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OM protein - protein search, using sw model

Run on: April 19, 2004, 17:13:16 ; Search time 7.93548 Seconds  
(without alignments)  
39.034 Million cell updates/sec

Title: US-10-726-692-14  
Perfect score: 28  
Sequence: 1 LKEKAK 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 50 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/prodata/2/iaa/5A COMB.pep:\*\*
- 2: /cgn2\_6/prodata/2/iaa/5B COMB.pep:\*\*
- 3: /cgn2\_6/prodata/2/iaa/6A COMB.pep:\*\*
- 4: /cgn2\_6/prodata/2/iaa/6B COMB.pep:\*\*
- 5: /cgn2\_6/prodata/2/iaa/PTUS COMB.pep:\*\*
- 6: /cgn2\_6/prodata/2/iaa/backfiles1.pep:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	100.0	171	4	US-09-540-236-2189
2	28	100.0	174	2	US-08-933-750C-27
3	28	100.0	174	3	US-09-234-613-27
4	28	100.0	322	4	US-09-634-955B-11
5	28	100.0	322	4	US-09-816-760-11
6	28	100.0	322	4	US-09-838-561-11
7	28	100.0	590	4	US-09-594-506-41
8	28	100.0	1044	4	US-09-107-532A-5229
9	28	100.0	1525	4	US-09-418-710-69
10	28	100.0	1527	4	US-09-418-710-27
11	28	100.0	1531	4	US-09-418-710-29
12	26	92.9	80	1	US-08-233-597-4
13	26	92.9	366	1	US-08-481-377-6
14	26	92.9	366	3	US-08-827-336-9
15	26	92.9	366	3	US-09-153-733A-6
16	26	92.9	366	4	US-09-389-705-6
17	26	92.9	366	4	US-09-357-905-9
18	26	92.9	366	4	US-09-787-351B-12
19	26	92.9	366	5	PCT-US94-00666-6
20	26	92.9	578	4	US-09-740-041-4
21	26	92.9	1086	4	US-09-543-681A-7696
22	26	92.9	3898	2	US-08-876-991-2
23	26	92.9	3898	2	US-09-059-853-2
24	26	92.9	3898	3	US-08-750-717-2
25	25	89.3	175	4	US-09-134-001C-4931
26	25	89.3	185	1	US-07-741-940-6
27	25	89.3	185	1	US-08-289-548A-6

28	25	89.3	185	1	US-08-452-654-6	Sequence 6, Appli
29	25	89.3	185	1	US-08-452-655B-6	Sequence 6, Appli
30	25	89.3	185	3	US-08-450-582-6	Sequence 6, Appli
31	25	89.3	185	4	US-08-449-731-6	Sequence 6, Appli
32	25	89.3	210	4	US-09-134-001C-3446	Sequence 3446, Ap
33	25	89.3	288	2	US-08-961-858-6	Sequence 6, Appli
34	25	89.3	288	3	US-09-089-593-6	Sequence 6, Appli
35	25	89.3	288	3	US-08-950-925-4	Sequence 4, Appli
36	25	89.3	288	4	US-09-368-819A-7	Sequence 7, Appli
37	25	89.3	288	4	US-09-565-286-4	Sequence 4, Appli
38	25	89.3	339	3	US-09-002-298-8	Sequence 8, Appli
39	25	89.3	339	4	US-09-481-277-8	Sequence 8, Appli
40	25	89.3	394	1	US-07-637-870-1	Sequence 1, Appli
41	25	89.3	394	1	US-07-637-870-2	Sequence 2, Appli
42	25	89.3	394	1	US-07-637-399-1	Sequence 1, Appli
43	25	89.3	394	1	US-07-637-399-2	Sequence 2, Appli
44	25	89.3	394	1	US-07-640-476-5	Sequence 5, Appli
45	25	89.3	394	1	US-07-640-476-8	Sequence 8, Appli
46	25	89.3	394	1	US-08-112-703-1	Sequence 1, Appli
47	25	89.3	394	1	US-08-112-703-2	Sequence 2, Appli
48	25	89.3	458	4	US-09-612-402B-36	Sequence 36, Appl
49	25	89.3	505	4	US-09-612-402B-17	Sequence 17, Appl
50	25	89.3	519	4	US-09-489-039A-11591	Sequence 11591, A

#### ALIGNMENTS

RESULT 1  
US-09-540-236-2189  
; Sequence 2189, Application US/09540236  
; Patent No. 6673910  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATENA  
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.2005-001  
; CURRENT APPLICATION NUMBER: US/09/540,236  
; CURRENT FILING DATE: 2000-04-04  
; NUMBER OF SEQ ID NOS: 3840  
; SEQ ID NO 2189  
; LENGTH: 171  
; TYPE: PRT  
; ORGANISM: M.catarrhalis  
US-09-540-236-2189

Query Match 100.0%; Score 28; DB 4; Length 171;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LKEKAK 6  
DB 38 LKEKAK 43

RESULT 2  
US-08-933-750C-27  
; Sequence 27, Application US/08933750C  
; Patent No. 5932442  
; GENERAL INFORMATION:  
; APPLICANT: Lal, Preeti  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Bandman, Olga  
; APPLICANT: Shah, Purvi  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Yue, Henry  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Corley, Neil C.  
; TITLE OF INVENTION: HUMAN REGULATORY MOLECULES  
; NUMBER OF SEQUENCES: 98  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive

;  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/933,750C  
; FILING DATE: September 23, 1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0356 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 174 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: LNODNOT03  
; CLONE: 1574624  
; US-08-933-750C-27

Query Match 100.0%; Score 28; DB 2; Length 174;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
Db 28 LKEKAK 33

RESULT 3  
US-09-234-613-27  
; Sequence 27, Application US/09234613  
; Patent No. 6132973  
; GENERAL INFORMATION:  
; APPLICANT: Lal, Preeti  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Bandman, Olga  
; APPLICANT: Shah, Purvi  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Yue, Henry  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Corey, Neil C.  
; TITLE OF INVENTION: HUMAN REGULATORY MOLECULES  
; NUMBER OF SEQUENCES: 98  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/234,613

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; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/933,750  
; FILING DATE: September 23, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0356 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 174 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: LNODNOT03  
; CLONE: 1574624  
; US-09-234-613-27

Query Match 100.0%; Score 28; DB 3; Length 174;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
Db 28 LKEKAK 33

RESULT 4  
US-09-634-955B-11  
; Sequence 11, Application US/09634955B  
; Patent No. 6511834  
; GENERAL INFORMATION:  
; APPLICANT: Meyers, Rachel  
; APPLICANT: Cook, William James  
; TITLE OF INVENTION: 32142, 21481, 25964, 21686, NOVEL HUMAN DEHYDROGENASE  
; FILE REFERENCE: MNI-134  
; CURRENT APPLICATION NUMBER: US/09/634,955B  
; CURRENT FILING DATE: 2000-08-08  
; PRIOR APPLICATION NUMBER: 60/192,002  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: FastSeq for Windows Version 4.  
; SEQ ID NO 11  
; LENGTH: 322  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-634-955B-11

Query Match 100.0%; Score 28; DB 4; Length 322;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
Db 316 LKEKAK 321

RESULT 5  
US-09-816-760-11  
; Sequence 11, Application US/09816760  
; Patent No. 6613555  
; GENERAL INFORMATION:  
; APPLICANT: Meyers, Rachel  
; APPLICANT: Cook, William James  
; APPLICANT: Williamson, Mark  
; APPLICANT: Rudolph-Owen, Laura A.





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Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
Db 194 LKEKAK 199

RESULT 9
US-09-418-710-69
; Sequence 69, Application US/09418710
; Patent No. 6596482
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-042001
; CURRENT APPLICATION NUMBER: US/09/418,710
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01783
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JP 9/310027
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: JP 9/116570
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69
; LENGTH: 1525
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-418-710-69

Query Match 100.0%; Score 28; DB 4; Length 1525;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
Db 558 LKEKAK 563

RESULT 10
US-09-418-710-27
; Sequence 27, Application US/09418710
; Patent No. 6596482
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-042001
; CURRENT APPLICATION NUMBER: US/09/418,710
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01783
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JP 9/310027
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: JP 9/116570
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 1527
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-418-710-27

Query Match 100.0%; Score 28; DB 4; Length 1527;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
Db 558 LKEKAK 563

RESULT 11
US-09-418-710-29
; Sequence 29, Application US/09418710
; Patent No. 6596482
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-042001
; CURRENT APPLICATION NUMBER: US/09/418,710
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01783
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JP 9/310027
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: JP 9/116570
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 1531
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-418-710-29

Query Match 100.0%; Score 28; DB 4; Length 1531;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
Db 558 LKEKAK 563

RESULT 12
US-08-233-597-4
; Sequence 4, Application US/08233597
; Patent No. 5763271
; GENERAL INFORMATION:
; APPLICANT: Lerner, Ethan A.
; APPLICANT: Remold, Heinz G.
; APPLICANT: Ribeiro, Jose M.C.
; APPLICANT: Titus, Richard G.
; APPLICANT: Shoemaker, Charles B.
; TITLE OF INVENTION: VASODILATORY AND IMMUNE SUPPRESSANT
; TITLE OF INVENTION: PEPTIDES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/233,597
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 778,159
; FILING DATE: 26-DEC-1991
; APPLICATION NUMBER: US 374,080
; FILING DATE: 29-JUN-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: HUI-003CP2
; TELECOMMUNICATION INFORMATION:
```

TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 80 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-233-597-4

Query Match 92.9%; Score 26; DB 1; Length 80;  
Best Local Similarity 83.3%; Pred. No. 1.8e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LXEKAK 6  
DB 69 MKEKAK 74

RESULT 13  
US-08-481-377-6  
Sequence 6, Application US/08481377  
Patent No. 5808007  
GENERAL INFORMATION:  
APPLICANT: JOHNS HOPKINS UNIVERSITY  
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ  
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR  
CITY: LOS ANGELES  
STATE: CALIFORNIA  
COUNTRY: US  
ZIP: 90067  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/481,377  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/00666  
FILING DATE: 12-JAN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: WETHERELL, JR. Ph.D., JOHN R.  
REGISTRATION NUMBER: 31,678  
REFERENCE/DOCKET NUMBER: FD2279 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 366 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-481-377-6

Query Match 92.9%; Score 26; DB 1; Length 366;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LXEKAK 6  
DB 117 IREKAK 122

RESULT 14  
US-08-827-336-9  
Sequence 9, Application US/08827336

Patent No. 6004780  
GENERAL INFORMATION:  
APPLICANT: SOPPET, DANIEL  
TITLE OF INVENTION: GROWTH FACTOR HTTTR36  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
STREET: 9410 KEY WEST AVENUE  
CITY: ROCKVILLE  
STATE: MARYLAND  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/827,336  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BROOKES, ANDY, A.  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PF230  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-309-8504  
TELEFAX: 301-309-8512  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 366 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-827-336-9

Query Match 92.9%; Score 26; DB 3; Length 366;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LXEKAK 6  
DB 117 IREKAK 122

RESULT 15  
US-09-153-733A-6  
Sequence 6, Application US/09153733A  
Patent No. 6025475  
GENERAL INFORMATION:  
APPLICANT: JOHNS HOPKINS UNIVERSITY  
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ  
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR  
CITY: LOS ANGELES  
STATE: CALIFORNIA  
COUNTRY: US  
ZIP: 90067  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/153,733A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/481,377  
FILING DATE:

ATTORNEY/AGENT INFORMATION:  
NAME: WETHERELL, JR. Ph.D., JOHN R.  
REGISTRATION NUMBER: 31,678  
REFERENCE/DOCKET NUMBER: FD2279 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 366 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-153-733A-6

Query Match 92.9%; Score 26; DB 3; Length 366;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
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Db 117 IKEKAK 122

RESULT 16  
US-09-389-705-6  
Sequence 6, Application US/09389705  
Patent No. 6391565  
GENERAL INFORMATION:  
APPLICANT: JOHNS HOPKINS UNIVERSITY  
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ  
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR  
CITY: LOS ANGELES  
STATE: CALIFORNIA  
COUNTRY: US  
ZIP: 90067  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/389,705  
FILING DATE: 03-Sep-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION NUMBER: 09/153,733  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: WETHERELL, JR. Ph.D., JOHN R.  
REGISTRATION NUMBER: 31,678  
REFERENCE/DOCKET NUMBER: FD2279 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 366 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-389-705-6

Query Match 92.9%; Score 26; DB 4; Length 366;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
:|||||

Db 117 IKEKAK 122  
RESULT 17  
US-09-357-905-9  
Sequence 9, Application US/09357905  
Patent No. 6413933  
GENERAL INFORMATION:  
APPLICANT: SOPPET, DANIEL  
TITLE OF INVENTION: GROWTH FACTOR HYTER36  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
STREET: 9410 KEY WEST AVENUE  
CITY: ROCKVILLE  
STATE: MARYLAND  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/357,905  
FILING DATE: 21-Jul-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/827,336  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: BROOKES, ANDY, A.  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PF230  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-309-8504  
TELEFAX: 301-309-8512  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 366 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
US-09-357-905-9

Query Match 92.9%; Score 26; DB 4; Length 366;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
:|||||  
Db 117 IKEKAK 122

RESULT 18  
US-09-787-351B-12  
Sequence 12, Application US/09787351B  
Patent No. 6656708  
GENERAL INFORMATION:  
APPLICANT: Yu, Long  
APPLICANT: Zhang, Honglai  
APPLICANT: Fu, Qiang  
APPLICANT: Dai, Fangyan  
APPLICANT: Zhao, Shouyuan  
TITLE OF INVENTION: NEW HUMAN GROWTH DIFFERENTIATION FACTOR ENCODING SEQUENCE AND  
POLYPEPTIDE ENCODED BY SUCH DNA SEQUENCE AND PRODUCING METHOD  
TITLE OF INVENTION: THEREOF  
FILE REFERENCE: 9548.49USWO  
CURRENT APPLICATION NUMBER: US/09/787,351B  
CURRENT FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: PCT/CN99/00138

; PRIOR FILING DATE: 1999-09-06  
; PRIOR APPLICATION NUMBER: CN 98119759.0  
; PRIOR FILING DATE: 1998-09-22  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 12  
; LENGTH: 366  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-787-351B-12

Query Match 92.9%; Score 26; DB 4; Length 366;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
:|||||  
Db 117 IKEKAK 122

RESULT 19  
PCT-US94-00666-6  
; Sequence 6, Application PC/TUS9400666  
; GENERAL INFORMATION:  
; APPLICANT: JOHNS HOPKINS UNIVERSITY  
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SPENSLY HORN JURAS & LUBITZ  
; STREET: 1890 CENTURY PARK EAST, FIFTH FLOOR  
; CITY: LOS ANGELES  
; STATE: CALIFORNIA  
; COUNTRY: US  
; ZIP: 90067  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/00666  
; FILING DATE: 12-JAN-1994  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WETHERELL, JR. Ph.D., JOHN R.  
; REGISTRATION NUMBER: 31,678  
; REFERENCE/DOCKET NUMBER: PD2279 PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 455-5100  
; TELEFAX: (619) 455-5110  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 366 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US94-00666-6

Query Match 92.9%; Score 26; DB 5; Length 366;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
:|||||  
Db 117 IKEKAK 122

RESULT 20  
US-09-740-041-4  
; Sequence 4, Application US/09740041  
; Patent No. 6562593  
; GENERAL INFORMATION:  
; APPLICANT: MERKULOV, Karl et al

; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: AND USES THEREOF  
; FILE REFERENCE: CL001001  
; CURRENT APPLICATION NUMBER: US/09/740,041  
; CURRENT FILING DATE: 2000-12-20  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 578  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-09-740-041-4

Query Match 92.9%; Score 26; DB 4; Length 578;  
Best Local Similarity 83.3%; Pred. No. 1.1e+03;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
:|||||  
Db 110 IKEKAK 115

RESULT 21  
US-09-543-681A-7696  
; Sequence 7696, Application US/09543681A  
; Patent No. 6605709  
; GENERAL INFORMATION:  
; APPLICANT: GARY BRETON  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.1002-001  
; CURRENT APPLICATION NUMBER: US/09/543,681A  
; CURRENT FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/128,706  
; PRIOR FILING DATE: 1999-04-09  
; NUMBER OF SEQ ID NOS: 8344  
; SEQ ID NO 7696  
; LENGTH: 1086  
; TYPE: PRT  
; ORGANISM: Proteus mirabilis  
US-09-543-681A-7696

Query Match 92.9%; Score 26; DB 4; Length 1086;  
Best Local Similarity 83.3%; Pred. No. 1.9e+03;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
:|||||  
Db 767 IKEKAK 772

RESULT 22  
US-08-876-991-2  
; Sequence 2, Application US/08876991  
; Patent No. 5925360  
; GENERAL INFORMATION:  
; APPLICANT: Gregor Meyers, Tillmann R menapf,  
; APPLICANT: Heinz-J rgen Thiel  
; TITLE OF INVENTION: Hog cholera virus vaccine and diagnostic  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Organon Teknika Corporation  
; ADDRESSEE: Biotechnology Research Institute  
; STREET: 1330-A Piccard Drive  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: U.S.A.  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/876,991
; FILING DATE: 16-JUN-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/747,577
; FILING DATE:
; APPLICATION NUMBER: US/08/650,584
; FILING DATE:
; APPLICATION NUMBER: US/08/469,702
; FILING DATE:
; APPLICATION NUMBER: US/08/123,596
; FILING DATE:
; APPLICATION NUMBER: 07/797,554
; FILING DATE: 22-NOV-1991
; APPLICATION NUMBER: US 07/494,991
; FILING DATE: 16-MAR-1990
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: William M. Blackstone
; REGISTRATION NUMBER: 29,772
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 258-5200
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3898 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-876-991-2

Query Match          92.9%; Score 26; DB 2; Length 3898;
Best Local Similarity 83.3%; Pred. No. 6.2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LKEKAK 6
Db      3152 IKEKAK 3157

RESULT 23
US-09-059-853-2
; Sequence 2, Application US/09059853
; Patent No. 5935582
; GENERAL INFORMATION:
; APPLICANT: Gregor Meyers, Tillmann R menapf,
; APPLICANT: Heinz-J tgen Thiel
; TITLE OF INVENTION: Hog cholera virus vaccine and diagnostic
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Organon Teknika Corporation
; ADDRESSEE: Biotechnology Research Institute
; STREET: 1330-A Piccard Drive
; CITY: Rockville
; STATE: Maryland
; COUNTRY: U.S.A.
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/059,853
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/797,554
; FILING DATE: 22-NOV-1991
; APPLICATION NUMBER: US 07/494,991
; FILING DATE: 16-MAR-1990
```

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; ATTORNEY/AGENT INFORMATION:
; NAME: William M. Blackstone
; REGISTRATION NUMBER: 29,772
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 258-5200
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3898 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-059-853-2

Query Match          92.9%; Score 26; DB 2; Length 3898;
Best Local Similarity 83.3%; Pred. No. 6.2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LKEKAK 6
Db      3152 IKEKAK 3157

RESULT 24
US-08-750-717-2
; Sequence 2, Application US/08750717
; Patent No. 6180109
; GENERAL INFORMATION:
; APPLICANT: MOORMANN, Robertus J. M.
; APPLICANT: VAN RIJN, Petrus A.
; TITLE OF INVENTION: Nucleotide Sequences of Pestivirus
; TITLE OF INVENTION: Strains, Polypeptides Encoded by These Sequences and Use
; TITLE OF INVENTION: Thereof for Diagnosis and Prevention of Pestivirus
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/750,717
; FILING DATE: 24-DEC-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94201743.5
; FILING DATE: 17-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/NL95/00214
; FILING DATE: 16-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: BO 39123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-521-2297
; TELEFAX: 703-685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3898 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-750-717-2
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Query Match      92.3%; Score 26; DB 3; Length 3898;
Best Local Similarity 83.3%; Pred. No. 6.2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LKEKAK 6
DB      3152 IKEKAK 3157

RESULT 25
US-09-134-001C-4931
; Sequence 4931, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4931
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4931

Query Match      89.3%; Score 25; DB 4; Length 175;
Best Local Similarity 83.3%; Pred. No. 5.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LKEKAK 6
DB      150 VKEKAK 155

RESULT 26
US-07-741-940-6
; Sequence 6, Application US/07741940
; Patent No. 5352775
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, HANS
; APPLICANT: ANAND, RAKESH
; APPLICANT: CARLSON, MARY
; APPLICANT: GRODEN, JOANNA
; APPLICANT: HEDGE, PHILIP J.
; APPLICANT: JOSLYN, GEOFF
; APPLICANT: KINZLER, KENNETH
; APPLICANT: MARKHAM, ALEXANDER P.
; APPLICANT: NAKAMURA, YUSUKE
; APPLICANT: THLIVERIS, ANDREW
; TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
; TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4598
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/741,940
; FILING DATE: 19920109
```

```
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 1107.035574
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: YS-39 (TB2)
US-07-741-940-6

Query Match      89.3%; Score 25; DB 1; Length 185;
Best Local Similarity 83.3%; Pred. No. 6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LKEKAK 6
DB      155 LKDKAK 160

RESULT 27
US-08-289-548A-6
; Sequence 6, Application US/08289548A
; Patent No. 5648212
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, HANS
; APPLICANT: ANAND, RAKESH
; APPLICANT: CARLSON, MARY
; APPLICANT: GRODEN, JOANNA
; APPLICANT: HEDGE, PHILIP J.
; APPLICANT: JOSLYN, GEOFF
; APPLICANT: KINZLER, KENNETH
; APPLICANT: MARKHAM, ALEXANDER P.
; APPLICANT: NAKAMURA, YUSUKE
; APPLICANT: THLIVERIS, ANDREW
; TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
; TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, LTD
; STREET: 1001 G Street, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4598
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/289,548A
; FILING DATE: 12-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 1107.46943
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
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/ LENGTH: 185 amino acids  
/ TYPE: amino acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: protein  
/ ORIGINAL SOURCE:  
/ ORGANISM: Homo sapiens  
/ IMMEDIATE SOURCE:  
/ CLONE: YS-39(TB2)  
US-08-289-548A-6

Query Match 89.3%; Score 25; DB 1; Length 185;  
Best Local Similarity 83.3%; Pred. No. 6e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
DB 155 LKDKAK 160

RESULT 28  
US-08-452-654-6

/ Sequence 6, Application US/08452654  
/ Patent No. 5691454  
/ GENERAL INFORMATION:  
/ APPLICANT: ALBERTSEN, HANS  
/ APPLICANT: ANAND, RAKESH  
/ APPLICANT: CARLSON, MARY  
/ APPLICANT: GRODEN, JOANNA  
/ APPLICANT: HEDGE, PHILIP J.  
/ APPLICANT: JOSLYN, GEOFF  
/ APPLICANT: KINZLER, KENNETH  
/ APPLICANT: MARKHAM, ALEXANDER P.  
/ APPLICANT: NAKAMURA, YUSUKE  
/ APPLICANT: THLIVERIS, ANDREW  
/ TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC  
/ NUMBER OF SEQUENCES: 94  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Banner, Birch, McKie & Beckett  
/ STREET: 1001 G Street, NW  
/ CITY: Washington  
/ STATE: D.C.  
/ COUNTRY: USA  
/ ZIP: 20001-4598  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: Patent In Release #1.0, Version #1.25  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/452,654  
/ FILING DATE: 25-MAY-1995  
/ CLASSIFICATION: 536  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US 07/741,940  
/ FILING DATE: 08-AUG-1991  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Kagan, Sarah A.  
/ REGISTRATION NUMBER: 32,141  
/ REFERENCE/DOCKET NUMBER: 1107.035574  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: 202-508-9100  
/ TELEFAX: 202-508-9299  
/ INFORMATION FOR SEQ ID NO: 6:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 185 amino acids  
/ TYPE: amino acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: protein  
/ ORIGINAL SOURCE:  
/ ORGANISM: Homo sapiens

/ IMMEDIATE SOURCE:  
/ CLONE: YS-39(TB2)  
US-08-452-654-6

Query Match 89.3%; Score 25; DB 1; Length 185;  
Best Local Similarity 83.3%; Pred. No. 6e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
DB 155 LKDKAK 160

RESULT 29  
US-08-452-655B-6

/ Sequence 6, Application US/08452655B  
/ Patent No. 5783666  
/ GENERAL INFORMATION:  
/ APPLICANT: ALBERTSEN, HANS  
/ APPLICANT: ANAND, RAKESH  
/ APPLICANT: CARLSON, MARY  
/ APPLICANT: GRODEN, JOANNA  
/ APPLICANT: HEDGE, PHILIP J.  
/ APPLICANT: JOSLYN, GEOFF  
/ APPLICANT: KINZLER, KENNETH  
/ APPLICANT: MARKHAM, ALEXANDER P.  
/ APPLICANT: NAKAMURA, YUSUKE  
/ APPLICANT: THLIVERIS, ANDREW  
/ TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC  
/ NUMBER OF SEQUENCES: 102  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Banner & Witcoff, Ltd.  
/ STREET: 1001 G Street, NW  
/ CITY: Washington  
/ STATE: D.C.  
/ COUNTRY: USA  
/ ZIP: 20001-4598  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: Patent In Release #1.0, Version #1.25  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/452,655B  
/ FILING DATE: 25-MAY-1995  
/ CLASSIFICATION: 530  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US 08/289,548  
/ FILING DATE: 12-AUG-1994  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US 07/741,940  
/ FILING DATE: 08-AUG-1991  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Kagan, Sarah A.  
/ REGISTRATION NUMBER: 32,141  
/ REFERENCE/DOCKET NUMBER: 1107.49964  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: 202-508-9100  
/ TELEFAX: 202-508-9299  
/ INFORMATION FOR SEQ ID NO: 6:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 185 amino acids  
/ TYPE: amino acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: protein  
/ ORIGINAL SOURCE:  
/ ORGANISM: Homo sapiens  
/ IMMEDIATE SOURCE:  
/ CLONE: YS-39(TB2)  
US-08-452-655B-6



Query Match 89.3%; Score 25; DB 1; Length 185;  
Best Local Similarity 83.3%; Pred. No. 6e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LXEKAK 6  
DB 155 LKDKAK 160

RESULT 30  
US-08-450-582-6  
; Sequence 6, Application US/08450582  
; Patent No. 6114124  
; GENERAL INFORMATION:  
; APPLICANT: ALBERTSEN, HANS  
; APPLICANT: ANAND, RAKESH  
; APPLICANT: CARLSON, MARY  
; APPLICANT: GRODEN, JOANNA  
; APPLICANT: HEDGE, PHILIP J.  
; APPLICANT: JOSLYN, GEOFF  
; APPLICANT: KINZLER, KENNETH  
; APPLICANT: MARKHAM, ALEXANDER F.  
; APPLICANT: NAKAMURA, YUSUKE  
; APPLICANT: THLIVERIS, ANDREW  
; TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC  
; NUMBER OF SEQUENCES: 102  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Banner & Witcoff, Ltd.  
; STREET: 1001 G Street, NW  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20001-4598  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/450,582  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/452,655  
; FILING DATE: 25-MAY-1995  
; APPLICATION NUMBER: US 08/289,548  
; FILING DATE: 12-AUG-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/741,940  
; FILING DATE: 08-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kagan, Sarah A.  
; REGISTRATION NUMBER: 32,141  
; REFERENCE/DOCKET NUMBER: 1107.49964  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-508-9100  
; TELEFAX: 202-508-9299  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 185 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; IMMEDIATE SOURCE:  
; CLONE: YS-39(TB2)

US-08-450-582-6

Query Match 89.3%; Score 25; DB 3; Length 185;  
Best Local Similarity 83.3%; Pred. No. 6e+02;

Matches 5; Conservative 0; Gaps 0;

QY 1 LXEKAK 6  
DB 155 LKDKAK 160

RESULT 31  
US-08-449-731-6  
; Sequence 6, Application US/08449731  
; Patent No. 6413727  
; GENERAL INFORMATION:  
; APPLICANT: ALBERTSEN, HANS  
; APPLICANT: ANAND, RAKESH  
; APPLICANT: CARLSON, MARY  
; APPLICANT: GRODEN, JOANNA  
; APPLICANT: HEDGE, PHILIP J.  
; APPLICANT: JOSLYN, GEOFF  
; APPLICANT: KINZLER, KENNETH  
; APPLICANT: MARKHAM, ALEXANDER F.  
; APPLICANT: NAKAMURA, YUSUKE  
; APPLICANT: THLIVERIS, ANDREW  
; TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC  
; NUMBER OF SEQUENCES: 102  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Banner & Allegretti, LTD  
; STREET: 1001 G Street, NW  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20001-4598  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/449,731  
; FILING DATE: 25-MAY-1995  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/289,548  
; FILING DATE: 12-AUG-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kagan, Sarah A.  
; REGISTRATION NUMBER: 32,141  
; REFERENCE/DOCKET NUMBER: 1107.46943  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-508-9100  
; TELEFAX: 202-508-9299  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 185 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; IMMEDIATE SOURCE:  
; CLONE: YS-39(TB2)  
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-08-449-731-6  
Query Match 89.3%; Score 25; DB 4; Length 185;  
Best Local Similarity 83.3%; Pred. No. 6e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LXEKAK 6  
DB 155 LKDKAK 160

RESULT 32  
US-09-134-001C-3446  
; Sequence 3446, Application US/09134001C  
; Patent No. 6380370  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134,001C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 3446  
; LENGTH: 210  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-3446

Query Match 89.3%; Score 25; DB 4; Length 210;  
Best Local Similarity 83.3%; Pred. No. 6.7e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
|:||||  
Db 42 LREKAK 47

RESULT 33  
US-08-961-858-6  
; Sequence 6, Application US/08961858  
; Patent No. 5834210  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Shigui  
; APPLICANT: Shi, Qinwei  
; TITLE OF INVENTION: STABLE TROPONIN SUBUNITS AND COMPLEXES  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klauber & Jackson  
; STREET: 411 Hackensack Avenue, 4th Floor  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/961,858  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 1112-1-044 CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-487-5800  
; TELEFAX: 201-343-1684  
; TELEX: 133521  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 288 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO

US-08-961-858-6

Query Match 89.3%; Score 25; DB 2; Length 288;  
Best Local Similarity 83.3%; Pred. No. 9e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
|:||||  
Db 229 LREKAK 234

RESULT 34  
US-09-089-593-6  
; Sequence 6, Application US/09089593  
; Patent No. 6060278  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Shigui  
; APPLICANT: Shi, Qinwei  
; TITLE OF INVENTION: STABLE TROPONIN SUBUNITS AND COMPLEXES  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klauber & Jackson  
; STREET: 411 Hackensack Avenue, 4th Floor  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/089,593  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/961,858  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 1112-1-044 CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-487-5800  
; TELEFAX: 201-343-1684  
; TELEX: 133521  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 288 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
US-09-089-593-6

Query Match 89.3%; Score 25; DB 3; Length 288;  
Best Local Similarity 83.3%; Pred. No. 9e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
|:||||  
Db 229 LREKAK 234

RESULT 35  
US-08-950-925-4  
; Sequence 4, Application US/08950925  
; Patent No. 6072040  
; GENERAL INFORMATION:  
; APPLICANT: Dave, Kirti I.  
; APPLICANT: Botyanszki, Janos

APPLICANT: Sintar, Eva  
TITLE OF INVENTION: Stabilized Conjugates of Uncomplexed  
SUBUNITS OF MULTIMERIC PROTEINS  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 PAGE MILL ROAD  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/950,925  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Axford, Laurie A  
REGISTRATION NUMBER: 35,053  
REFERENCE/DOCKET NUMBER: 32260-20004.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-813-5600  
TELEFAX: 650-494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 288 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-950-925-4

Query Match 89.3%; Score 25; DB 3; Length 288;  
Best Local Similarity 83.3%; Pred. No. 9e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
DB 229 LREKAK 234

RESULT 36  
US-09-368-819A-7  
Sequence 7, Application US/09368819A  
Patent No. 6475785  
GENERAL INFORMATION:  
APPLICANT: Shi, Qinwei  
APPLICANT: Ling, Mingfu  
APPLICANT: Liu, Shiqui  
TITLE OF INVENTION: SINGLE-CHAIN POLYPEPTIDES COMPRISING TROPONIN I  
TITLE OF INVENTION: N-TERMINAL FRAGMENTS AND TROPONIN C  
FILE REFERENCE: 1112-1-071  
CURRENT APPLICATION NUMBER: US/09/368,819A  
CURRENT FILING DATE: 1999-08-05  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 7  
LENGTH: 288  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-368-819A-7

Query Match 89.3%; Score 25; DB 4; Length 288;  
Best Local Similarity 83.3%; Pred. No. 9e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LKEKAK 6  
DB 229 LREKAK 234  
RESULT 37  
US-09-565-286-4  
Sequence 4, Application US/09565286  
Patent No. 6491923  
GENERAL INFORMATION:  
APPLICANT: Dave, Kirti I.  
APPLICANT: Botyanszki, Janos  
APPLICANT: Sintar, Eva  
TITLE OF INVENTION: STABILIZED CONJUGATES OF UNCOMPLEXED  
SUBUNITS OF MULTIMERIC PROTEINS  
FILE REFERENCE: 35574-22004.10  
CURRENT APPLICATION NUMBER: US/09/565,286  
CURRENT FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 08/950,925  
PRIOR FILING DATE: 1997-10-15  
PRIOR APPLICATION NUMBER: 08/730,111  
PRIOR FILING DATE: 1996-10-15  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 4  
LENGTH: 288  
TYPE: PRT  
ORGANISM: homo sapien  
US-09-565-286-4

Query Match 89.3%; Score 25; DB 4; Length 288;  
Best Local Similarity 83.3%; Pred. No. 9e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
DB 229 LREKAK 234

RESULT 38  
US-09-002-298-8  
Sequence 8, Application US/09002298  
Patent No. 6046001  
GENERAL INFORMATION:  
APPLICANT: Bandman, Olga  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Guegler, Karl J.  
APPLICANT: Corley, Neil C.  
APPLICANT: Tang, Y. Tom  
APPLICANT: Shah, Purvi  
TITLE OF INVENTION: HUMAN FATTY ACID BETA-OXIDATION ENZYMES  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Dr.  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/002,298  
FILING DATE: Filed Herewith  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:

```
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0453 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 780241
;
US-09-002-298-8
Query Match 89.3%; Score 25; DB 3; Length 339;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
Db 143 LKERAK 148

RESULT 39
US-09-481-277-8
; Sequence 8, Application US/09481277
; Patent No. 6511833
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; Hillman, Jennifer L.
; Guegler, Karl J.
; Corley, Neil C.
; Tang, Y. Tom
; Shah, Purvi
;
TITLE OF INVENTION: HUMAN FATTY ACID BETA-OXIDATION ENZYMES
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSES: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
;
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/481,277
FILING DATE: 11-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/002,298
FILING DATE: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0453 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
;
INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 780241
```

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; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-481-277-8
Query Match 89.3%; Score 25; DB 4; Length 339;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
Db 143 LKERAK 148

RESULT 40
US-07-637-870-1
; Sequence 1, Application US/07637870
; Patent No. 5310685
; GENERAL INFORMATION:
; APPLICANT: Lambier, Anne-Marie
; APPLICANT: Lasters, Ignace
; APPLICANT: Quax, Wilhemus J.
; APPLICANT: Van Der Laan, Jan M.
;
TITLE OF INVENTION: NOVEL GLUCOSE ISOMERASES HAVING
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSES: Morrison & Foerster
STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: California
COUNTRY: USA
ZIP: 94025
;
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/637,870
FILING DATE: 19910104
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 24615-20019.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFAX: 415-327-2951
TELEX: 706141
;
INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 394 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-07-637-870-1
Query Match 89.3%; Score 25; DB 1; Length 394;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
Db 318 LKERAK 323

RESULT 41
US-07-637-870-2
; Sequence 2, Application US/07637870
; Patent No. 5310685
; GENERAL INFORMATION:
; APPLICANT: Lambier, Anne-Marie
; APPLICANT: Lasters, Ignace
; APPLICANT: Quax, Wilhemus J.
```



Query Match 89.3%; Score 25; DB 1; Length 394;  
Best Local Similarity 83.3%; Pred. No. 1.2e+03;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
|||:|  
Db 318 LKERAK 323

RESULT 44  
US-07-640-476-5  
; Sequence 5, Application US/07640476  
; Patent No. 5376536  
; GENERAL INFORMATION:  
; APPLICANT: QUAX, WILHELMUS  
; APPLICANT: LUITEN, RUDOLF G.M.  
; APPLICANT: SCHUURHUIZEN, PAUL W.  
; APPLICANT: MRABET, NADIR  
; TITLE OF INVENTION: NOVEL GLUCOSE ISOMERASE ENZYMES AND  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morrison & Foerster  
; STREET: 545 Middlefield Road, Suite 200  
; CITY: Menlo Park  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94025  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; SOFTWARE:  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/640,476  
; FILING DATE: 19910110  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kate H. Murashige  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 24615-20009.20  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 327-7250  
; TELEFAX: (415) 327-2951  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 394 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-640-476-5

Query Match 89.3%; Score 25; DB 1; Length 394;  
Best Local Similarity 83.3%; Pred. No. 1.2e+03;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
|||:|  
Db 318 LKERAK 323

RESULT 45  
US-07-640-476-8  
; Sequence 8, Application US/07640476  
; Patent No. 5376536  
; GENERAL INFORMATION:  
; APPLICANT: QUAX, WILHELMUS  
; APPLICANT: LUITEN, RUDOLF G.M.  
; APPLICANT: SCHUURHUIZEN, PAUL W.  
; APPLICANT: MRABET, NADIR  
; TITLE OF INVENTION: NOVEL GLUCOSE ISOMERASE ENZYMES AND

; TITLE OF INVENTION: THEIR USE  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morrison & Foerster  
; STREET: 545 Middlefield Road, Suite 200  
; CITY: Menlo Park  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94025  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; SOFTWARE:  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/640,476  
; FILING DATE: 19910110  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kate H. Murashige  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 24615-20009.20  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 327-7250  
; TELEFAX: (415) 327-2951  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 394 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Ampullaxiella species  
; STRAIN: ATCC 31351  
; FEATURE:  
; NAME/KEY: Protein  
; LOCATION: 1..394  
; PUBLICATION INFORMATION:  
; AUTHORS: Saari, J  
; JOURNAL: J. Bacteriol.  
; VOLUME: 169  
; PAGES: 612-  
; DATE: 1987  
US-07-640-476-8

Query Match 89.3%; Score 25; DB 1; Length 394;  
Best Local Similarity 83.3%; Pred. No. 1.2e+03;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
|||:|  
Db 318 LKERAK 323

RESULT 46  
US-08-112-703-1  
; Sequence 1, Application US/08112703  
; Patent No. 5384257  
; GENERAL INFORMATION:  
; APPLICANT: Lambair, Anne-Marie  
; APPLICANT: Lasters, Ignace  
; APPLICANT: Mrabet, Nadir  
; APPLICANT: Quax, Wilhelms J.  
; APPLICANT: Van Der Laan, Jan M.  
; APPLICANT: Misset, Onno  
; TITLE OF INVENTION: NOVEL GLUCOSE ISOMERASES WITH AN  
; TITLE OF INVENTION: ALTERED PH OPTIMUM  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morrison & Foerster

STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/112,703  
FILING DATE: 26-AUG-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 4615002001  
TELEPHONE: 415-813-5600  
TELEFAX: 415-494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 394 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-112-703-1

Query Match 89.3%; Score 25; DB 1; Length 394;  
Best Local Similarity 83.3%; Pred. No. 1.2e+03;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
DB 318 LKERAK 323

RESULT 47  
US-08-112-703-2  
Sequence 2, Application US/08112703  
Patent No. 5384257  
GENERAL INFORMATION:  
APPLICANT: Lambert, Anne-Marie  
APPLICANT: Lasters, Ignace  
APPLICANT: Mrabet, Nadir  
APPLICANT: Quax, Wilhelmus J.  
APPLICANT: Van Der Laan, Jan M.  
APPLICANT: Misset, Onno  
TITLE OF INVENTION: NOVEL GLUCOSE ISOMERASES WITH AN  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/112,703  
FILING DATE: 26-AUG-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 4615002001

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-813-5600  
TELEFAX: 415-494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 394 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-112-703-2

Query Match 89.3%; Score 25; DB 1; Length 394;  
Best Local Similarity 83.3%; Pred. No. 1.2e+03;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
DB 318 LKERAK 323

RESULT 48  
US-09-612-402B-36  
Sequence 36, Application US/09612402B  
Patent No. 6642023  
GENERAL INFORMATION:  
APPLICANT: Jackson, W. James  
TITLE OF INVENTION: Chlamydia Protein, Gene Sequence and Uses Thereof  
Patent No. 6642023  
FILE REFERENCE: 7969-086-999  
CURRENT APPLICATION NUMBER: US/09/612,402B  
CURRENT FILING DATE: 2000-07-06  
PRIOR APPLICATION NUMBER: 08/942,596  
PRIOR FILING DATE: 1997-10-02  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: Patent In version 3.0  
SEQ ID NO 36  
LENGTH: 458  
TYPE: PRT  
ORGANISM: Chlamydia sp.  
US-09-612-402B-36

Query Match 89.3%; Score 25; DB 4; Length 458;  
Best Local Similarity 83.3%; Pred. No. 1.4e+03;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
DB 307 LREKAK 312

RESULT 49  
US-09-612-402B-17  
Sequence 17, Application US/09612402B  
Patent No. 6642023  
GENERAL INFORMATION:  
APPLICANT: Jackson, W. James  
TITLE OF INVENTION: Chlamydia Protein, Gene Sequence and Uses Thereof  
Patent No. 6642023  
FILE REFERENCE: 7969-086-999  
CURRENT APPLICATION NUMBER: US/09/612,402B  
CURRENT FILING DATE: 2000-07-06  
PRIOR APPLICATION NUMBER: 08/942,596  
PRIOR FILING DATE: 1997-10-02  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: Patent In version 3.0  
SEQ ID NO 17  
LENGTH: 505  
TYPE: PRT  
ORGANISM: Chlamydia sp.  
US-09-612-402B-17

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Query Match      89.3%; Score 25; DB 4; Length 505;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LKEKAK 6
      |:|||||
Db      495 LREKAK 500

RESULT 50
US-09-489-039A-11591
; Sequence 11591, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11591
; LENGTH: 519
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11591

Query Match      89.3%; Score 25; DB 4; Length 519;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LKEKAK 6
      |:|||||
Db      450 LKERAK 455

Search completed: April 19, 2004, 17:24:45
Job time : 8.93548 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 19, 2004, 17:11:35 ; Search time 17.8065 Seconds  
(without alignments)  
106.316 Million cell updates/sec

Title: US-10-726-692-14

Perfect score: 28

Sequence: 1 LKEKAK 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database :

SPTREMBL 25:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phase:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	44	5 Q818J9	Q818J9 drosophila
2	28	100.0	74	17 Q8ZUJ2	Q8ZUJ2 pyroaculum
3	28	100.0	78	4 Q8WWE9	Q8WWE9 homo sapien
4	28	100.0	112	13 Q9DG75	Q9DG75 oncorhynchu
5	28	100.0	148	16 Q9KEP6	Q9KEP6 bacillus ha
6	28	100.0	165	5 Q9V535	Q9V535 drosophila
7	28	100.0	165	5 Q8ZA6	Q8ZA6 drosophila
8	28	100.0	165	5 Q95X08	Q95X08 drosophila
9	28	100.0	172	13 Q8JUC5	Q8JUC5 oryzias lat
10	28	100.0	173	11 Q9D6U5	Q9D6U5 mus musculu
11	28	100.0	173	11 Q9CWZ3	Q9CWZ3 mus musculu
12	28	100.0	173	13 Q8JUC6	Q8JUC6 oryzias lat
13	28	100.0	174	13 Q9DF42	Q9DF42 xenopus lae
14	28	100.0	182	16 Q8EST1	Q8EST1 oceanobacil
15	28	100.0	185	2 Q9R8Q0	Q9R8Q0 borrelia ga
16	28	100.0	205	17 Q8TWK4	Q8TWK4 methanopyru

17	28	100.0	223	13 Q93376	Q93376 salmo salar
18	28	100.0	224	16 Q24983	Q24983 helicobacte
19	28	100.0	235	16 Q7U7M1	Q7U7M1 synechococ
20	28	100.0	236	16 Q9ZMP9	Q9ZMP9 helicobacte
21	28	100.0	241	17 Q58271	Q58271 pyrococcus
22	28	100.0	242	16 Q8EYN0	Q8EYN0 leptospira
23	28	100.0	246	11 Q9R2C8	Q9R2C8 rattus norv
24	28	100.0	254	16 Q9JUL7	Q9JUL7 neisseria m
25	28	100.0	270	16 Q8RGJ9	Q8RGJ9 fusbacteri
26	28	100.0	288	11 Q9CSP8	Q9CSP8 mus musculu
27	28	100.0	304	16 Q8R8P7	Q8R8P7 thermoanaer
28	28	100.0	326	10 Q39108	Q39108 arabidopsis
29	28	100.0	326	10 Q9SZM6	Q9SZM6 arabidopsis
30	28	100.0	326	10 Q9FPK0	Q9FPK0 arabidopsis
31	28	100.0	338	16 Q06452	Q06452 streptococ
32	28	100.0	343	13 Q818H9	Q818H9 xenopus lae
33	28	100.0	365	16 Q81F64	Q81F64 bacillus ce
34	28	100.0	367	16 Q93M86	Q93M86 clostridium
35	28	100.0	367	17 Q9VOV9	Q9VOV9 pyrococcus
36	28	100.0	372	16 Q8YS20	Q8YS20 anabaena sp
37	28	100.0	373	11 Q8BJQ6	Q8BJQ6 mus musculu
38	28	100.0	374	16 Q9JSV1	Q9JSV1 neisseria m
39	28	100.0	374	16 Q92F23	Q92F23 rickettsia
40	28	100.0	374	16 Q8DPV9	Q8DPV9 streptococ
41	28	100.0	377	16 Q9KI28	Q9KI28 neisseria m
42	28	100.0	383	11 Q8BSH9	Q8BSH9 mus musculu
43	28	100.0	386	16 Q93HB1	Q93HB1 streptomyce
44	28	100.0	393	13 Q7ZY81	Q7ZY81 xenopus lae
45	28	100.0	405	16 Q81S74	Q81S74 bacillus an
46	28	100.0	411	17 Q8ZT93	Q8ZT93 pyroaculum
47	28	100.0	456	10 Q9SFL5	Q9SFL5 arabidopsis
48	28	100.0	458	16 Q67311	Q67311 aquifex aeo
49	28	100.0	482	10 Q8H0F2	Q8H0F2 gentiana tr
50	28	100.0	485	16 Q8XMD5	Q8XMD5 clostridium

## ALIGNMENTS

RESULT 1

Q818J9 PRELIMINARY; PRT; 44 AA.  
ID Q818J9  
AC Q818J9; 01-MAR-2003 (TREMREL. 23, Created)  
DT 01-MAR-2003 (TREMREL. 23, Last sequence update)  
DT 01-OCT-2003 (TREMREL. 25, Last annotation update)  
DE Histone H2A (Fragment).  
GN HIS2B.  
OS Drosophila fuscipila (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=30025;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Y001353;  
RA Yang Y., Zhang Y.P.;  
RT "Phylogenetic Relationships of Drosophila melanogaster Species Group  
Deduced from Spacer Regions of Histone Gene H2A-H2B.";  
DR Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY147443; AA87240.1;  
DR FlyBase; FBgn0064592; Df1c\HIS2B.  
DR GO; GO:0000786; C:nucleus; IEA.  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0003677; F:DNA binding; IEA.  
DR GO; GO:0007001; P:chromosome organization and biogenesis (sen. . .; IEA.  
DR GO; GO:0006334; P:nucleosome assembly; IEA.  
DR InterPro; IPR007125; Histone core D.  
DR InterPro; IPR002119; Histone\_H2A.  
DR Pfam; PF00125; histone; 1.  
DR PRINTS; PR00620; HISTONEH2A.  
DR ProDom; PD000522; Histone\_H2A; 1.  
FT NON\_TER 44 44

SQ SEQUENCE 44 AA; 4998 MW; E5463A43F68F12E1 CRC64;  
Query Match 100.0%; Score 28; DB 5; Length 44;  
Best Local Similarity 100.0%; Pred. No. 92;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LKEKAK 6  
| | | | |  
DB 10 LKEKAK 15  
| | | | |  
RESULT 2  
Q8ZUJ2 PRELIMINARY; PRT; 74 AA.  
ID Q8ZUJ2  
AC Q8ZUJ2  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Hypothetical protein PAE2755.  
GN PAE2755.  
OS Pyrobaculum aerophilum.  
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;  
OC Thermoproteaceae; Pyrobaculum.  
OX NCBI\_TaxID=13773;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=IW2 / ATCC 51768 / DSM 7523;  
RX MEDLINE=21664397; PubMed=1192869;  
RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,  
RA Miller J.H.;  
RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum  
RT aerophilum".  
RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989 (2002).  
DR EMBL; AF009892; AAL64415.1; -.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 74 AA; 8826 MW; AALAFD604B5D3646 CRC64;  
Query Match 100.0%; Score 28; DB 17; Length 74;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LKEKAK 6  
| | | | |  
DB 13 LKEKAK 18  
| | | | |  
RESULT 3  
Q8WWE9 PRELIMINARY; PRT; 78 AA.  
ID Q8WWE9  
AC Q8WWE9  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RA Strausberg R.;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC017770; AAH17770.1; -.  
KW Hypothetical protein.  
SQ SEQUENCE 78 AA; 8421 MW; 53C8FA33D0DD2D8B CRC64;  
Query Match 100.0%; Score 28; DB 4; Length 78;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LKEKAK 6  
| | | | |

DB 28 LKEKAK 33  
| | | | |  
RESULT 4  
Q9DG75 PRELIMINARY; PRT; 112 AA.  
ID Q9DG75  
AC Q9DG75  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE Apolipoprotein CII.  
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
OX NCBI\_TaxID=8022;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=20432101; PubMed=10974550;  
RA Shen Y., Lindberg A., Olivecrona G.;  
RT "Apolipoprotein CII from rainbow trout (Oncorhynchus mykiss) is  
RT functionally active but structurally very different from mammalian  
RT apolipoprotein CII".  
RL Gene 254:189-198 (2000).  
DR EMBL; AF140783; AAG11410.1; -.  
KW Lipoprotein.  
SQ SEQUENCE 112 AA; 12071 MW; 4820749CF0D43EAB CRC64;  
Query Match 100.0%; Score 28; DB 13; Length 112;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LKEKAK 6  
| | | | |  
DB 79 LKEKAK 84  
| | | | |  
RESULT 5  
Q9KEP6 PRELIMINARY; PRT; 148 AA.  
ID Q9KEP6  
AC Q9KEP6  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Hypothetical protein BH0803.  
GN BH0803.  
OS Bacillus halodurans.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=86665;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C-125 / JCM 9153;  
RX MEDLINE=20512582; PubMed=11058132;  
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,  
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,  
RA Horikoshi K.;  
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus  
RT halodurans and genomic sequence comparison with Bacillus subtilis.";  
RL Nucleic Acids Res. 28:4317-4331 (2000).  
DR EMBL; AP001509; BAB04522.1; -.  
DR PIR; C83750; C83750.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 148 AA; 15691 MW; 59DB7FBCA86C45D6 CRC64;  
Query Match 100.0%; Score 28; DB 16; Length 148;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LKEKAK 6  
| | | | |  
DB 32 LKEKAK 37  
| | | | |

```

RESULT 6
Q9V535 PRELIMINARY; PRT; 165 AA.
AC Q9V535;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CG8781 protein.
GN TSU OR CG8781.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Prannkuch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo S., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Flossler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hosten D., Kaulous K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleib J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stappleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL: AE003834; AAF58987.1; -.
DR FlyBase: FBgn0033378; tsu.
DR GO: GO:0005737; C:cytoplasm; IDA.
DR GO: GO:0005634; C:nucleus; IDA.
DR GO: GO:0000226; P:microtubule cytoskeleton organization and b...; IMP.
DR GO: GO:0007314; P:ococyte anterior/posterior axis determination; IMP.
DR GO: GO:0007310; P:ococyte dorsal/ventral axis determination; IMP.
DR GO: GO:0007312; P:ococyte nucleus migration; IMP.
DR GO: GO:0007311; P:regulation of pole plasm oskar mRNA localiz...; IMP.
DR InterPro: IPR008111; RNA_bind.8.
DR Pfam: PF00076; rtm; 1.
DR PRINTS: PR01738; RNABINDINGM8.
DR SMART: SM00360; RRM; 1.
DR PROSITE: PS50102; RRM; 1.
SQ SEQUENCE 165 AA; 19011 MW; A47BE9BD37CCA045 CRC64;

Query Match 100.0%; Score 28; DB 5; Length 165;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
DB 26 LKEKAK 31

RESULT 7
Q8SZA6 PRELIMINARY; PRT; 165 AA.
AC Q8SZA6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RE09075p.
GN TSU OR CG8781.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dreenek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleib J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AV071005; AAL48627.1; -.
DR FlyBase: FBgn0033378; tsu.
DR GO: GO:0005737; C:cytoplasm; IDA.
DR GO: GO:0005634; C:nucleus; IDA.
DR GO: GO:0000226; P:microtubule cytoskeleton organization and b...; IMP.
DR GO: GO:0007314; P:ococyte anterior/posterior axis determination; IMP.
DR GO: GO:0007310; P:ococyte dorsal/ventral axis determination; IMP.
DR GO: GO:0007312; P:ococyte nucleus migration; IMP.
DR GO: GO:0007311; P:regulation of pole plasm oskar mRNA localiz...; IMP.
DR InterPro: IPR008111; RNA_bind.8.
DR Pfam: PF00076; rtm; 1.
DR PRINTS: PR01738; RNABINDINGM8.
DR SMART: SM00360; RRM; 1.
DR PROSITE: PS50102; RRM; 1.
SQ SEQUENCE 165 AA; 19011 MW; B59A19FCD63CB775 CRC64;

Query Match 100.0%; Score 28; DB 5; Length 165;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
DB 26 LKEKAK 31

RESULT 8
Q95X08 PRELIMINARY; PRT; 165 AA.
AC Q95X08;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tsunagi.
GN TSU OR CG8781.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Prannkuch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo S., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Flossler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hosten D., Kaulous K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleib J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stappleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL: AE003834; AAF58987.1; -.
DR FlyBase: FBgn0033378; tsu.
DR GO: GO:0005737; C:cytoplasm; IDA.
DR GO: GO:0005634; C:nucleus; IDA.
DR GO: GO:0000226; P:microtubule cytoskeleton organization and b...; IMP.
DR GO: GO:0007314; P:ococyte anterior/posterior axis determination; IMP.
DR GO: GO:0007310; P:ococyte dorsal/ventral axis determination; IMP.
DR GO: GO:0007312; P:ococyte nucleus migration; IMP.
DR GO: GO:0007311; P:regulation of pole plasm oskar mRNA localiz...; IMP.
DR InterPro: IPR008111; RNA_bind.8.
DR Pfam: PF00076; rtm; 1.
DR PRINTS: PR01738; RNABINDINGM8.
DR SMART: SM00360; RRM; 1.
DR PROSITE: PS50102; RRM; 1.
SQ SEQUENCE 165 AA; 19011 MW; A47BE9BD37CCA045 CRC64;

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OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21549073; PubMed=11691839;
RA Mohr S.E., Dillon S.T., Boswell R.E.;
RT "The RNA-binding protein Tsunagi interacts with Mago Nashi to
RT establish polarity and localize oskar mRNA during Drosophila
RT oogenesis.";
RL Genes Dev. 15:2886-2899(2001).
DR EMBL; AF173550; AAL29185.1; -.
DR FlyBase; FBgn0033378; tsu.
DR GO; GO:0005737; C:cytoplasm; IDA.
DR GO; GO:0005634; C:nucleus; IDA.
DR GO; GO:0002026; P:microtubule cytoskeleton organization and b...; IMP.
DR GO; GO:0007314; P:ocyte anterior/posterior axis determination; IMP.
DR GO; GO:0007310; P:ocyte dorsal/ventral axis determination; IMP.
DR GO; GO:0007312; P:ocyte nucleus migration; IMP.
DR GO; GO:0007317; P:regulation of pole plasm oskar mRNA localiz...; IMP.
DR InterPro; IPR008111; RNA_bind_8.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00076; rrm; 1.
DR PRINTS; PR01738; RNABINDINGM8.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS0102; RRM; 1.
SQ SEQUENCE 165 AA; 18983 MW; D56D0A5DC12CBD86 CRC64;

Query Match 100.0%; Score 28; DB 5; Length 165;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
DB 26 LKEKAK 31
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RESULT 9
Q8JUC5 PRELIMINARY; PRT; 172 AA.
AC Q8JUC5;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RNA binding motif protein 8 (Fragment).
GN RBM8;
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=himedaka;
RX MEDLINE=22050021; PubMed=12054603;
RA Okubo K., Mitani H., Naruse K., Kondo M., Shima A., Tanaka M.,
RA Aida K.;
RT "Conserved physical linkage of GnRH-R and RBM8 in the medaka and human
RT genomes.";
RL Biochem. Biophys. Res. Commun. 293:327-331(2002).
DR EMBL; AB069906; BAB92097.1; -.
DR PIR; JC7836; JC7836.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0006396; P:RNA processing; IEA.
DR InterPro; IPR008111; RNA_bind_8.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00076; rrm; 1.
DR PRINTS; PR01738; RNABINDINGM8.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS0102; RRM; 1.
FT NON TER 1
SQ SEQUENCE 172 AA; 19589 MW; 482CE2B71A608B40 CRC64;

Query Match 100.0%; Score 28; DB 11; Length 173;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
DB 28 LKEKAK 33
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RESULT 11
Q9CWZ3 PRELIMINARY; PRT; 173 AA.
ID Q9CWZ3
AC Q9CWZ3;

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DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE 2310057C03Rik protein (RNA binding motif protein 8A).  
GN RBM8 OR 2310057C03RIK.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Embryonic stem cells;  
RX MEDLINE=21085660; PubMed=1117851;  
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gibbs C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Suzuki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Breast tumor;  
RA Strausberg R.;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK010284; BAB26820.1; -;  
DR EMBL; BC020086; AAH20086.1; -;  
DR HSSP; P19339; 1SXL.  
DR MGD; MGI:1313129; Rbm8.  
DR GO; GO:0005634; C:nucleus; IDA.  
DR GO; GO:0003729; F:mRNA binding; IDA.  
DR InterPro; IPR008111; RNA\_bind\_8.  
DR InterPro; IPR000504; RNA\_rec\_mot.  
DR Pfam; PF00076; rtm; 1.  
DR PRINTS; PR01738; RNABINDINGM8.  
DR PROSITE; PS50102; RRM; 1.  
SQ SEQUENCE 173 AA; 19760 MW; 6710C1BD9CFAF92E CRC64;  
Query Match 100.0%; Score 28; DB 11; Length 173;  
Best Local Similarity 100.0%; Pred. No. 3e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 6; Conservative 0;  
QY 1 LKEKAK 6  
DB 28 LKEKAK 33  
RESULT 12  
Q8JJC6 PRELIMINARY; PRT; 173 AA.  
AC Q8JJC6  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DE 2310057C03Rik protein (RNA binding motif protein 8).  
DE RNA binding motif protein 8.  
GN RBM8.  
OS Oryzias latipes (Medaka fish) (Japanese ricefish).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;

OC Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.  
OX NCBI\_TaxID=8090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=himedaka; TISSUE=Brain;  
RX MEDLINE=22050021; PubMed=12054603;  
RA Okubo K., Mitani H., Naruse K., Kondo M., Shima A., Tanaka M.,  
RA Aida K.;  
RT "Conserved physical linkage of GnRH-R and RBM8 in the medaka and human  
genomes.";  
RL Biochem. Biophys. Res. Commun. 293:327-331(2002).  
DR EMBL; AB069905; BAB92096.1; -;  
DR FIR; JC7836; JC7836.  
DR GO; GO:0005737; C:cytoplasm; IEA.  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0003723; F:RNA binding; IEA.  
DR GO; GO:0006396; P:RNA processing; IEA.  
DR InterPro; IPR008111; RNA\_bind\_8.  
DR InterPro; IPR000504; RNA\_rec\_mot.  
DR Pfam; PF00076; rtm; 1.  
DR PRINTS; PR01738; RNABINDINGM8.  
DR SMART; SM00360; RRM; 1.  
DR PROSITE; PS50102; RRM; 1.  
SQ SEQUENCE 173 AA; 19721 MW; 438EABEA8F506B84 CRC64;  
Query Match 100.0%; Score 28; DB 13; Length 173;  
Best Local Similarity 100.0%; Pred. No. 3e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 6; Conservative 0;  
QY 1 LKEKAK 6  
DB 26 LKEKAK 31  
RESULT 13  
Q9DF42 PRELIMINARY; PRT; 174 AA.  
AC Q9DF42  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE RNA-binding protein Y14.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20483263; PubMed=11030346;  
RA Kataoka N., Yong J., Kim V.N., Velazquez F., Perkinson R.A., Wang F.,  
RA Drevfuss G.;  
RT "Pre-mRNA splicing imprints mRNA in the nucleus with a novel RNA-  
binding protein that persists in the cytoplasm.";  
RL Mol. Cell 6:673-682(2000).  
DR EMBL; AF299119; AAG27092.1; -;  
DR HSSP; P26368; 2U2F.  
DR GO; GO:0005737; C:cytoplasm; IEA.  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0003723; F:RNA binding; IEA.  
DR GO; GO:0006396; P:RNA processing; IEA.  
DR InterPro; IPR008111; RNA\_bind\_8.  
DR InterPro; IPR000504; RNA\_rec\_mot.  
DR Pfam; PF00076; rtm; 1.  
DR PRINTS; PR01738; RNABINDINGM8.  
DR SMART; SM00360; RRM; 1.  
DR PROSITE; PS50102; RRM; 1.  
SQ SEQUENCE 174 AA; 19720 MW; A0E5177923AC0B2C CRC64;  
Query Match 100.0%; Score 28; DB 13; Length 174;  
Best Local Similarity 100.0%; Pred. No. 3e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 6; Conservative 0;

QY 1 LKEKAK 6  
 Db 28 LKEKAK 33

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 14

Q8EST1 PRELIMINARY; PRT; 182 AA.  
 ID Q8EST1  
 AC Q8EST1  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical conserved protein.  
 OB0536.  
 OS Oceanobacillus iheyensis.  
 OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Oceanobacillus.  
 OX NCBI\_TaxID=182710;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=HTE831 / DSM 14371 / JCM 11309;  
 RX MEDLINE=22220767; PubMed=12235376;  
 RA Takami H., Takaki Y., Uchiyama I.;  
 RT "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya  
 RT Ridge and its unexpected adaptive capabilities to extreme  
 RT environments.";  
 RL Nucleic Acids Res. 30:3927-3935(2002).  
 DR EMBL; AP004594; BAC12492.1; -  
 GO; GO:0003824; Fcatalytic activity; IEA.  
 DR InterPro; IPR006674; HD.  
 DR InterPro; IPR003607; Met\_phosphohydro.  
 DR SMART; PF01966; HD; 1.  
 DR SMART; SM00471; HDC; 1.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 182 AA; 21030 MW; 53B44E253B675C5 CRC64;

Query Match 100.0%; Score 28; DB 16; Length 182;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
 Db 2 LKEKAK 7

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 15

Q9R8Q0 PRELIMINARY; PRT; 185 AA.  
 ID Q9R8Q0  
 AC Q9R8Q0  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Decorin binding protein A.  
 GN DBPA.  
 OS Borrelia garinii.  
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.  
 OX NCBI\_TaxID=29519;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PBR;  
 RX MEDLINE=99003139; PubMed=9784533;  
 RA Roberts W.C., Mullikin B.A., Lathigra R., Hanson M.S.;  
 RT "Molecular analysis of sequence heterogeneity among genes encoding  
 RT decorin binding proteins A and B of Borrelia burgdorferi sensu lato.";  
 RL Infect. Immun. 66:5278-5285(1998).  
 DR EMBL; AF069281; AAC70059.1; -  
 DR InterPro; IPR003332; Decorin bind.  
 DR InterPro; IPR000437; Prok\_lipo\_prot\_s.  
 DR Pfam; PF02352; Decorin bind. 1  
 DR PROSITE; PS00013; PROKAR\_LIPOPROTEIN; 1.  
 SQ SEQUENCE 185 AA; 20227 MW; 458DBBA69C30E038 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 185;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;

QY 1 LKEKAK 6  
 Db 175 LKEKAK 180

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 16

Q8TWK4 PRELIMINARY; PRT; 205 AA.  
 ID Q8TWK4  
 AC Q8TWK4  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Uncharacterized protein.  
 GN MK1029.  
 OS Methanopyrus kandleri.  
 OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;  
 OX NCBI\_TaxID=2320;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=AV19 / DSM 6324 / JCM 9639;  
 RX MEDLINE=21927647; PubMed=11930014;  
 RA Slesarev A.I., Mezheva K.V., Makarova K.S., Polushin N.N.,  
 RA Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,  
 RA Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,  
 RA Malykh A.G., Koonin E.V., Kozyavkin S.A.;  
 RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19  
 RT and monophyly of archaeal methanogens.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).  
 DR EMBL; AE010391; AAM02242.1; -  
 KW Complete proteome.  
 SQ SEQUENCE 205 AA; 22552 MW; 6FF2083F4C138002 CRC64;

Query Match 100.0%; Score 28; DB 17; Length 205;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
 Db 132 LKEKAK 137

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 17

O93376 PRELIMINARY; PRT; 223 AA.  
 ID O93376  
 AC O93376  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Fast myotomal muscle troponin-T.  
 OS Salmo salar (Atlantic salmon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.  
 OX NCBI\_TaxID=8030;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Myotomal muscle;  
 RA Jackman D.M., Heeley D.H.;  
 RT "Salmo salar fast myotomal muscle troponin-T mRNA, complete cds.";  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF072687; AAC24595.1; -  
 DR InterPro; IPR001978; Troponin.  
 DR Pfam; PF00992; Troponin; 1.  
 SQ SEQUENCE 223 AA; 26649 MW; 83B29B428612443C CRC64;

Query Match 100.0%; Score 28; DB 13; Length 223;  
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6

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Db      168 LKEKAK 173
|||||
RESULT 18
O24983 PRELIMINARY; PRT; 224 AA.
AC O24983;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein HP0181.
GN HP0181.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=26695 / ATCC 700392;
RX MEDLINE=97394467; PubMed=9252185;
RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
RA McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,
RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,
RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
RA Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
pylori."
RL Nature 388:539-547(1997).
DR EMBL; AE000538; AAD07253.1; -.
DR PIR; E64542; E64542.
DR TIGR; HP0181; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0009403; P:toxin biosynthesis; IEA.
DR InterPro; IPR003825; Colicin V.
DR Pfam; PF02674; Colicin V; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 224 AA; 24909 MW; B27185B3874D42F7 CRC64;

Query Match 100.0%; Score 28; DB 16; Length 224;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
|||
Db 193 LKEKAK 198

RESULT 19
Q7U7M1 PRELIMINARY; PRT; 235 AA.
AC Q7U7M1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN SYN0960.
OS Synechococcus sp. (strain WH8102).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=84588;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22825697; PubMed=12917641;
RA Palenik B., Brahamsha B., Larimer P.W., Land M., Hauser L., Chain P.,
RA Lamerdin J., Regala W., Allen E.E., McCarren J., Paulsen I.,
RA Dufresne A., Partensky F., Webb E.A., Waterbury J.;
RT "The genome of a motile marine Synechococcus."
RL Nature 424:1037-1042(2003).
DR EMBL; BX569691; CAE07475.1; -.

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KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 235 AA; 27056 MW; 580A5E2EF48917B1 CRC64;

Query Match 100.0%; Score 28; DB 16; Length 235;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
|||||
Db 100 LKEKAK 105

RESULT 20
Q9ZMP9 PRELIMINARY; PRT; 236 AA.
AC Q9ZMP9;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative.
GN JHP0169.
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99120557; PubMed=9923682;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.B., Vovis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
gastric pathogen Helicobacter pylori."
RL Nature 397:176-180(1999).
DR EMBL; AE001455; AAD05750.1; -.
DR PIR; E71965; E71965.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0009403; P:toxin biosynthesis; IEA.
DR InterPro; IPR003825; Colicin V.
DR Pfam; PF02674; Colicin V; 1.
KW Complete proteome.
SQ SEQUENCE 236 AA; 26137 MW; E9898531E7E4D0E4 CRC64;

Query Match 100.0%; Score 28; DB 16; Length 236;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
|||||
Db 202 LKEKAK 207

RESULT 21
O58271 PRELIMINARY; PRT; 241 AA.
AC O58271;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein PH0536.
GN PH0536.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=53953;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OT3;
RX MEDLINE=98344137; PubMed=9679194;
RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,

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RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:55-76(1998).
DR EMBL; AF000002; BAA29625.1; -.
DR FIR; D71167; D71167.
DR GO; GO:0000049; F:RNA binding; IEA.
DR InterPro; IPR008994; Nucleic acid_OB.
DR Pfam; PF01588; trna bind. 1.
DR PROSITE; PS50886; TRBD; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 241 AA; 28918 MW; 7EB9B82F19EC03CE CRC64;

Query Match 100.0%; Score 28; DB 17; Length 241;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
DB 71 LKEKAK 76

RESULT 22
Q8EYN0
ID Q8EYN0 PRELIMINARY; PRT; 242 AA.
AC Q8EYN0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Flagellar motor protein MotB.
GN MOTB4 OR LA4183.
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=173;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RA Ren S.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB011572; AAN51381.1; -.
KW Complete proteome.
SQ SEQUENCE 242 AA; 28044 MW; C94096D8523CF474 CRC64;

Query Match 100.0%; Score 28; DB 16; Length 242;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
DB 105 LKEKAK 110

RESULT 23
Q9R2C8
ID Q9R2C8 PRELIMINARY; PRT; 246 AA.
AC Q9R2C8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mast cell protease 5 precursor (fragment).
GN MCP-5.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague Dawley;
RX MEDLINE=97149430; PubMed=8996238;

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RA Lutzelschwab C., Pejler G., Aveskog M., Hellman L.;
RT "Secretory granule proteases in rat mast cells. Cloning of 10
RT different serine proteases and a carboxypeptidase A from various rat
RT mast cell populations.";
RL J. Exp. Med. 185:13-29(1997).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; U67908; AAB48261.1; -.
DR FIR; S59135; S59135.
DR HSSP; P23946; 1KLT.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRY1 SPC; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease; Signal.
FT NON_TER 1
FT SIGNAL <1 18 POTENTIAL.
FT CHAIN 19 246 MAST CELL PROTEASE 5.
SQ SEQUENCE 246 AA; 27438 MW; A525FC4F1BFDEF87 CRC64;

Query Match 100.0%; Score 28; DB 11; Length 246;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
DB 115 LKEKAK 120

RESULT 24
Q9JUI7
ID Q9JUI7 PRELIMINARY; PRT; 254 AA.
AC Q9JUI7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein NMA1544.
GN NMA1544.
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=22491 / Serogroup A / Serotype 4A;
RX MEDLINE=2022556; PubMed=10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA Jagsels K., Leather S., Moule S., Mungall K., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrall B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
RT meningitidis 22491.";
RL Nature 404:502-508(2000).
DR EMBL; AL162756; CAB84771.1; -.
DR FIR; C81846; C81846.
DR InterPro; IPR007478; Kila N.
DR Pfam; PF04383; Kila-N; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 254 AA; 29410 MW; 55C08C8FDCBCCB34 CRC64;

Query Match 100.0%; Score 28; DB 16; Length 254;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 LKEKAK 6
DB      225 LKEKAK 230

RESULT 25
Q8RGJ9  PRELIMINARY;      PRT;      270 AA.
AC      Q8RGJ9;
DT      01-JUN-2002 (TrEMBLrel. 21, Created)
DT      01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT      01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE      Transketolase subunit A (EC 2.2.1.1).
GN      FN0294.
OS      Fusobacterium nucleatum (subsp. nucleatum).
OC      Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;
OC      Fusobacterium.
OX      NCBI_TaxID=76856;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=ATCC 25586;
RX      MEDLINE=21886394; PubMed=11889109;
RA      Kapatal V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
RA      Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
RA      Vasteva O., Chu L., Kogan Y., Chaga O., Goltzman E., Bernal A.,
RA      Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
RA      Fongstein M., Kyripides N., Overbeek R.;
RT      "Genome sequence and analysis of the oral bacterium Fusobacterium
RT      nucleatum strain ATCC 25586";
RL      J. Bacteriol. 184:2005-2018(2002).
DR      EMBL; AE010542; AAL94500.1; -.
DR      HSSP; P06958; 1L8A.
DR      GO; GO:0016740; F:transferase activity; IEA.
DR      GO; GO:0004802; F:transketolase activity; IEA.
DR      InterPro; IPR005474; Transketolase_N.
DR      Pfam; PF00456; transketolase; 1.
DR      PROSITE; PS00801; TRANSKETOLASE_1; 1.
KW      Transferase; Complete proteome.
SQ      SEQUENCE 270 AA; 29577 MW; 7A394B05C3D050E3 CRC64;

Query Match      100.0%; Score 28; DB 16; Length 270;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LKEKAK 6
DB      7 LKEKAK 12

RESULT 26
Q9CSP8  PRELIMINARY;      PRT;      288 AA.
AC      Q9CSP8;
DT      01-JUN-2001 (TrEMBLrel. 17, Created)
DT      01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Nucleosome assembly protein 1-like 1 (Fragment).
GN      NAP1L1.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J; TISSUE=Embryo;
RX      MEDLINE=21085660; PubMed=11217851;
RA      Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA      Arakawa T., Hara A., Fushiki Y., Konno H., Adachi J., Fukuda S.,
RA      Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA      Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA      Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA      Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

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RA      Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA      Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA      Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA      Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA      Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA      Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA      Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA      Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA      Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA      Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA      Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA      Hayashizaki Y.;
RT      "Functional annotation of a full-length mouse cDNA collection.";
RL      Nature 409:685-690(2001).
DR      EMBL; AK012250; BAB28118.1; -.
DR      MGD; MGI:1855693; Nap1l1.
DR      GO; GO:0005634; C:nucleus; IEA.
DR      GO; GO:0003677; F:DNA binding; IEA.
DR      GO; GO:0006334; P:nucleosome assembly; IEA.
DR      InterPro; IPR002164; NAP_family.
DR      Pfam; PF00956; NAP; 1.
FT      NON TER      1
SQ      SEQUENCE 288 AA; 33486 MW; 65B14B91317B151A CRC64;

Query Match      100.0%; Score 28; DB 11; Length 288;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LKEKAK 6
DB      43 LKEKAK 48

RESULT 27
Q8R8P7  PRELIMINARY;      PRT;      304 AA.
AC      Q8R8P7;
DT      01-JUN-2002 (TrEMBLrel. 21, Created)
DT      01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Sugar phosphate isomerases/epimerases.
GN      IOLE OR TSL1948.
OS      Thermoanaerobacter tengcongensis.
OC      Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
OC      Thermoanaerobacteriaceae; Thermoanaerobacter.
OX      NCBI_TaxID=119072;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=MB4 / JCM 11007;
RX      MEDLINE=21992816; PubMed=11997336;
RA      Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA      Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA      Tan H., Chen R., Wang J., Yu J., Yang H.;
RT      "A complete sequence of T. tengcongensis genome.";
RL      Genome Res. 12:689-700(2002).
DR      EMBL; AE013146; AAM25127.1; -.
DR      GO; GO:0005622; C:intracellular; IEA.
DR      GO; GO:0003677; F:DNA binding; IEA.
DR      GO; GO:0004519; F:endonuclease activity; IEA.
DR      GO; GO:0016853; F:isomerase activity; IEA.
DR      GO; GO:0006281; P:DNA repair; IEA.
DR      InterPro; IPR001719; AP_endonuclease2.
DR      Pfam; PF01261; AP_endonuc 2; 1.
KW      Isomerase; Complete proteome.
SQ      SEQUENCE 304 AA; 35581 MW; 3382E3A01359C36D CRC64;

Query Match      100.0%; Score 28; DB 16; Length 304;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LKEKAK 6
DB      15 LKEKAK 20

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RESULT 28
Q39108      PRELIMINARY;      PRT;      326 AA.
ID Q39108;
AC Q39108;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Geranylgeranyl pyrophosphate synthase-related protein precursor.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RN
SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RA Scolnik P.A., Bartley G.E.;
RT "Nucleotide sequence of a putative geranylgeranyl pyrophosphate
RT synthase (GenBank L40577) from Arabidopsis (F095-018).";
RL Plant Physiol. 108:1343-1343 (1995).
DR EMBL; L40577; AAA81879.1; -.
DR GO; GO:0008299; P:isoprenoid biosynthesis; IEA.
DR InterPro; IPR000092; Polyprenyl synth.
DR Pfam; PF00348; polyprenyl synth.
DR PROSITE; PS00723; POLYPRENYL_SYNTHET_1; 1.
KW TRANSIT peptide.
FT TRANSIT 1 47 POTENTIAL.
FT CHAIN 48 326 GERANYLGERANYL PYROPHOSPHATE SYNTHASE-
FT RELATED PROTEIN.
SQ SEQUENCE 326 AA; 35240 MW; FF9224BCC2D7B570 CRC64;

Query Match 100.0%; Score 28; DB 10; Length 326;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
DB 286 LKEKAK 291
|||||

RESULT 29
Q9SZM6      PRELIMINARY;      PRT;      326 AA.
ID Q9SZM6;
AC Q9SZM6;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Geranylgeranyl pyrophosphate synthase-related protein
DE (AT4G38460/F20M13.20).
DE F20M13.20 OR AT4G38460.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RN
SEQUENCE FROM N.A.
RA Bevan M., Wedler H., Kutzner M., Wambutt R., Bancroft I., Mewes H.W.,
RA Mayer K.F.X., Schueller C.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RN
SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RN
SEQUENCE FROM N.A.
RA Wedler H., Kutzner M., Wambutt R., Mewes H.W., Lemcke K.,
RA Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RN

SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RN
SEQUENCE FROM N.A.
RA Liu S.X., Sakano H., Pham P.K., Yamada K., Banh J., Etgu P., Lee J.M.,
RA Toriumi M., Yu G., Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT "Full length cDNA of gene F20M13.20/AT4G38460 (GI:7270829).";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RN
SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.D., Lee J.M., Toriumi M., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayaishizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Full length cDNA of gene F20M13.20/AT4G38460 (GI:7270829).";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [7]
RN
SEQUENCE FROM N.A.
RA Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayaishizaki Y.,
RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis ORF clones.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [8]
RN
SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Meyers M.C., Shinn P., Banh J.,
RA Bowser L., Carninci P., Chung M.K., Goldsmith A.D., Hayaishizaki Y.,
RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
RA Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M.,
RA Palm C.J., Pham P.K., Quach H.L., Sakurai T., Satou M.,
RA Seki M., Southwick A., Toriumi M., Sakano H., Sakurai T., Satou M.,
RA Davis R.W., Theologis A., Toriumi M., Yamada K., Yu G., Shinozaki K.,
RA Ecker J.R.;
RT "Arabidopsis cDNA clones.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [9]
RN
SEQUENCE FROM N.A.
RA Haas B.J., Volfovsky N., Town C.D., Trukhan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT "Full-length messenger RNA sequences greatly improve genome
RT annotation.";
RL Genome Biol. 0:0-0(2002).
RN [10]
RN
SEQUENCE FROM N.A.
RA Brover V., Trukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RT "Full-length cDNA from Arabidopsis thaliana.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL035540; CAB37502.1; -.
DR EMBL; AL161593; CAB80510.1; -.
DR EMBL; AF326906; AAG41488.1; -.
DR EMBL; AF339725; AAK00407.1; -.
DR EMBL; AY057734; AAL15364.1; -.
DR EMBL; AF372915; AAK49631.1; -.
DR EMBL; AY086829; AAM63877.1; -.
DR FIR; T05674; T05674.
DR GO; GO:0008299; P:isoprenoid biosynthesis; IEA.
DR InterPro; IPR000092; Polyprenyl synth.
DR InterPro; IPR000849; Terpenoid synth.
DR Pfam; PF00348; polyprenyl synth.
DR PROSITE; PS00723; POLYPRENYL_SYNTHET_1; 1.
SQ SEQUENCE 326 AA; 35188 MW; 89494E00740CD475 CRC64;

Query Match 100.0%; Score 28; DB 10; Length 326;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;

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Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKEKAK 6
DB 286 LKEKAK 291

RESULT 30
Q9PPKO PRELIMINARY; PRT; 326 AA.
AC Q9PPKO;
DT 01-WAR-2001 (TrEMBLrel. 16, Created)
DT 01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE AT4938460.
GN AT4938460/F20M13.20.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Shinn P., Chen H., Cheuk R., Kim C.J., Banh J., Bowser L.,
RA Carninci P., Chung M.K., Goldsmith A.D., Hayashizaki Y., Ishida J.,
RA Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M.,
RA Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
RA Pham P.K., Quach H.L., Sakano H., Sakurai T., Satou M., Seki M.,
RA Southwick A., Toriumi M., Yamada K., Yu G., Shinozaki K., Davis R.W.,
RA Theologis A., Ecker J.R.;
RT "Arabidopsis cDNA clones."
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF324662; RAG40013.1; -.
DR GO; GO:0008299; P:isoprenoid biosynthesis; IEA.
DR InterPro; IPR000092; Polyprenyl_synth.
DR InterPro; IPR008949; Terpenoid_synth.
DR Pfam; PF00348; polyprenyl_synth; 1.
DR PROSITE; PS00723; POLYPRENYL_SYNTHET_1; 1.
SQ SEQUENCE 326 AA; 35246 MW; 894C5A00740CD475 CRC64;

Query Match 100.0%; Score 28; DB 10; Length 326;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKEKAK 6
DB 286 LKEKAK 291

RESULT 31
O06452 PRELIMINARY; PRT; 338 AA.
AC O06452;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE DNAG, RPOD, CPOA genes and ORF3 and ORF5 (Glycosyl transferase CPOA).
DE CPOA.
GN CPOA OR SP1075.
OS Streptococcus pneumoniae (strain ATCC BAA-255 / R6), and
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=171101, 1313;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=ATCC BAA-255 / R6;
RX MEDLINE=97294477; PubMed=9150233;
RA Grebe T., Paik J., Hakenbeck R.;
RT "A novel resistance mechanism against beta-lactams in Streptococcus pneumoniae involves CpoA, a putative glycosyltransferase."
RL J. Bacteriol. 179:3342-3349 (1997).
RN [2]

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RP SEQUENCE FROM N.A.
RC STRAIN=ATCC BAA-334 / TIGR4;
RX MEDLINE=21357209; PubMed=11463916;
RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
RA Durkin A.S., Gwinn M., Kolonay J.P., Nelson W.C., Peterson J.D.,
RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
RA Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RT "Complete genome sequence of a virulent isolate of Streptococcus pneumoniae."
RL Science 293:498-506 (2001).
DR EMBL; Y11463; CAA72249.1; -.
DR EMBL; AE007409; RAK75188.1; -.
DR PIR; C95124; C95124.
DR TIGR; SP1075; -.
DR GO; GO:0016740; P:transferase activity; IEA.
DR GO; GO:0009058; P:biosynthesis; IEA.
DR InterPro; IPR001296; Glyco_transf_1.
DR Pfam; PF00534; Glycos_transf_1; 1.
DR Transferase; Complete_protocoe.
SQ SEQUENCE 338 AA; 38826 MW; DD9ED42C748F8565 CRC64;

Query Match 100.0%; Score 28; DB 16; Length 338;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKEKAK 6
DB 305 LKEKAK 310

RESULT 32
Q918H9 PRELIMINARY; PRT; 343 AA.
AC Q918H9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Nucleosome assembly protein 1 (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Oliver C.J., Shenolikar S.;
RT "Identification of Protein Phosphatase-1 Binding Proteins in a Xenopus laevis Gastrula Stage Embryo Library."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF278538; AAF86278.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006334; P:nucleosome assembly; IEA.
DR InterPro; IPR002164; NAP_family.
DR Pfam; PF00956; NAP; 1.
DR NON_TER 1.
SQ SEQUENCE 343 AA; 39706 MW; 6A4524C1E1BB8FFD CRC64;

Query Match 100.0%; Score 28; DB 13; Length 343;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKEKAK 6
DB 120 LKEKAK 125

RESULT 33
Q81F64

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ID Q81F64 PRELIMINARY; PRT; 365 AA.  
AC Q81F64;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Cardiolipin synthetase (BC 2.7.8.-).  
GN BC1737.  
OS Bacillus cereus (strain ATCC 14579 / DSM 31).  
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=226900;  
RN [1]  
RP MEDLINE=22608415; PubMed=12721630;  
RX Imanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,  
RA Kapralov V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,  
RA Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,  
RA Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,  
RA Overbeek R., Kyrpides N.;  
RT "Genome sequence of Bacillus cereus and comparative analysis with  
RT Bacillus anthracis.";  
RL Nature 423:87-91(2003).  
DR EMBL; A8017003; AAP08713.1; -.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0008152; P:metabolism; IEA.  
DR InterPro; IPR001064; Crystallin.  
DR InterPro; IPR001736; PLD.  
DR Pfam; PF00614; PLDC; 2.  
DR SMART; SM00155; PLDC; 2.  
DR PROSITE; PS00225; CRYSTALLIN\_BETAGAMMA; 1.  
DR PROSITE; PS00335; PLD; 2.  
KW Transferase; Complete proteome.  
SQ SEQUENCE 365 AA; 42508 MW; 67688A56FDAA9A6E CRC64;  
Query Match 100.0%; Score 28; DB 16; Length 365;  
Best Local Similarity 100.0%; Pred. No. 5.6e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LKEKAK 6  
DB 56 LKEKAK 61  
RESULT 34  
Q93M86 PRELIMINARY; PRT; 367 AA.  
ID Q93M86;  
AC Q93M86;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Probable transcription regulator phage-related.  
GN PCP61.  
OS Clostridium perfringens.  
OG Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
OC Clostridium  
OX NCBI\_TaxID=1502;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=13 / Type A;  
RX MEDLINE=21664373; PubMed=11792842;  
RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,  
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayaishi H.;  
RT "Complete genome sequence of Clostridium perfringens, an anaerobic  
RT flesh-eater.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).  
DR EMBL; AP003515; BAB62499.1; -.  
DR GO; GO:0046921; C:extrachromosomal DNA; IEA.  
DR GO; GO:0003677; F:DNA binding; IEA.  
DR GO; GO:0008236; F:serine-type peptidase activity; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR001387; HTH 3.  
DR InterPro; IPR006198; Peptidase\_S24\_C.  
DR Pfam; PF01381; HTH\_3; 1.

DR Pfam; PF00717; Peptidase\_S24; 1.  
DR SMART; SM00530; HTH\_XRE\_1.  
KW Plasmid; Complete proteome.  
SQ SEQUENCE 367 AA; 43223 MW; 036437980A3BE704 CRC64;  
Query Match 100.0%; Score 28; DB 16; Length 367;  
Best Local Similarity 100.0%; Pred. No. 5.6e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LKEKAK 6  
DB 223 LKEKAK 228  
RESULT 35  
Q9V0V9 PRELIMINARY; PRT; 367 AA.  
ID Q9V0V9;  
AC Q9V0V9;  
DT 01-WAY-2000 (TrEMBLrel. 13, Created)  
DT 01-WAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Hypothetical protein PYRAB06810.  
GN PYRAB06810 OR PAB0463.  
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;  
OS Pyrococcus abyssi.  
OC Pyrococcus  
OX NCBI\_TaxID=29292;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=GE5 / Orsay;  
RA Heilig R.;  
RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome  
RT structure and evolution.";  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBSJ databases.  
DR EMBL; AJ248285; CAB49594.1; -.  
DR PIR; A75110; A75110.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 367 AA; 43396 MW; 649D6B87670431CB CRC64;  
Query Match 100.0%; Score 28; DB 17; Length 367;  
Best Local Similarity 100.0%; Pred. No. 5.6e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LKEKAK 6  
DB 167 LKEKAK 172  
RESULT 36  
Q8YS20 PRELIMINARY; PRT; 372 AA.  
ID Q8YS20;  
AC Q8YS20;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Hypothetical protein All3271.  
GN All3271.  
OS Anabaena sp. (strain PCC 7120).  
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.  
OX NCBI\_TaxID=103690;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21595285; PubMed=11759840;  
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,  
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,  
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,  
RA Nakazaki N., Shimpō S., Sugimoto M., Takazawa M., Yamada M.,  
RA Yasuda M., Tabata S.;  
RT "Complete genomic sequence of the filamentous nitrogen-fixing  
RT cyanobacterium Anabaena sp. strain PCC 7120.";  
RL DNA Res. 8:205-213(2001).  
DR EMBL; AP003592; BAB74970.1; -.  
DR PIR; AH2214; AH2214.

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DR InterPro; IPR007345; PS_pyruv_trans.
DR Pfam; PF04230; PS_pyruv_trans; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 372 AA; 43535 MW; 9D60D1D8311F0CF8 CRC64;

Query Match          100.0%; Score 28; DB 16; Length 372;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
DB 72 LKEKAK 77
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RESULT 37
Q8BJQ6 PRELIMINARY; PRT; 373 AA.
AC Q8BJQ6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical acyl-CoA dehydrogenase containing protein.
GN 9330129D05RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/60; TISSUE=Brain;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL; AK080793; BAC38023.1; -.
DR PIR; PT0596; PT0596.
DR PIR; PT0635; PT0696.
DR MGD; MGI:2443320; 9330129D05RIK.
DR GO; GO:0003995; F:acyl-CoA dehydrogenase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006091; Acyl-CoA_dh_M.
DR Pfam; PF02770; Acyl-CoA_dh_M; 1.
KW Hypothetical protein.
SQ SEQUENCE 373 AA; 41426 MW; 9FCA71873D1FA08E CRC64;

Query Match          100.0%; Score 28; DB 11; Length 373;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
DB 195 LKEKAK 200
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RESULT 38
Q9JSV1 PRELIMINARY; PRT; 374 AA.
AC Q9JSV1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein NMA2122.
GN NMA2122.
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=22491 / Serogroup A / Serotype 4A;
RX MEDLINE=20222556; PubMed=10761919;

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RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrell B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
RL Nature 404:502-506(2000).
DR EMBL; AL162758; CAB85335.1; -.
DR PIR; H81783; H81783.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 374 AA; 42758 MW; 7BF09DC15037185F CRC64;

Query Match          100.0%; Score 28; DB 16; Length 374;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
DB 99 LKEKAK 104
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RESULT 39
Q92FZ3 PRELIMINARY; PRT; 374 AA.
AC Q92FZ3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE NAD(P) transhydrogenase subunit alpha.
GN PNTAA OR RC1334.
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=781;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=Malish 7;
RX MEDLINE=21442074; PubMed=11557893;
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
RA Raoult D.;
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii."
RL Science 293:2093-2098(2001).
DR EMBL; AE008679; AAL03872.1; -.
DR PIR; P97866; P97866.
DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR007698; Aladh_PNT_C.
DR InterPro; IPR007886; Aladh_PNT_N.
DR InterPro; IPR000169; SHprot_acsite.
DR Pfam; PF01262; Aladh_PNT_C; 1.
DR Pfam; PF05222; Aladh_PNT_N; 1.
DR PROSITE; PS00639; THIOI_PROTEASE_HIS; 1.
KW Complete proteome.
SQ SEQUENCE 374 AA; 40617 MW; 4A41408DD9A19A81 CRC64;

Query Match          100.0%; Score 28; DB 16; Length 374;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
DB 6 LKEKAK 11
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RESULT 40
Q8DPV9 PRELIMINARY; PRT; 374 AA.
ID Q8DPV9
AC Q8DPV9;

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DT 01-WAR-2003 (TReMBLrel. 23, Created)  
 DT 01-WAR-2003 (TReMBLrel. 23, Last sequence update)  
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
 DE Glycosyltransferase.  
 GN CPOA OR SPR0981.  
 OS Streptococcus pneumoniae (strain ATCC BAA-255 / R6).  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 OC Streptococcus.  
 OX NCBI\_TaxID=171101;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21429245; PubMed=11544234;  
 RA Hoskins J., Alborn W.E. Jr., Arnold J., Blaszcak L.C., Burgett S.,  
 RA DeHoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C.,  
 RA Gilmore R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E.,  
 RA LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P.,  
 RA McAhren S.M., McHenry M., McLeaster K., Mundy C.W., Nicas T.I.,  
 RA Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rocky P.,  
 RA Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G.,  
 RA Zook C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R. Jr., Skatrud P.L.,  
 RA Glaes J.I.;  
 RT "Genome of the bacterium Streptococcus pneumoniae strain R6.";  
 RL J. Bacteriol. 183:5709-5717(2001).  
 DR EMBL; AE008471; AAK99785.1; -.  
 DR PIR; E97994; E97994.  
 DR GO; GO:0016740; P:transferase activity; IEA.  
 DR GO; GO:0009058; P:biosynthesis; IEA.  
 DR InterPro; IPR001296; Glyco\_transf\_1.  
 DR Pfam; PF00534; Glycosyl\_transf\_1; 1.  
 KW Transferase; Complete proteome.  
 SQ SEQUENCE 374 AA; 43093 MW; 03D9D0642D1470B2 CRC64;  
  
 Query Match 100.0%; Score 28; DB 16; Length 374;  
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 LKEKAK 6  
 Db 341 LKEKAK 346  
 |||||  
  
 RESULT 41  
 Q9K128 ID Q9K128 PRELIMINARY; PRT; 377 AA.  
 AC Q9K128;  
 DT 01-OCT-2000 (TReMBLrel. 15, Created)  
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
 DE Hypothetical protein NMB0366.  
 GN NMB0366.  
 OS Neisseria meningitidis (serogroup B).  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
 OC Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=491;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NC58 / Serogroup B;  
 RX MEDLINE=201175755; PubMed=10710307;  
 RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,  
 RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,  
 RA Nelson W.C., Gunn M.L., DeBoy R., Peterson J.D., Hickey E.K.,  
 RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,  
 RA Mason T., Cleeck A., Parksey D.S., Blair E., Citron H., Clark E.B.,  
 RA Cotton M.D., Uterback T.R., Khouri H., Qin H., Vamathevan J.,  
 RA Gill J., Scarlato V., Masignani V., Pizzo M., Grandi G., Sun L.,  
 RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;  
 RT "Complete genome sequence of Neisseria meningitidis serogroup B strain  
 NC58.";  
 RL Science 287:1809-1815(2000).  
 DR EMBL; AE002393; AAF40808.1; -.  
 DR PIR; D81206; D81206.  
 DR TIGR; NMB0366; -.  
 KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 377 AA; 43158 MW; 9B1930636F732E3F CRC64;  
  
 Query Match 100.0%; Score 28; DB 16; Length 377;  
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 LKEKAK 6  
 Db 102 LKEKAK 107  
 |||||  
  
 RESULT 42  
 Q8BSH9 ID Q8BSH9 PRELIMINARY; PRT; 383 AA.  
 AC Q8BSH9;  
 DT 01-WAR-2003 (TReMBLrel. 23, Created)  
 DT 01-WAR-2003 (TReMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
 DE Nucleosome assembly protein 1-like 1.  
 GN NAP1L1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CS7BL/6J; TISSUE=Meiosephros;  
 RX MEDLINE=22354883; PubMed=12466851;  
 RA The FANTOM Consortium,  
 RA The RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 DR EMBL; AK032896; BAC28075.1; -.  
 DR MGD; MGI:1855693; Nap1l1.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003677; F:DNA binding; IEA.  
 DR GO; GO:0006334; P:nucleosome assembly; IEA.  
 DR InterPro; IPR002164; NAP\_family.  
 DR Pfam; PF00956; NAP; 1.  
 SQ SEQUENCE 383 AA; 44597 MW; 6C579ADB4A29E3A7 CRC64;  
  
 Query Match 100.0%; Score 28; DB 11; Length 383;  
 Best Local Similarity 100.0%; Pred. No. 5.8e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 LKEKAK 6  
 Db 146 LKEKAK 151  
 |||||  
  
 RESULT 43  
 Q93HB1 ID Q93HB1 PRELIMINARY; PRT; 386 AA.  
 AC Q93HB1;  
 DT 01-DEC-2001 (TReMBLrel. 19, Created)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
 DE Cytochrome P450.  
 GN CYP11 OR SAV2385.  
 OS Streptomyces avermitilis.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Streptomycineae; Streptomycetaceae; Streptomyces.  
 OX NCBI\_TaxID=33903;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;  
 RX MEDLINE=21477403; PubMed=11572948;  
 RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,  
 RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,  
 RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;  
 RT "Genome sequence of an industrial microorganism Streptomyces  
 avermitilis: Deducing the ability of producing secondary

```

RT metabolites.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=NA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=22608306; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis.";
RL Nat. Biotechnol. 21:526-531(2003).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
DR EMBL; AB070947; BAB69278.1; -;
DR EMBL; AB005030; BAC70096.1; -;
DR GO; GO:0004497; F:monooxygenase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001128; Cytochrome_P450.
DR Pfam; PF00067; P450; 1.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
KW Heme; Monooxygenase; Oxidoreductase; Complete proteome.
SQ SEQUENCE 386 AA; 43694 MW; 38BE1F563D061F86 CRC64;

Query Match 100.0%; Score 28; DB 16; Length 386;
Best Local Similarity 100.0%; Pred. No. 5.8e+02; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

QY 1 LKEKAK 6
DB 181 LKEKAK 186

RESULT 44
Q7ZY81 PRELIMINARY; PRT; 393 AA.
AC Q7ZY81;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to nucleosome assembly protein 1-like 1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC043903; AAH43903.1; -;
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006334; P:nucleosome assembly; IEA.
DR InterPro; IPR002164; NAP_family.
DR Pfam; PF00956; NAP; 1.
SQ SEQUENCE 393 AA; 45516 MW; E0EBC9D50FBADF44 CRC64;

Query Match 100.0%; Score 28; DB 13; Length 393;
Best Local Similarity 100.0%; Pred. No. 5.9e+02; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

QY 1 LKEKAK 6
DB 147 LKEKAK 152

RESULT 45
Q81S74 PRELIMINARY; PRT; 405 AA.
AC Q81S74;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

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DE Cardiolipin synthetase domain protein.
GN BAI1796.
OS Bacillus anthracis (strain Ames).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=198094;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22608414; PubMed=12721629;
RA Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Okstad O.A., Helgason E., Ristone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.,
RA DeBoy R.T., Madpu R., Dougherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahmoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,
RA Thomson B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,
RA Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria.";
RL Nature 423:81-86(2003).
DR EMBL; AE017029; AAP25707.1; -;
DR TIGR; BAI1796; -;
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR001736; PLD.
DR Pfam; PF00614; PLDC; 2.
DR SMART; SM00155; PLDC; 2.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
DR PROSITE; PS00335; PLD; 2.
KW Complete proteome.
SQ SEQUENCE 405 AA; 47150 MW; 50E76BE54F424962 CRC64;

Query Match 100.0%; Score 28; DB 16; Length 405;
Best Local Similarity 100.0%; Pred. No. 6.1e+02; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

QY 1 LKEKAK 6
DB 96 LKEKAK 101

RESULT 46
Q8ZT93 PRELIMINARY; PRT; 411 AA.
AC Q8ZT93;
DT 01-WAR-2002 (TrEMBLrel. 20, Created)
DT 01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein PAE3368.
GN PAE3368.
OS Pyrobaculum aerophilum.
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
OC Thermoproteaceae; Pyrobaculum.
OX NCBI_TaxID=13773;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=IM2 / ATCC 51768 / DSM 7523;
RX MEDLINE=21664397; PubMed=11792869;
RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
RA Miller J.H.;
RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
RT aerophilum.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
DR EMBL; AE009927; AAL64870.1; -;
DR InterPro; IPR005912; Cons_hypoth1213.
DR TIGRFAMs; TIGR01213; TIGR01213; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 411 AA; 46961 MW; A5981BC80603F623 CRC64;

Query Match 100.0%; Score 28; DB 17; Length 411;

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Best Local Similarity 100.0%; Pred. No. 6.2e+02; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

QY 1 LKEKAK 6
DB 294 LKEKAK 299

RESULT 47
Q9SF15 ID Q9SF15 PRELIMINARY; PRT; 456 AA.
AC Q9SF15;
DT 01-WAY-2000 (TrEMBLrel. 13, Created)
DT 01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE F26K24.13 protein (Hypothetical protein).
DE F26K24.13.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurooids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia.
RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
RA Rowning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
RA Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RT "Arabidopsis thaliana chromosome III BAC F26K24 genomic sequence.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Haas B.J., Volkovsky N., Town C.D., Troupkan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT "Full-length messenger RNA sequences greatly improve genome
RT annotation.";
RL Genome Biol. 0:0-0 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RA Brover V., Troupkan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RT "Full-length cDNA from Arabidopsis thaliana.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC016795; AAF23200.1; -.
DR EMBL; AY084238; AAM67265.1; -.
DR InterPro; IPR008938; ARM.
DR Pfam; PF04564; U-box; 1.
KW Hypothetical protein.
SQ SEQUENCE 456 AA; 51286 MW; 509873CAC065BB8D CRC64;

Query Match 100.0%; Score 28; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
DB 417 LKEKAK 422

RESULT 48
O67311 ID O67311 PRELIMINARY; PRT; 458 AA.
AC O67311;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cytoplasmic axial filament protein.
DE CAFA OR AQ_1275.
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]

Best Local Similarity 100.0%; Pred. No. 6.2e+02; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RP SEQUENCE FROM N.A.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.B., Overbeek R., Sneed M.A., Keller M., Aujay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus.";
RL Nature 392:353-358 (1998).
DR EMBL; AB000732; AAC07269.1; -.
DR PIR; D70410; D70410.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0004540; F:ribonuclease activity; IEA.
DR GO; GO:0006396; P:RNA processing; IEA.
DR InterPro; IPR008994; Nucleic_acid_OB.
DR InterPro; IPR004659; RNaseEG.
DR InterPro; IPR003029; S1.
DR SMART; SM00316; S1; 1.
DR TIGRFAMs; TIGR00757; RNaseEG; 1.
KW Complete proteome.
SQ SEQUENCE 458 AA; 52508 MW; BC453A3AA266065C CRC64;

Query Match 100.0%; Score 28; DB 16; Length 458;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
DB 178 LKEKAK 183

RESULT 49
Q8H0F2 ID Q8H0F2 PRELIMINARY; PRT; 482 AA.
AC Q8H0F2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anthocyanin 3'-glucosyltransferase.
GN 3'GT.
OS Gentiana triflora.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Gentianales; Gentianaceae; Gentiana.
OX NCBI_TaxID=55190;
RN [1]
RP SEQUENCE FROM N.A.
RA Mizutani M., Fukui Y., Nakao M., Okuhara H., Katsumoto Y.,
RA Yonekura-Sakakibara K., Kusumi T., Hase T., Tanaka Y.;
RT "Gentian anthocyanin 3'-glucosyltransferase.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB076697; BAC54092.1; -.
DR GO; GO:0016740; F:transferase activity, transferring hexosyl . . .; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002213; UDP_gluco_trans.
DR Pfam; PF00201; UDEGT; 1.
KW Transferase.
SQ SEQUENCE 482 AA; 54041 MW; BDBC12F21C7F7147 CRC64;

Query Match 100.0%; Score 28; DB 10; Length 482;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
DB 451 LKEKAK 456

RESULT 50
Q8XMD5 ID Q8XMD5 PRELIMINARY; PRT; 485 AA.
OX Q8XMD5;
RN [1]
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DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Cardiolipin synthase.  
 GN CLSC OR CPE0754.  
 OS Clostridium perfringens.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 OC Clostridium.  
 OX NCBI\_TaxID=1502;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=13 / Type A;  
 RX MEDLINE=21664373; PubMed=11792842;  
 RA Shimizu T., Ohnani K., Hirakawa H., Ohshima K., Yamashita A.,  
 RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;  
 RT "Complete genome sequence of Clostridium perfringens, an anaerobic  
 RT flesh-eater.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).  
 DR EMBL, AF003188; BAB80460.1; -.  
 DR GO; GO:0003824; F:catalytic activity; IEA.  
 DR GO; GO:0008152; P:metabolism; IEA.  
 DR InterPro; IPR001736; PLD.  
 DR Pfam; PF00614; PLDC; 2.  
 DR SMART; SM00155; PLDC; 2.  
 DR PROSITE; PS50035; PLD; 2.  
 KW Complete proteome.  
 SQ SEQUENCE 485 AA; 56193 MW; B988569756D97CD6 CRC64;

Query Match 100.0%; Score 28; DB 16; Length 485;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
 |||||  
 Db 160 LKEKAK 165

Search completed: April 19, 2004, 17:21:58  
 Job time : 20.8065 secs

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OM protein - protein search, using sw model

Run on: April 19, 2004, 17:08:15 ; Search time 3.3871 Seconds  
(without alignments)  
92.239 Million cell updates/sec

Title: US-10-726-692-14

Perfect score: 28  
Sequence: 1 LKEKAK 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 50 summaries  
Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	100.0	132	Y33A METJA	P81306 methanococ
2	28	100.0	159	YMOU YEAST	Q03713 saccharomyc
3	28	100.0	174	RB8A HUMAN	Q9Y589 homo sapien
4	28	100.0	177	Y105 PASMU	Q9CK30 pasteurella
5	28	100.0	247	MCT3 MERUN	P50341 meriones un
6	28	100.0	247	MCT3 RAT	P50339 rattus norv
7	28	100.0	247	MCT5 MOUSE	P21844 mus musculu
8	28	100.0	284	TPM ECHMU	Q95pu1 echinococcu
9	28	100.0	390	NPL1 RAT	Q9Z2G8 rattus norv
10	28	100.0	391	NPL1 HUMAN	P55209 homo sapien
11	28	100.0	391	NPL1 MOUSE	P28656 mus musculu
12	28	100.0	426	PYRC THEAQ	P96081 thermus aqu
13	28	100.0	431	TIG CLOAB	Q97f66 clostridium
14	28	100.0	434	Y830 THEMA	Q9WZT7 thermocoga
15	28	100.0	442	ENGA UREPA	Q9PQA7 ureaplasma
16	28	100.0	453	UFOG GENTR	Q96493 gentiana tr
17	28	100.0	508	ATPO PHAVU	P24459 phaseolus v
18	28	100.0	590	THIC BACSU	P45740 bacillus su
19	28	100.0	701	ORA PLAFN	P16405 plasmodium
20	28	100.0	1231	CFAH HUMAN	P08603 homo sapien
21	28	100.0	1451	MYM1 HUMAN	P52179 homo sapien
22	28	100.0	1483	BA1B HUMAN	Q9UIG0 homo sapien
23	28	100.0	2459	MAPB RAT	P15205 rattus norv
24	28	100.0	2869	RB01 PLAVB	Q00798 plasmodium
25	26	92.9	219	VB02 VACCC	P20999 vaccinia vi
26	26	92.9	219	VB02 VACCV	Q01225 vaccinia vi
27	26	92.9	236	PLL SHEEP	P16038 ovis aries
28	26	92.9	263	LPSA PASHA	Q05770 pasteurella
29	26	92.9	336	FEN THEAC	Q9HID4 thermoplasm
30	26	92.9	366	GDF3 MOUSE	Q07104 mus musculu
31	26	92.9	431	PURE BACSU	P12047 bacillus su
32	26	92.9	787	PFL LACLA	Q32797 lactococcus
33	26	92.9	787	PFL LACLC	Q32799 lactococcus

34	26	92.9	1411	1	TCOF HUMAN	Q13428 homo sapien
35	26	92.9	1565	1	DMN HUMAN	Q15061 homo sapien
36	26	92.9	3898	1	POLG HCVA	P19712 hog cholera
37	26	92.9	3898	1	POLG HCVB	P21530 hog cholera
38	25	89.3	115	1	Y112 METWA	Q8Q0M4 methanosarc
39	25	89.3	115	1	Y469 METAC	Q8TKX4 methanosarc
40	25	89.3	155	1	Y941 STRAP	Q8C8T6 staphylococ
41	25	89.3	167	1	PTGA BUCAP	Q8K451 buchnera ap
42	25	89.3	168	1	YJ00 AQUAE	Q67738 aquifex aeo
43	25	89.3	183	1	DEF STAEF	Q8CPN4 staphylococ
44	25	89.3	185	1	DPI HUMAN	Q00765 homo sapien
45	25	89.3	185	1	YE46 AQUAE	Q67433 aquifex aeo
46	25	89.3	209	1	RS4 CHLPN	Q9Z7H2 chlamydia p
47	25	89.3	209	1	RS4 CHLTH	Q84G31 chlamydia t
48	25	89.3	235	1	FRHG METTH	P19498 methanobact
49	25	89.3	240	1	YDFB SCHPO	Q10483 schizosacch
50	25	89.3	256	1	UT11 YEAST	P34247 saccharomyc

ALIGNMENTS

RESULT 1

ID	Y33A METJA	STANDARD	PRT	132 AA
AC	P81306			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Hypothetical protein MJ0332.1.			
GN	MJ0332.1.			
OS	Methanococcus jannaschii.			
OC	Archaea; Euryarchaeota; Methanococci; Methanococcales;			
OC	Methanocaldococcaceae; Methanocaldococcus.			
OX	NCBI_TaxID=2190;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAINE-JAL-1 / DSM 2661 / ATCC 43067;			
RX	MEDLINE=96337999; PubMed=8688087;			
RA	Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,			
RA	Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,			
RA	Kerlavage A.R., Dougherty B.A., Tomb J.-P., Adams M.D., Reich C.I.,			
RA	Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,			
RA	Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,			
RA	Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,			
RA	Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,			
RA	Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;			
RT	"Complete genome sequence of the methanogenic archaeon, Methanococcus			
RT	jannaschii."			
RL	Science 273:1058-1073(1996).			
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).			
CC	-----			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
CC	EMBL; U67487; AAB98330.1; -			
DR	TIGR; MJ0332.1; -			
KW	Hypothetical protein; Transmembrane; Complete proteome.			
FT	TRANSMEM 12 32 POTENTIAL.			
FT	TRANSMEM 37 57 POTENTIAL.			
SQ	SEQUENCE 132 AA; 14971 MW; 6E1E1A58AB1641D CRC64;			

Query Match 100.0%; Score 28; DB 1; Length 132;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LKEKAK 6  
|||||

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Db          94 LKEKAK 99

RESULT 2
ID YMD0_YEAST STANDARD; PRT; 159 AA.
AC Q03713;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical 18.5 kDa protein in NDC1-TSA1 intergenic region.
GN YML030W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE=97313268; PubMed=9169872;
RA Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,
RA Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,
RA Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A.,
RA Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome
RT XIII."
RL Nature 387:90-93(1997).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
RX MEDLINE=20483263; PubMed=11030346;
RA Kataoka N., Yong J., Kim V.N., Velazquez F., Parkinson R.A., Wang F.,
RA Dreyfuss G.;
RT "Pre-mRNA splicing imprints mRNA in the nucleus with a novel
RT RNA-binding protein that persists in the cytoplasm."
RL Mol. Cell 6:673-682(2000).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM 2), AND INTERACTION WITH MAGOH.
RX MEDLINE=20130124; PubMed=10662555;
RA Zhao X.F., Nowak N.J., Shows T.B., Aplan P.D.;
RT "MAGOH interacts with a novel RNA-binding protein."
RL Genomics 63:145-148(2000).
RN [7]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND INTERACTION WITH OVCA1.
RC TISSUE=Brain;
RX MEDLINE=20469404; PubMed=11013075;
RA Salicioni A.M., Xi M., Vanderveer L.A., Balsara B., Testa J.R.,
RA Dunbrack R.L. Jr., Godwin A.K.;
RT "Identification and structural analysis of human RRM8A and RRM8B: two
RT highly conserved RNA-binding motif proteins that interact with OVCA1,
RT a candidate tumor suppressor."
RL Genomics 69:54-62(2000).
RN [8]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX MEDLINE=21564198; PubMed=11707068;
RA Faurholm B., Millar R.P., Katz A.A.;
RT "The genes encoding the type II gonadotropin-releasing hormone
RT receptor and the ribonucleoprotein RRM8A in humans overlap in two
RT genomic loci."
RL Genomics 78:15-18(2001).
RN [9]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McKean P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.J., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.M., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RN [1]
RP "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."

```

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[9]  
 RN INTERACTION WITH THOC4 AND THE EXON JUNCTION COMPLEX.  
 RX MEDLINE=21564074; PubMed=11707413;  
 RA Kataoka N., Diem M.D., Kim V.N., Yong J., Dreyfuss G.,  
 RT "Magoh, a human homolog of Drosophila mago nashi protein, is a  
 RT component of the splicing-dependent exon-exon junction complex.";  
 RL EMBO J. 20:6424-6433(2001).  
 CC -!- FUNCTION: Associates preferentially with mRNAs produced by  
 CC splicing. Does not interact with pre-mRNAs, introns, or mRNAs  
 CC produced from intronless cDNAs. Associates with both nuclear mRNAs  
 CC and newly exported cytoplasmic mRNAs.  
 CC -!- SUBUNIT: Interacts with MAGOH and OVCA1 and is part of the exon  
 CC junction complex (EJC) containing NCBP1, NCBP2, RNPS1, RNPS2,  
 CC SRRM1, NXF1, NXF2, NXF3, NXF4, NXF5, NXF6, NXF7, NXF8, NXF9,  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1; Synonyms=BOV-1a;  
 CC IsoId=Q9Y5S9-1; Sequence=Displayed;  
 CC Name=2; Synonyms=BOV-1b;  
 CC IsoId=Q9Y5S9-2; Sequence=VSP 005810;  
 CC -!- TISSUE SPECIFICITY: Ubiquitous.  
 CC -!- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.  
 CC -!- CAUTION: Ref.6 (AAG16782) sequence differs from that shown due to  
 CC the translation of a chimeric cDNA originating from chromosomes 1  
 CC and 5.  
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 CC -----  
 DR EMBL; AF127761; AAD21089.1; -;  
 DR EMBL; AF161463; AAF29078.1; -;  
 DR EMBL; AF182415; AAG14951.1; ALT\_INIT.  
 DR EMBL; AF299118; AAG27091.1; -;  
 DR EMBL; AF198620; AAF37551.1; -;  
 DR EMBL; AF231511; AAG16781.1; -;  
 DR EMBL; AF231512; AAG16782.1; ALT\_INIT.  
 DR EMBL; AF403012; AAL26999.1; -;  
 DR EMBL; BC017088; AAH17088.1; -;  
 DR HSP; P19339; 1SLX.  
 DR Genew; HGNC:9905; RBM8A.  
 DR GK; Q9Y5S9; -;  
 DR MIM; 605313; -;  
 DR GO; GO:0005737; C:cytoplasm; NAS.  
 DR GO; GO:0005634; C:nucleus; NAS.  
 DR GO; GO:0003729; F:mRNA binding; NAS.  
 DR InterPro; IPR008111; RNA\_bind\_8.  
 DR InterPro; IPR000504; RNA\_rec\_mot.  
 DR Pfam; PF00076; rrm; 1.  
 DR PRINTS; PR01738; RNABINDINGM8.  
 DR SMART; SM00360; RRM; 1.  
 DR PROSITE; PS0102; RRM; 1.  
 DR PROSITE; PS00030; RRM\_RNP\_1; FALSE NEG.  
 DR Transport; mRNA transport; mRNA splicing; Nuclear protein;  
 KW RNA-binding; Alternative splicing.  
 FT DOMAIN 73 151  
 FT VARSPLIC 44 44 Missing (in isoform 2).  
 FT RNA-BINDING (RRM).  
 FT /FTId=VSP 005810.  
 FT -----  
 SQ SEQUENCE 174 AA; 19889 MW; 70BED03CDDFECEFC CRC64;  
 Query Match 100.0%; Score 28; DB 1; Length 174;  
 Best Local Similarity 100.0%; Pred. No. 47;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LKEKAK 6  
 DB 28 LKEKAK 33

RESULT 4  
 YI05\_PASMU STANDARD; PRT; 177 AA.  
 AC O9CK30;  
 DT 10-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Hypothetical protein PM1805 precursor.  
 GN PM1805.  
 OS Pasteurella multocida.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
 OC Pasteurellaceae; Pasteurella.  
 OX NCBI\_TaxID=747;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PM70;  
 RX MEDLINE=21145866; PubMed=11248100;  
 RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;  
 RT "Complete genomic sequence of Pasteurella multocida Pm70.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).  
 CC -----  
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 CC -----  
 DR EMBL; AE006217; AAK03889.1; -;  
 DR InterPro; IPR000437; Prok\_lipoprot\_S.  
 DR PROSITE; PS00013; PROKAR\_LIPOPROTEIN; UNKNOWN 1.  
 KW Hypothetical protein; Signal; Complete proteome.  
 FT SIGNAL 1 19 Potential.  
 FT CHAIN 20 177 Hypothetical protein PM1805.  
 SQ SEQUENCE 177 AA; 19439 MW; E415DFA63FE5A28 CRC64;  
 Query Match 100.0%; Score 28; DB 1; Length 177;  
 Best Local Similarity 100.0%; Pred. No. 48;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LKEKAK 6  
 DB 113 LKEKAK 118

RESULT 5  
 MCT2\_MERUN STANDARD; PRT; 247 AA.  
 AC P50341;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Mast cell protease 2 precursor (EC 3.4.21.-).  
 OS Meriones unguiculatus (Mongolian jird).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;  
 OC Meriones.  
 OX NCBI\_TaxID=10047;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MGS/SEA; TISSUE=Intestine;  
 RX MEDLINE=96177868; PubMed=8615790;  
 RA Itoh H., Murakumo Y., Tomita M., Ide H., Kobayashi T., Maruyama H.,  
 RA Horii Y., Nawa Y.;  
 RT "Cloning of the cDNAs for mast-cell chymases from the jejunum of  
 RT Mongolian gerbils, Meriones unguiculatus, and their sequence  
 RT similarities with chymases expressed in the connective-tissue mast  
 RT cells of mice and rats.";  
 RL Biochem. J. 314:923-929(1996).  
 CC -!- SIMILARITY: Belongs to peptidase family S1. Granzyme subfamily.

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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D45174; BAA08122.1; -.
CC FIRM; S64708; S64708.
CC HSP; P23946; 1KLT.
CC MEROPS; S01.140; -.
CC InterPro; IPR009003; Cys_Ser_trypsin.
CC InterPro; IPR001254; Peptidase_S1.
CC InterPro; IPR001314; Peptidase_S1A.
CC Pfam; PF00089; trypsin; 1.
CC PRINTS; PR00722; CHYMOTRYPSIN.
CC SMART; SM00020; Tryp_SPC; 1.
CC PROSITE; PS0240; TRYPSIN_DOM; 1.
CC PROSITE; PS00134; TRYPSIN_HIS; 1.
CC PROSITE; PS00135; TRYPSIN_SER; 1.
CC Hydrolase; Serine protease; Signal; Glycoprotein; Zymogen;
KW Multigene family.
FT SIGNAL 1 19 POTENTIAL.
FT PROPEP 20 21 ACTIVATION PEPTIDE (BY SIMILARITY).
FT CHAIN 22 247 MAST CELL PROTEASE 2.
FT ACT_SITE 66 66 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 110 110 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 203 203 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 51 67 BY SIMILARITY.
FT DISULFID 144 209 BY SIMILARITY.
FT DISULFID 175 188 BY SIMILARITY.
FT CARBOHYD 80 80 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 247 AA; 27633 MW; CA737B5CD43FBE30 CRC64;

Query Match 100.0%; Score 28; DB 1; Length 247;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
DB 116 LKEKAK 121

RESULT 6
MCT3_RAT
ID MCT3_RAT STANDARD; PRT; 247 AA.
AC P50339;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Mast cell protease III precursor (EC 3.4.21.-) (RMCP-III) (RMCP-3).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96033070; PubMed=7487912;
RA Ide H., Itoh H., Tomita M., Murakumo Y., Kobayashi T.,
RA Maruyama H., Osada Y., Nawa Y.;
RT "Cloning of the cDNA encoding a novel rat mast-cell proteinase,
RT rMCP-3, and its expression in comparison with other rat mast-cell
RT proteinases."
RL Biochem. J. 311:675-680(1995).
CC -1- SUBCELLULAR LOCATION: Secretory granules.
CC -1- TISSUE SPECIFICITY: Mast cells.
CC -1- SIMILARITY: Belongs to peptidase family S1. Granzyme subfamily.
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CC -----
CC EMBL; D38495; BAA07507.1; -.
CC FIRM; S59135; S59135.
CC HSP; P23946; 1KLT.
CC MEROPS; S01.150; -.
CC InterPro; IPR009003; Cys_Ser_trypsin.
CC InterPro; IPR001254; Peptidase_S1.
CC InterPro; IPR001314; Peptidase_S1A.
CC Pfam; PF00089; trypsin; 1.
CC PRINTS; PR00722; CHYMOTRYPSIN.
CC SMART; SM00020; Tryp_SPC; 1.
CC PROSITE; PS0240; TRYPSIN_DOM; 1.
CC PROSITE; PS00134; TRYPSIN_HIS; 1.
CC PROSITE; PS00135; TRYPSIN_SER; 1.
CC Hydrolase; Serine protease; Signal; Glycoprotein; Zymogen;
KW Multigene family.
FT SIGNAL 1 19 POTENTIAL.
FT PROPEP 20 21 ACTIVATION PEPTIDE.
FT CHAIN 22 247 MAST CELL PROTEASE III.
FT ACT_SITE 66 66 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 110 110 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 203 203 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 51 67 BY SIMILARITY.
FT DISULFID 144 209 BY SIMILARITY.
FT DISULFID 175 188 BY SIMILARITY.
FT CARBOHYD 80 80 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 247 AA; 27569 MW; 6525D7BF1BFDF053 CRC64;

Query Match 100.0%; Score 28; DB 1; Length 247;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
DB 116 LKEKAK 121

RESULT 7
MCT5_MOUSE
ID MCT5_MOUSE STANDARD; PRT; 247 AA.
AC P21844; Q9R1F0;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Mast cell protease 5 precursor (EC 3.4.21.-) (MMCP-5) (Mast cell
DE chymase 1).
GN MCPT5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92041862; PubMed=1939089;
RA McNeil H.P., Austen K.F., Somerville L.L., Gurish M.F., Stevens R.L.;
RT "Molecular cloning of the mouse mast cell protease-5 gene. A novel
RT secretory granule protease expressed early in the differentiation of
RT serosal mast cells."
RL J. Biol. Chem. 266:20316-20322(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Leaden X A1; TISSUE=Connective tissue;
RX MEDLINE=91285010; PubMed=2060576;
RA Huang R., Blom T., Hellman L.;
RT "Cloning and structural analysis of MMCP-1, MMCP-4 and MMCP-5, three
RT mouse mast cell-specific serine proteases."
RL Eur. J. Immunol. 21:1611-1621(1991).
RN [3]

```

RP SEQUENCE FROM N.A.  
RX MEDLINE=92287966; PubMed=1376147;  
RA Chu W., Johnson D.A., Musich P.R.;  
RT "Molecular cloning and characterization of mouse mast cell chymases.";  
RL Mol. Cell. Biochem. 199; 121:83-87(1992).  
[4]  
RN SEQUENCE OF 1-19 FROM N.A.  
RC STRAIN=129/SV;  
RX MEDLINE=21291700; PubMed=11398967;  
RA Lunderius C., Hellman L.;  
RT "Characterization of the gene encoding mouse mast cell protease 8  
(mMCP-8), and a comparative analysis of hematopoietic serine protease  
genes.";  
RL Immunogenetics 53:225-232(2001).  
[5]  
RN SEQUENCE OF 22-51.  
RX MEDLINE=90222202; PubMed=2326280;  
RA Reynolds D.S., Stevens R.L., Lane W.S., Carr M.H., Austen K.F.,  
RA Serafin W.B.;  
RT "Different mouse mast cell populations express various combinations  
of at least six distinct mast cell serine proteases.";  
RL Proc. Natl. Acad. Sci. U.S.A. 87:3230-3234(1990).  
[6]  
RN SUBCELLULAR LOCATION.  
RX MEDLINE=92407343; PubMed=1527387;  
RA McNeil H.P., Frenkel D.P., Austen F., Friend D.S., Stevens R.L.;  
RT "Translation and granule localization of mouse mast cell protease-5.  
Immunodetection with specific antipeptide Ig.";  
RL J. Immunol. 149:2466-2472(1992).  
CC -|- SUBCELLULAR LOCATION: Secretory granules.  
CC -|- TISSUE SPECIFICITY: Mast cells.  
CC -|- SIMILARITY: Belongs to peptidase family S1. Granzyme subfamily.  
CC  
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CC  
CC EMBL; X6805; CAA48705.1; ALT\_INIT.  
CC EMBL; M73759; AAA40105.1; -.  
CC EMBL; M73760; -; NOT ANNOTATED\_CDS.  
CC EMBL; M68898; AAA39492.1; -.  
CC EMBL; AF113364; AAD43901.1; -.  
CC PIR; S23504; S23504.  
CC PIR; S26043; S26043.  
CC HSSP; P23946; IKLT.  
CC MEROPS; S01.150; -.  
CC MGD; MGI:96941; Mcpt5.  
CC InterPro; IPR009003; Cys Ser trypsin.  
CC InterPro; IPR001254; Peptidase S1.  
CC InterPro; IPR001314; Peptidase\_S1A.  
CC Pfam; PF00089; trypsin; 1.  
CC PRINTS; PR00722; CHYMOTRYPSIN.  
CC SMART; SM00020; TRYPSIN\_DOM; 1.  
CC PROSITE; PS0240; TRYPSIN\_DOM; 1.  
CC PROSITE; PS00134; TRYPSIN\_HIS; 1.  
CC PROSITE; PS00135; TRYPSIN\_SER; 1.  
KW Hydrolase; Serine protease; signal; Glycoprotein; Zymogen.  
FT SIGNAL 1 19  
FT PROPEP 20 21 POTENTIAL.  
FT CHAIN 22 27 ACTIVATION PEPTIDE.  
FT ACT\_SITE 22 27 MAST CELL PROTEASE 5.  
FT ACT\_SITE 66 66 CHARGE RELAY SYSTEM (BY SIMILARITY).  
FT ACT\_SITE 110 110 CHARGE RELAY SYSTEM (BY SIMILARITY).  
FT ACT\_SITE 203 203 CHARGE RELAY SYSTEM (BY SIMILARITY).  
FT DISULFID 51 67 BY SIMILARITY.  
FT DISULFID 144 209 BY SIMILARITY.  
FT DISULFID 175 188 BY SIMILARITY.  
FT CARBOHYD 80 80 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT CONFLICT 5 5 T -> A (IN REF. 1).  
FT CONFLICT 51 51 C -> R (IN REF. 5).

FT CONFLICT 224 224 A -> R (IN REF. 3).  
SQ SEQUENCE 247 AA; 27586 MW; 24C290CF61237DC7 CRC64;  
Query Match 100.0%; Score 28; DB 1; Length 247;  
Best Local Similarity 100.0%; Pred. No. 64;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LKEKAK 6  
DB 116 LKEKAK 121  
|||||  
RESULT 8  
TPM ECHMU STANDARD; PRT; 284 AA.  
ID TPM ECHMU  
AC Q95PUL;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Tropomyosin.  
OS Echinococcus multilocularis.  
OC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;  
OC Cyclophyllidae; Taeniidae; Echinococcus.  
OX NCBI\_TaxID=6211;  
OX [1]  
RN SEQUENCE FROM N.A.  
RA Hubert K., Frosch M., Brehm K.;  
RT "Characterisation of a E. multilocularis tropomyosin encoding mRNA.";  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
CC -|- SUBUNIT: Homodimer (By similarity).  
CC -|- DOMAIN: The molecule is in a coiled coil structure. The sequence  
exhibits a prominent seven-residues periodicity.  
CC -|- SIMILARITY: Belongs to the tropomyosin family.  
CC  
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or send an email to license@isb-sib.ch).  
CC  
CC EMBL; AJ314792; CAC85552.1; -.  
CC DR HSSP; P04268; IIC2.  
CC InterPro; IPR002017; Spectrin.  
CC DR InterPro; IPR000533; Tropomyosin.  
CC DR Pfam; PF00261; Tropomyosin; 1.  
CC DR PRINTS; PR00194; TROPOMYOSIN.  
CC Coiled coil; Repeat.  
KW Coiled coil; Repeat.  
SQ SEQUENCE 284 AA; 32986 MW; 01431F074BF8A73A CRC64;  
Query Match 100.0%; Score 28; DB 1; Length 284;  
Best Local Similarity 100.0%; Pred. No. 73;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LKEKAK 6  
DB 29 LKEKAK 34  
|||||  
RESULT 9  
ID NPL1 RAT STANDARD; PRT; 390 AA.  
AC Q92ZG8;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Nucleosome assembly protein 1-like 1 (NAP-1 related protein).  
GN NAP1L1 OR NRP.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;

```

RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=Sprague-Dawley;
RA  Cataldo L.M., Zhang Y., Ravid K.;
RT  "Mpi-ligand stimulates the expression of multiple mRNAs encoding a
RL  family of nucleosome assembly proteins.";
RT  Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
CC  -!- FUNCTION: May be involved in modulating chromatin formation and
CC  contribute to regulation of cell proliferation (By similarity).
CC  -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC  -!- DOMAIN: The acidic domains are probably involved in the
CC  interaction with histones.
CC  -!- SIMILARITY: Belongs to the nucleosome assembly protein (NAP)
CC  family.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; AF062594; AAC67388.1; -
DR  InterPro; IPR002164; NAP_family.
DR  Pfam; PF00956; NAP; 1.
KW  Nuclear protein.
FT  DOMAIN 10 30 ASP/GLU-RICH (ACIDIC).
FT  DOMAIN 129 145 ASP/GLU-RICH (ACIDIC).
FT  DOMAIN 347 377 ASP/GLU-RICH (ACIDIC).
FT  DOMAIN 272 278 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
SQ  SEQUENCE 390 AA; 45313 MW; 3D59D3C2AE1A71EB CRC64;

Query Match 100.0%; Score 28; DB 1; Length 390;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
DB 146 LKEKAK 151
|||||

RESULT 10
NP1L_HUMAN STANDARD; PRT; 391 AA.
AC P5209;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Nucleosome assembly protein 1-like 1 (NAP-1 related protein) (hNRP).
GN NP1L1 OR NRP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thymus;
RX MEDLINE=94128073; PubMed=8297347;
RA Simon H.-U., Mills G.B., Kozlowski M., Hogg D., Branch D.,
RA Ishini Y., Siminovich K.A.;
RT "Molecular characterization of hNRP, a cDNA encoding a human
RT nucleosome-assembly-protein-1-related gene product involved in the
RT induction of cell proliferation.";
RL Biochem. J. 297:389-397(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Melanoma;
RA Bloecker H., Boecker M., Brandt P., Mewes H.-W., Weil B., Wiemann S.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Kainline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,

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RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length CDSs in BD Creator(TM) system donor
RT vector.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle, and Placenta;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: May be involved in modulating chromatin formation
CC and contribute to regulation of cell proliferation.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: Ubiquitously expressed.
CC -!- DOMAIN: The acidic domains are probably involved in the
CC interaction with histones.
CC -!- SIMILARITY: Belongs to the nucleosome assembly protein (NAP)
CC family.
CC -----
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CC -----
DR  EMBL; M86667; AAC37544.1; -
DR  EMBL; AL162068; CAB82405.1; -
DR  EMBL; BT007023; AAP35669.1; -
DR  EMBL; BC002387; AAH02387.1; -
DR  EMBL; BC015593; AAH15599.1; -
DR  F1R; S40510; S40510.
DR  Genew; HGNC:7637; NAP1L1.
DR  MIM; 164060; -
DR  GO; GO:0005678; C:chromatin assembly complex; TAS.
DR  GO; GO:0006260; P:DNA replication; TAS.
DR  GO; GO:0006334; P:nucleosome assembly; TAS.
DR  GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
DR  InterPro; IPR002164; NAP_family.
DR  Pfam; PF00956; NAP; 1.
KW  Nuclear protein.
FT  DOMAIN 10 30 ASP/GLU-RICH (ACIDIC).
FT  DOMAIN 129 145 ASP/GLU-RICH (ACIDIC).
FT  DOMAIN 348 378 ASP/GLU-RICH (ACIDIC).
FT  DOMAIN 273 279 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
SQ  SEQUENCE 391 AA; 45374 MW; E5B2EAA4EAE551D2 CRC64;

Query Match 100.0%; Score 28; DB 1; Length 391;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
|||||

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Db 146 LXEKAK 151

RESULT 11

NPL1 MOUSE

AC P2856; STANDARD; PRT; 391 AA.

DT 01-DEC-1992 (Rel. 24, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Nucleosome assembly protein 1-like 1 (NAP-1 related protein)

DE (Brain protein DN38).

GN NAP1L1 OR NRP.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]\_TaxID=10090;

RP SEQUENCE FROM N.A.

RA Okuda A.;

RL Submitted (JUL-1992) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=liver;

RX MEDLINE=22354683; PubMed=12466851;

RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Schriml L.M., Kanapin A., Mateuda H., Batalov S., Beisel K.W.,

RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,

RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Grimmer S., Gustinch S., Hirokawa N., Jackson I.J., Jarvis E.D.,

RA Kanai A., Kawai H., Kawasawa Y., Kedzierka R.M., King B.L.,

RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RA Nagashima T., Numata K., Okido T., Pavan W.J., Perte G., Pesole G.,

RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,

RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

RA Verrardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,

RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,

RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,

RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,

RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,

RA Hara A., Hashizume W., Inotani K., Ishii Y., Itoh M., Kagawa I.,

RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,

RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,

RA Birney E., Hayashizaki Y.;

RT "Analysis of the mouse transcriptome based on functional annotation of

RT 60,770 full-length cDNAs.;"

RL Nature 420:563-573 (2002).

RN [3]

RP SEQUENCE OF 50-391 FROM N.A.

RC STRAIN=BALB/c; TISSUE=Brain;

RA Kato K.;

RT "A collection of cDNA clones with specific expression patterns in

RT mouse brain.;"

RL Eur. J. Neurosci. 2:704-711 (1991).

CC -!- FUNCTION: May be involved in modulating chromatin formation and

CC contribute to regulation of cell proliferation.

CC -!- SUBCELLULAR LOCATION: Nuclear.

CC -!- TISSUE SPECIFICITY: High expression in cerebral cortex, not in

CC cerebellar cortex.

CC -!- DOMAIN: The acidic domains are probably involved in the

CC interaction with histones.

CC -!- SIMILARITY: Belongs to the nucleosome assembly protein (NAP)

CC family.

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CC -----

CC EMBL; Y09536; CAA70731.1; -.

CC HAMAP; MF\_00220; -; 1.

CC InterPro; IPR006680; Amidohydro 1.

CC InterPro; IPR004722; Pept\_M38\_dHOMult.

CC InterPro; IPR002195; Pept\_M38\_nph.

CC InterPro; IPR005847; Pept\_M38\_regn.

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CC -----

CC EMBL; D12618; BAA02142.1; -.

CC EMBL; X61449; CAA43689.1; -.

CC EMBL; AK050375; BAC34219.1; -.

CC FIR; JS0707; JS0707.

CC MGD; MGI:1855693; Nap1l1.

CC InterPro; IPR002164; NAP\_family.

CC Pfam; PF00956; NAP; 1.

CC Nuclear protein.

CC DOMAIN 11 30 ASP/GLU-RICH (ACIDIC).

CC DOMAIN 129 145 ASP/GLU-RICH (ACIDIC).

CC DOMAIN 348 378 ASP/GLU-RICH (ACIDIC).

CC DOMAIN 273 279 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

CC CONFLICT 377 390 YDPKQONPAECKQ -> MTQRRITQPSASSSE (IN

CC REF. 3).

CC SEQUENCE 391 AA; 45345 MW; 48F17F3A44D9A597 CRC64;

CC -----

CC Query Match 100.0%; Score 28; DB 1; Length 391;

CC Best Local Similarity 100.0%; Pred. No. 96;

CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC -----

CC QY 1 LXEKAK 6

CC Db 146 LXEKAK 151

CC -----

CC RESULT 12

CC PYRC THEAQ

CC ID PYRC THEAQ STANDARD; PRT; 426 AA.

CC AC P96081;

CC DT 15-JUL-1998 (Rel. 36, Created)

CC DT 15-JUL-1998 (Rel. 36, Last sequence update)

CC DT 10-OCT-2003 (Rel. 42, Last annotation update)

CC DE Dihydroorotase (EC 3.5.2.3) (DHOase).

CC GN PYRC.

CC OS Thermus aquaticus.

CC Bacteria; Deinococcus-Thermus; Deinococci; Thermaceae;

CC Thermus.

CC NCBI\_TaxID=271;

CC [1]

CC RP SEQUENCE FROM N.A.

CC RC STRAIN=Z05;

CC MEDLINE=97315215; PubMed=9171389;

CC RA van de Castele M., Chen P., Roovers M., Legrain C., Glansdorff N.;

CC RT "Structure and expression of a pyrimidine gene cluster from the

CC extreme thermophile Thermus strain Z05.;"

CC RL J. Bacteriol. 179:3470-3481 (1997).

CC -!- CATALYTIC ACTIVITY: (S)-dihydroorotate + H(2)O = N-carbamoyl-L-

CC aspartate.

CC -!- COFACTOR: Binds 2 zinc ions per subunit (By similarity).

CC -!- PATHWAY: Pyrimidine biosynthesis; third step.

CC -!- SUBUNIT: Homodimer (By similarity).

CC -!- SIMILARITY: Belongs to the DHOase family. Subfamily 2.

CC -----

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CC -----

CC EMBL; Y09536; CAA70731.1; -.

CC HAMAP; MF\_00220; -; 1.

CC InterPro; IPR006680; Amidohydro 1.

CC InterPro; IPR004722; Pept\_M38\_dHOMult.

CC InterPro; IPR002195; Pept\_M38\_nph.

CC InterPro; IPR005847; Pept\_M38\_regn.

CC -----

```

DR Pfam; PF01979; Amidohydro 1; 1.
DR ProDom; PD000518; Urease; 1.
DR TIGRPFAMs; TIGR00857; pyrC_multi; 1.
DR PROSITE; PS00482; DIHYDROOROTASE_1; 1.
DR PROSITE; PS00483; DIHYDROOROTASE_2; 1.
KW Pyrimidine biosynthesis; Hydrolase; Metal-binding; Zinc.
FT METAL 55 55 ZINC 1 (BY SIMILARITY).
FT METAL 57 57 ZINC 1 (BY SIMILARITY).
FT METAL 174 174 ZINC 2 (BY SIMILARITY).
FT METAL 233 233 ZINC 2 (BY SIMILARITY).
FT METAL 306 306 ZINC 1 (BY SIMILARITY).
SQ SEQUENCE 426 AA; 45929 MW; B957DD829F3E227F CRC64;

Query Match 100.0%; Score 28; DB 1; Length 426;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
Db 103 LKEKAK 108

RESULT 13
TIG_CLOAB
ID TIG_CLOAB STANDARD; PRT; 431 AA.
AC Q97F6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Trigger factor (TF).
GN TIG OR CAC2641.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
RA Noelling J., Breton G., Ometchenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA Bennett G.N., Koonin E.V., Smith D.R.;
RT "Genome sequence and comparative analysis of the solvent-producing
RT bacterium Clostridium acetobutylicum.";
RL J. Bacteriol. 183:4823-4838(2001).
CC -!- FUNCTION: Involved in protein export. Acts as a chaperone by
CC maintaining the newly synthesized protein in an open conformation
CC (By similarity).
CC -!- SIMILARITY: Belongs to the FKBP-type PPIase family. Tig subfamily.
CC
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CC
CC EMBL; AE007761; AAK80588.1; -.
CC PIR; A97225; A97225.
CC HAMAP; MF_00303; -.
CC InterPro; IPR001179; FKBP_PPIase.
CC InterPro; IPR005215; Trig_fac.
CC InterPro; IPR008880; Trigger_C.
CC InterPro; IPR008881; Trigger_N.
CC Pfam; PF00254; FKBP; 1.
CC Pfam; PF05698; Trigger_C; 1.
CC Pfam; PF05697; Trigger_N; 1.
CC TIGRPFAMs; TIGR001115; tig; 1.
CC PROSITE; PS00453; FKBP_PPIASE_1; FALSE_NEG.
CC PROSITE; PS00454; FKBP_PPIASE_2; FALSE_NEG.
CC PROSITE; PS00059; FKBP_PPIASE_3; 1.

KW Cell division; Chaperone; Isomerase; Rotamase; Complete proteome.
FT DOMAIN 164 249 PPIASE, FKBP-TYPE.
SQ SEQUENCE 431 AA; 49539 MW; 2B620438ADEA6285 CRC64;

Query Match 100.0%; Score 28; DB 1; Length 431;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
Db 379 LKEKAK 384

RESULT 14
Y830_THENA
ID Y830_THENA STANDARD; PRT; 434 AA.
AC Q9WZT7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Hypothetical protein TW0830.
GN TW0830.
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OX NCBI_TaxID=2336;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MSB8 / DSM 3109 / ATCC 43589;
RX MEDLINE=99287316; PubMed=10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L., Uterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA Stewart A.M., Coston M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
RT genome sequence of Thermotoga maritima.";
RL Nature 399:323-329(1999).
CC -!- SIMILARITY: Belongs to the UPF0004 family.
CC
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CC
CC EMBL; AE001750; AAD35912.1; -.
CC PIR; B72328; B72328.
CC TIGR; TW0830; -.
CC InterPro; IPR006638; Elp3.
CC InterPro; IPR006467; Miab_like_C.
CC InterPro; IPR007197; Radical_SAM.
CC InterPro; IPR005839; UPF0004.
CC Pfam; PF04055; Radical_SAM; 1.
CC Pfam; PF00919; UPF0004; 1.
CC SMART; SM00729; Elp3; 1.
CC TIGRPFAMs; TIGR01579; Miab-like-C; 1.
CC TIGRPFAMs; TIGR00089; TIGR00089; 1.
CC PROSITE; PS01278; UPF0004; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 434 AA; 49324 MW; C33186CD10545B20 CRC64;

Query Match 100.0%; Score 28; DB 1; Length 434;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
Db 352 LKEKAK 357

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RESULT 15
ENG_UREPA
ID ENG_UREPA STANDARD; PRT; 442 AA.
AC Q9PQA7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE GTP-binding protein engA.
GN ENG OR U0383.
OS Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma.
OX NCBI_TaxID=134821;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Serovar 3;
RX MEDLINE=20500219; PubMed=11048724;
RA Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y.,
RA Cassell G.H.;
RT "The complete sequence of the mucosal pathogen Ureaplasma
urealyticum."
RL Nature 407:757-762(2000).
CC -!- FUNCTION: GTPase of unknown physiological role.
CC -!- SIMILARITY: Belongs to the era/trmE family of GTP-binding
CC proteins. EngA subfamily.
CC
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CC
CC -----
CC EMBL; AEO02135; AAF30793.1; -.
CC DR HAMAP; MF 00195; -.
CC DR InterPro; IPR005289; GTP-binding_dom.
CC DR InterPro; IPR006073; GTP_OBG.
CC DR InterPro; IPR002917; MMR_HSR1.
CC DR InterPro; IPR005225; Small_GTP.
CC DR Pfam; PF01926; MMR_HSR1; 1.
CC DR PRINTS; PR00326; GTP_OBG.
CC DR TIGRFAMS; TIGR00650; MG442; 2.
CC DR TIGRFAMS; TIGR00231; small_GTP; 2.
CC KW GTP-binding; Repeat; Complete proteome.
FT NP_BIND 8 15 GTP 1 (POTENTIAL).
FT NP_BIND 55 59 GTP 1 (POTENTIAL).
FT NP_BIND 119 122 GTP 1 (POTENTIAL).
FT NP_BIND 181 188 GTP 2 (POTENTIAL).
FT NP_BIND 228 232 GTP 2 (POTENTIAL).
FT NP_BIND 293 296 GTP 2 (POTENTIAL).
SQ SEQUENCE 442 AA; 50547 MW; 11D7C67C92902932 CRC64;

Query Match 100.0%; Score 28; DB 1; Length 442;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
Db 105 LKEKAK 110
|||||

RESULT 16
UFOG_GENTR
ID UFOG_GENTR STANDARD; PRT; 453 AA.
AC Q96493;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Flavonol 3-O-glucosyltransferase (EC 2.4.1.91) (UDP-glucose flavonoid
DE 3-O-glucosyltransferase)
OS Gentiana triflora (Clustered gentian).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;

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OC lamids; Gentianales; Gentianaceae; Gentiana.
OX NCBI_TaxID=55190;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Petal;
RX MEDLINE=96416435; PubMed=8819318;
RA Tanaka Y., Yonekura K., Fukuchi-Mizutani M., Fukui Y.,
RA Fujiwara H., Ashikari T., Kusumi T.;
RT "Molecular and biochemical characterization of three anthocyanin
RT synthetic enzymes from Gentiana triflora."
RL Plant Cell Physiol. 37:711-716(1996).
CC -!- FUNCTION: In the presence of other necessary color factors, this
CC glycosylation reaction allows the accumulation of anthocyanin
CC pigments (by similarity).
CC -!- CATALYTIC ACTIVITY: UDP-glucose + a flavonol = UDP + flavonol
CC 3-O-D-glucoside.
CC -!- PATHWAY: Anthocyanin biosynthesis.
CC -!- SIMILARITY: Belongs to the UDP-glycosyltransferase family.
CC
CC -----
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CC
CC -----
CC EMBL; D85186; BAAL2737.1; -.
CC DR InterPro; IPR002213; UDP_gluco_trans.
CC DR Pfam; PF00201; UDPGT_1.
CC DR PROSITE; PS00375; UDPGT; 1.
CC KW Transferase; Glycosyltransferase.
CC SQ SEQUENCE 453 AA; 50009 MW; BF738B0A2DA76C05 CRC64;

Query Match 100.0%; Score 28; DB 1; Length 453;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6.
Db 423 LKEKAK 428
|||||

RESULT 17
ATP0_PHAVU
ID ATP0_PHAVU STANDARD; PRT; 508 AA.
AC P24459;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE ATP synthase alpha chain, mitochondrial (EC 3.6.3.14).
GN ATPA.
OS Phaseolus vulgaris (Kidney bean) (French bean).
OG Mitochondrion.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.
OX NCBI_TaxID=3885;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93046798; PubMed=1423717;
RA Chase C.D., Ortega V.M.;
RT "Organization of ATPA coding and 3' flanking sequences associated
RT with cytoplasmic male sterility in Phaseolus vulgaris L.;"
RL Curr. Genet. 22:147-153(1992).
CC -!- FUNCTION: Produces ATP from ADP in the presence of a proton
CC gradient across the membrane. The alpha chain is a regulatory
CC subunit.
CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (in) = ADP + phosphate +
CC H(+) (out).
CC -!- SUBUNIT: F-type ATPases have 2 components, CF(1) - the catalytic
CC core - and CF(0) - the membrane proton channel. CF(1) has five
CC subunits: alpha(3), beta(3), gamma(1), delta(1), epsilon(1). CF(0)

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CC      has three main subunits: a, b and c.
CC      -!- SUBCELLULAR LOCATION: Mitochondrial.
CC      -!- SIMILARITY: Belongs to the ATPase alpha/beta chains family.
CC
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CC
CC      EMBL; M64246; AAB01582.1; -.
CC      PIR; S26979; S26979.
CC      HSSP; P19483; 1BME.
CC      InterPro; IPR005294; ATP_synthF1_alph.
CC      InterPro; IPR000793; ATPase_a/b_C.
CC      InterPro; IPR000194; ATPase_a/bCentre.
CC      InterPro; IPR004100; ATPase_a/bN.
CC      InterPro; IPR000790; ATPase_a_C.
CC      InterPro; IPR009005; F1_ATPase_a/bN.
CC      Pfam; PF00006; ATP-synt_ab; 1.
CC      Pfam; PF00306; ATP-synt_ab_C; 1.
CC      Pfam; PF02874; ATP-synt_ab_N; 1.
CC      ProDom; PD001099; ATPase_aC; 1.
CC      TIGRfam; TIGR00962; atpA; 1.
CC      PROSITE; PS00152; ATPASE_ALPHA_BETA; 1.
CC      ATP synthesis; CF(1); Hydrogen ion transport;
KW      Hydrolyase; ATP-binding; Mitochondrion.
FT      NP BIND 171 178 ATP (BY SIMILARITY).
FT      ACT SITE 373 373 BY SIMILARITY.
SQ      SEQUENCE 508 AA; 55344 MW; 2198F396E8C0A79 CRC64;

Query Match 100.0%; Score 28; DB 1; Length 508;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
DB 499 LKEKAK 504

RESULT 18
THIC_BACSU STANDARD; PRT; 590 AA.
AC P45740; P71090;
DT 01-NOV-1995 (Rel. 32, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Thiamine biosynthesis protein thic.
GN THIC OR THIA OR BSU08790.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Zhang Y., Begley T.P.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=97346037; PubMed=9202460;
RA Cummings N.J., Connerton I.F.;
RT "The Bacillus subtilis 168 chromosome from sspE to katA.";
RL Microbiology 143:1855-1859(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borries R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,

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RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
RA Guisepi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinols S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Furnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Yasumoto K., Yata K.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis".
RL Nature 390:249-256(1997).
CC      -!- FUNCTION: Required for the synthesis of the hydromethylpyrimidine
CC      (HMP) moiety of thiamine (4-amino-2-methyl-5-
CC      hydroxymethylpyrimidine) (By similarity).
CC      -!- PATHWAY: Thiamine biosynthesis.
CC      -!- SIMILARITY: Belongs to the thic family.
CC
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CC
CC      EMBL; U26178; AAA68243.1; -.
CC      EMBL; 282044; CAB04805.1; -.
CC      EMBL; 299108; CAB12707.1; -.
CC      PIR; D69722; D69722.
CC      Subtilist; BG11246; thic.
CC      HAMAP; MF_00089; -.
CC      InterPro; IPR002817; Thic.
CC      Pfam; PF01964; Thic; 1.
CC      ProDom; PD007048; Thic; 1.
CC      TIGRfam; TIGR00190; thic; 1.
CC      Thiamine biosynthesis; Complete proteome.
KW Thiamine biosynthesis; Complete proteome.
FT CONFLICT 140 140 K -> Q (IN REF. 1).
FT CONFLICT 170 174 AIIP -> RLFLP (IN REF. 1).
FT CONFLICT 334 334 F -> L (IN REF. 1).
FT CONFLICT 547 547 C -> G (IN REF. 1).
SQ SEQUENCE 590 AA; 65916 MW; E43A62C6B8A530E2 CRC64;

Query Match 100.0%; Score 28; DB 1; Length 590;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
DB 574 LKEKAK 579

RESULT 19
ORA_PLAFN STANDARD; PRT; 701 AA.
ID ORA_PLAFN
AC P16405;
DT 01-AUG-1990 (Rel. 15, Created)

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DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Octapeptide-repeat antigen (ORA) (Fragment).  
 OS Plasmodium falciparum (isolate NF7 / Ghana).  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 ON NCBI\_TaxID=5842;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89181826; PubMed=2564637;  
 RA Favaloro J.M., Marshall V.M., Crewther P.E., Coppel R.L.,  
 RA Kemp D.J., Anders R.F.;  
 RT "cDNA sequence predicting an octapeptide-repeat antigen of Plasmodium  
 RT falciparum";  
 RL Mol. Biochem. Parasitol. 32:297-299(1989).  
 CC -I- SUBCELLULAR LOCATION: Probably in the parasitophorous  
 CC vacuole.  
 CC -I- DEVELOPMENTAL STAGE: In trophozoites, schizonts, and  
 CC merozoites.  
 CC -I- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme  
 CC family.  
 CC -----  
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 CC -----  
 CC EMBL; J04007; AAA29713.1; --  
 DR InterPro; IPR000873; AMP-bind.  
 DR Pfam; PF00501; AMP-binding; 1.  
 DR PROSITE; PS00455; AMP BINDING; 1.  
 KW Repeat; Glycoprotein; Antigen.  
 FT NON\_TER 1  
 FT DOMIN 653 700 6 X 8 AA APPROXIMATE TANDEM REPEATS.  
 FT REPEAT 653 660 1.  
 FT REPEAT 661 668 2.  
 FT REPEAT 669 676 3.  
 FT REPEAT 677 684 4.  
 FT REPEAT 685 692 5.  
 FT REPEAT 693 700 6.  
 FT CARBOHYD 40 40 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 41 41 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 76 76 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 111 111 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 127 127 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 139 139 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 181 181 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 189 189 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 311 311 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 334 334 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 344 344 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 477 477 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 557 557 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT NON\_TER 701 701  
 SQ SEQUENCE 701 AA; 79048 MW; 0E4AB302011391C CRC64;  
 Query Match 100.0%; Score 28; DB 1; Length 701;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LKEKAK 6  
 |||||  
 DB 165 LKEKAK 170  
 RESULT 20  
 ID CFAH HUMAN STANDARD; PRT; 1231 AA.  
 AC P08603; P78435; Q14570; Q9NU86;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Complement factor H precursor (H factor 1).  
 GN HF1 OR HF OR CFH.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 ON NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND VARIANT TYR-402.  
 RC TISSUE=Liver;  
 RX MEDLINE=88134059; PubMed=2963625;  
 RA Ripoché J., Day A.J., Harris T.J.R., Sim R.B.;  
 RT "The complete amino acid sequence of human complement factor H";  
 RL Biochem. J. 249:593-602(1988).  
 RN [2]  
 RP SEQUENCE OF 53-445 FROM N.A.  
 RX MEDLINE=87054207; PubMed=2946589;  
 RA Schulz T.P., Schwaible W., Stanley K.K., Weiss E., Dierich M.P.;  
 RT "Human complement factor H: isolation of cDNA clones and partial cDNA  
 RT sequence of the 38-kDa tryptic fragment containing the binding site  
 RT for C3b";  
 RL Eur. J. Immunol. 16:1351-1355(1986).  
 RN [3]  
 RP SEQUENCE OF 236-449 FROM N.A., AND PARTIAL SEQUENCE.  
 RX MEDLINE=86169701; PubMed=2937845;  
 RA Kristensen T., Wetsel R.A., Tack B.F.;  
 RT "Structural analysis of human complement protein H: homology with C4b  
 RT binding protein, beta 2-glycoprotein I, and the Ba fragment of B2";  
 RL J. Immunol. 136:3407-3411(1986).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM 2).  
 RA Bird C.;  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE OF 1047-1231 FROM N.A.  
 RX MEDLINE=91201892; PubMed=1826708;  
 RA Esteller C., Koistinen V., Schwaible W., Dierich M.P., Weiss E.H.;  
 RT "Cloning of the 1.4-kb mRNA species of human complement factor H  
 RT reveals a novel member of the short consensus repeat family related  
 RT to the carboxy terminal of the classical 150-kDa molecule";  
 RL J. Immunol. 146:3190-3196(1991).  
 RN [6]  
 RP SEQUENCE OF 19-35.  
 RX MEDLINE=83048213; PubMed=6215918;  
 RA Sim R.B., Discipio R.G.;  
 RT "Purification and structural studies on the complement-system control  
 RT protein beta 1H (Factor H)";  
 RL Biochem. J. 205:285-293(1982).  
 RN [7]  
 RP SEQUENCE OF 1-19 FROM N.A.  
 RA Vik D.P., Williams S.A.;  
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.  
 RN [8]  
 RP SEQUENCE OF 1-9 FROM N.A.  
 RA Dominguez O.;  
 RL Thesis (1993), Hospital Trias I Pujol, Spain.  
 RN [9]  
 RP STRUCTURE BY NMR OF 927-985 (SUSHI 16).  
 RX MEDLINE=91278097; PubMed=1829116;  
 RA Norman D.G., Barlow P.N., Baron M., Day A.J., Sim B., Campbell I.D.;  
 RT "Three-dimensional structure of a complement control protein module  
 RT in solution";  
 RL J. Mol. Biol. 219:717-725(1991).  
 RN [10]  
 RP STRUCTURE BY NMR OF 264-322 (SUSHI 5).  
 RX MEDLINE=92232649; PubMed=1533152;  
 RA Barlow P.N., Norman D.G., Steinkasserer A., Horne T.J., Pearce J.,  
 RA Driscoll P.C., Sim B., Campbell I.D.;  
 RT "Solution structure of the fifth repeat of factor H: a second example  
 RT of the complement control protein module";  
 RL Biochemistry 31:3626-3634(1992).  
 RN [11]  
 RP STRUCTURE BY NMR OF 866-985 (SUSHI 15 AND 16).

```

RX MEDLINE=93323119; PubMed=8331663;
RA Barlow P.N., Steinkasserer A., Norman D.G., Kieffer B., Wiles A.P.,
RA Sim B., Campbell I.D.;
RT "Solution structure of a pair of complement modules by nuclear
magnetic resonance.";
RL J. Mol. Biol. 232:268-284(1993).
CC -!- FUNCTION: Factor H functions as a cofactor in the inactivation of
CC C3b by factor I and also increases the rate of dissociation of the
CC C3bb complex (C3 convertase) and the (C3b)NBB complex (C5
CC convertase) in the alternative complement pathway.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P08603-1; Sequence=Displayed;
CC Name=2; Synonyms=FHL-1;
CC IsoId=P08603-2; Sequence=VSP_001190, VSP_001191;
CC -!- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
CC -!- SIMILARITY: Contains 20 Sushi (SCR) domains.
CC -!- CAUTION: Ref.2 sequence differs from that shown due to a
CC frameshift in position 341.
CC -----
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CC -----
DR EMBL; Y00716; CAA68704.1; -;
DR EMBL; X04697; CAB41739.1; ALT_FRAME.
DR EMBL; X07523; CAA30403.1; -;
DR EMBL; M12383; AAA52013.1; -;
DR EMBL; AL049744; -; NOT_ANNOTATED_CDS.
DR EMBL; M65294; AAA35948.1; -;
DR EMBL; U56979; AAB01987.1; -;
DR EMBL; Z29665; CAA82763.1; -;
DR FIR; S0254; NBH0H.
DR FIR; S03013; NBH0H.
DR PDB; 1HCC; 15-APR-92.
DR PDB; 1HFI; 15-JUL-93.
DR PDB; 1HFI; 15-JUL-93.
DR PDB; 1HAQ; 05-APR-02.
DR PDB; 1KOV; 23-JAN-02.
DR Genew; HGNC:4883; HFI.
DR MIM; 134370; -;
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0003811; F:complement activity; TAS.
DR GO; GO:0006956; P:complement activation; TAS.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00084; sushi; 20.
DR SMART; SM00032; CCP; 20.
KW Complement alternate pathway; Plasma; Glycoprotein; Repeat; Sushi;
KW Signal; 3D-structure; Polymorphism; Alternative splicing.
FT SIGNAL 1 18
FT CHAIN 19 1231 COMPLEMENT FACTOR H.
FT DOMAIN 20 81 SUSHI 1.
FT DOMAIN 84 142 SUSHI 2.
FT DOMAIN 145 206 SUSHI 3.
FT DOMAIN 209 263 SUSHI 4.
FT DOMAIN 266 321 SUSHI 5.
FT DOMAIN 324 386 SUSHI 6.
FT DOMAIN 388 443 SUSHI 7.
FT DOMAIN 447 506 SUSHI 8.
FT DOMAIN 508 565 SUSHI 9.
FT DOMAIN 568 624 SUSHI 10.
FT DOMAIN 629 685 SUSHI 11.
FT DOMAIN 690 745 SUSHI 12.
FT DOMAIN 752 804 SUSHI 13.
FT DOMAIN 810 865 SUSHI 14.
FT DOMAIN 869 927 SUSHI 15.
FT DOMAIN 930 985 SUSHI 16.

```

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FT DOMAIN 988 1044 SUSHI 17.
FT DOMAIN 1047 1103 SUSHI 18.
FT DOMAIN 1108 1164 SUSHI 19.
FT DOMAIN 1166 1229 SUSHI 20.
FT DISULFID 21 66 BY SIMILARITY.
FT DISULFID 52 80 BY SIMILARITY.
FT DISULFID 85 129 BY SIMILARITY.
FT DISULFID 114 141 BY SIMILARITY.
FT DISULFID 146 192 BY SIMILARITY.
FT DISULFID 178 205 BY SIMILARITY.
FT DISULFID 210 251 BY SIMILARITY.
FT DISULFID 237 262 BY SIMILARITY.
FT DISULFID 267 309 BY SIMILARITY.
FT DISULFID 294 320 BY SIMILARITY.
FT DISULFID 325 374 BY SIMILARITY.
FT DISULFID 357 385 BY SIMILARITY.
FT DISULFID 389 431 BY SIMILARITY.
FT DISULFID 416 442 BY SIMILARITY.
FT DISULFID 448 494 BY SIMILARITY.
FT DISULFID 477 505 BY SIMILARITY.
FT DISULFID 509 553 BY SIMILARITY.
FT DISULFID 536 564 BY SIMILARITY.
FT DISULFID 569 611 BY SIMILARITY.
FT DISULFID 623 673 BY SIMILARITY.
FT DISULFID 630 673 BY SIMILARITY.
FT DISULFID 659 684 BY SIMILARITY.
FT DISULFID 691 733 BY SIMILARITY.
FT DISULFID 719 744 BY SIMILARITY.
FT DISULFID 753 792 BY SIMILARITY.
FT DISULFID 781 803 BY SIMILARITY.
FT DISULFID 811 853 BY SIMILARITY.
FT DISULFID 839 864 BY SIMILARITY.
FT DISULFID 870 915 BY SIMILARITY.
FT DISULFID 901 926 BY SIMILARITY.
FT DISULFID 931 973 BY SIMILARITY.
FT DISULFID 959 984 BY SIMILARITY.
FT DISULFID 989 1032 BY SIMILARITY.
FT DISULFID 1018 1043 BY SIMILARITY.
FT DISULFID 1048 1091 BY SIMILARITY.
FT DISULFID 1077 1102 BY SIMILARITY.
FT DISULFID 1109 1152 BY SIMILARITY.
FT DISULFID 1138 1163 BY SIMILARITY.
FT DISULFID 1167 1218 BY SIMILARITY.
FT DISULFID 1201 1228 BY SIMILARITY.
FT CARBOHYD 529 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 718 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 802 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 822 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 882 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 911 N-LINKED (GLCNAC. .) (POTENTIAL).

```

Query Match 100.0%; Score 28; DB 1; Length 1231;

Best Local Similarity 100.0%; Pred. No. 2.7e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKEKAK 6

Db 469 LKEKAK 474

RESULT 21

MYM1\_HUMAN

ID MYM1\_HUMAN STANDARD; PRT; 1451 AA.

AC F521779;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Myomesin 1 (190 kDa titin-associated protein) (190 kDa connectin-associated protein).

DE M1OM1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.





frameshift in position 1478.  
 -!- CAUTION: Ref.4 sequence differs from that shown due to erroneous gene model prediction.

-----  
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 -----

EMBL; AF084479; RAD08675.1; -  
 EMBL; AF072810; RAC97879.1; ALT\_FRAME.  
 EMBL; AB032253; BRA89210.1; ALT\_FRAME.  
 EMBL; AC005074; AAD04720.1; ALT\_SEQ.  
 EMBL; AC005089; -; NOT\_ANNOTATED\_CDS.  
 HSSP; Q92831; 1B91.  
 TRANSFAC; T04145; -.  
 Genew; HGNC:961; BAZ1B.  
 MIM; 605681; -; C.nucleus; NAS.  
 GO; GO:0005634; -; C.nucleus; NAS.  
 GO; GO:0003700; F:transcription factor activity; NAS.  
 GO; GO:0008270; F:zinc ion binding; NAS.  
 GO; GO:0006350; P:transcription; NAS.  
 InterPro; IPR001487; Bromodomain.  
 InterPro; IPR004022; DDT\_dom.  
 InterPro; IPR001965; Znf\_PHD.  
 Pfam; PF00439; bromodomain; 1.  
 Pfam; PF00628; PHD; 1.  
 PRINTS; PR00503; BROMODOMAIN.  
 SMART; SM00297; BROMO; 1.  
 SMART; SM00571; DDT; 1.  
 SMART; SM00249; PHD; 1.  
 PROSITE; PS00633; BROMODOMAIN\_1; FALSE\_NEG.  
 PROSITE; PS00114; BROMODOMAIN\_2; 1.  
 PROSITE; PS00827; DDT; 1.  
 PROSITE; PS01359; ZF\_PHD\_1; 1.  
 PROSITE; PS00016; ZF\_PHD\_2; 1.  
 Transcription regulation; Bromodomain; Zinc-finger; Coiled coil;  
 Nuclear protein; Alternative splicing; Williams-Beuren syndrome.  
 FT DOMAIN 20 126 WAC.  
 FT DOMAIN 604 668 DDT.  
 FT ZN\_FING 1184 1234 PHD-TYPE.  
 FT DOMAIN 1356 1426 BROMODOMAIN.  
 FT DOMAIN 306 578 LYS-RICH.  
 FT DOMAIN 533 586 COILED COIL (POTENTIAL).  
 FT DOMAIN 768 814 COILED COIL (POTENTIAL).  
 FT DOMAIN 850 893 COILED COIL (POTENTIAL).  
 FT DOMAIN 1245 1283 COILED COIL (POTENTIAL).  
 FT DOMAIN 1261 1273 Poly-Glu.  
 FT VARSPIC 660 663 Missing (in isoform 2).  
 FT CONFLICT 14 14 K -> N (IN REF. 3).  
 FT CONFLICT 22 22 L -> F (IN REF. 3).  
 FT CONFLICT 136 136 K -> E (IN REF. 1).  
 FT CONFLICT 191 191 N -> D (IN REF. 4).  
 FT CONFLICT 298 298 Y -> V (IN REF. 4).  
 FT CONFLICT 823 823 E -> R (IN REF. 3).  
 FT CONFLICT 1191 1191 R -> P (IN REF. 3).  
 FT CONFLICT 1354 1354 K -> M (IN REF. 2).  
 FT CONFLICT 1438 1438 A -> V (IN REF. 3).  
 SQ SEQUENCE 1483 AA; 170902 MW; 0CC146FEBB954261 CRC64;

Query Match 100.0%; Score 28; DB 1; Length 1483;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
 |||||  
 Db 558 LKEKAK 563

RESULT 23  
 MAPB RAT  
 ID MAPB RAT STANDARD; PRT; 2459 AA.  
 AC P15205; Q62958; Q9ER21; Q9QW92;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Microtubule-associated protein 1B (MAP 1B) (Neuraxin) [Contains: MAP1  
 DE light chain LCL].  
 GN MAP1B.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE OF 1-142 FROM N.A.  
 RC STRAIN=Sprague-Dawley; TISSUE=Testis;  
 RX MEDLINE=96257242; PubMed=8666295;  
 RA Liu D., Fischer I.;  
 RT "Isolation and sequencing of the 5' end of the rat microtubule-  
 RT associated protein (MAP1B)-encoding cDNA.";  
 RL Gene 172:307-308(1996).  
 RN [2]  
 RP SEQUENCE OF 96-2459 FROM N.A., DOMAIN, AND INDUCTION.  
 RC STRAIN=Sprague-Dawley; TISSUE=Brain, and Gliat tumor;  
 RX MEDLINE=92347374; PubMed=1639092;  
 RA Zauner W., Kratz J., Staunton J., Feick P., Wiche G.;  
 RT Identification of two distinct microtubule binding domains on  
 RT recombinant rat MAP 1B.";  
 RL Eur. J. Cell Biol. 57:66-74(1992).  
 RN [3]  
 RP SEQUENCE OF 1541-2459 FROM N.A., AND TISSUE SPECIFICITY.  
 RC TISSUE=Spinal cord;  
 RX MEDLINE=90059871; PubMed=2555150;  
 RA Rienitz A., Grenningloh G., Hermans-Borgmeyer I., Kirsch J.,  
 RA Littauer U.Z., Prior P., Gundelfinger E.D., Schmitt B., Betz H.;  
 RT "Neuraxin, a novel putative structural protein of the rat central  
 RT nervous system that is immunologically related to microtubule-  
 RT associated protein 5.";  
 RL EMBO J. 8:2879-2888(1989).  
 RN [4]  
 RP DEVELOPMENTAL STAGE, AND PHOSPHORYLATION.  
 RX MEDLINE=97405699; PubMed=9260743;  
 RA Ma D., Nothias F., Boyne L.J., Fischer I.;  
 RT "Differential regulation of microtubule-associated protein 1B (MAP1B)  
 RT in rat CNS and PNS during development.";  
 RL J. Neurosci. Res. 49:319-332(1997).  
 CC -!- FUNCTION: The function of brain MAPS is essentially unknown.  
 CC Phosphorylated MAP1B may play a role in the cytoskeletal changes  
 CC that accompany neurite extension. Possibly MAP1B binds to at least  
 CC two tubulin subunits in the polymer, and this bridging of subunits  
 CC might be involved in nucleating microtubule polymerization and in  
 CC stabilizing microtubules.  
 CC -!- SUBUNIT: 3 different light chains, LC1, LC2 and LC3, can associate  
 CC with MAP1A and MAP1B proteins.  
 CC -!- TISSUE SPECIFICITY: Nervous system (spinal cord, brain stem,  
 CC cerebellum and cerebrum). Not expressed in liver, spleen, kidney,  
 CC heart or muscle.  
 CC -!- DEVELOPMENTAL STAGE: In cerebral cortex, spinal cord and sciatic  
 CC nerve levels are high early in development but decrease during  
 CC postnatal development and are low in adults. In dorsal root  
 CC ganglia levels remain high throughout development.  
 CC -!- INDUCTION: By nerve growth factor.  
 CC -!- DOMAIN: Has a highly basic region with many copies of the sequence  
 CC KKEE and KKEI/V, repeated but not at fixed intervals, which is  
 CC responsible for the binding of MAP1B to microtubules.  
 CC -!- PTM: LC1 is coexpressed with MAP1B. It is a polypeptide generated  
 CC from MAP1B by proteolytic processing. It is free to associate with  
 CC both MAP1A and MAP1B. It interacts with the amino-terminal region  
 CC of MAP1B (by similarity).  
 CC -!- PTM: Phosphorylated.  
 CC -!- SIMILARITY: TO MAP1A.  
 CC -!- CAUTION: A C-terminal fragment of this protein (residues 1597 to



2459) was originally described as neuraxin in Ref.3.

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 CC -----  
 CC EMBL; U52950; AAB17068.1; --  
 CC EMBL; X60370; CAC16162.1; --  
 CC EMBL; X16623; CAA34620.1; ALT\_SEQ.  
 CC PIR; A56577; A56577.  
 CC InterPro; IPR000102; MAP1B\_neuraxin.  
 CC Pfam; PF00414; MAP1B\_neuraxin; 10.  
 CC PROSITE; PS00230; MAP1B\_NEURAXIN; 8.  
 CC Microtubule; Repeat; Phosphorylation.  
 CC CHAIN ? 2459  
 CC REPEAT 1869 1885  
 CC REPEAT 1886 1902  
 CC REPEAT 1903 1919  
 CC REPEAT 1920 1936  
 CC REPEAT 1937 1953  
 CC REPEAT 1954 1970  
 CC REPEAT 1988 2004  
 CC REPEAT 2005 2021  
 CC REPEAT 2022 2038  
 CC REPEAT 2039 2055  
 CC DOMAIN 559 1035  
 CC DOMAIN 588 786  
 CC LYS-RICH (HIGHLY BASIC, CONTAINS MANY  
 CC KEE AND KKEI/V REPEATS).  
 CC LYS-RICH.  
 CC M -> V (IN REF. 1).  
 CC T -> S (IN REF. 1).  
 CC R -> K (IN REF. 3).  
 CC L -> I (IN REF. 3).  
 CC SEQUENCE 2459 AA; 269497 MW; 2E3F6872DEDB8BA2 CRC64;  
 CC  
 CC Query Match 100.0%; Score 28; DB 1; Length 2459;  
 CC Best Local Similarity 100.0%; Pred. No. 5e+02;  
 CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC QY 1 LKEKAK 6  
 CC |||||  
 CC Db 2230 LKEKAK 2235  
 CC  
 CC RESULT 24  
 CC RBPI\_PLAVB STANDARD; PRT; 2869 AA.  
 CC AC Q00798;  
 CC DT 01-APR-1993 (Rel. 25, Created)  
 CC DT 01-APR-1993 (Rel. 25, Last sequence update)  
 CC DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 CC DE Reticulocyte binding protein 1 precursor.  
 CC GN RBPI.  
 CC OS Plasmodium vivax (strain Belem).  
 CC OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 CC OX NCBI\_TaxID=31273;  
 CC RN [1]  
 CC RP MEDLINE=92315338; PubMed=1617731;  
 CC RA Galinski M.R., Medina C.C., Ingravallo P., Barnwell J.W.;  
 CC RT "A reticulocyte-binding protein complex of Plasmodium vivax  
 CC merozoites";  
 CC RL Cell 69:1213-1226(1992).  
 CC CC -!- FUNCTION: Involved in reticulocyte adhesion. Specifically binds to  
 CC human reticulocyte cells.  
 CC CC -!- SUBUNIT: Homodimer (Potential).  
 CC CC -!- SUBCELLULAR LOCATION: Membrane-bound.  
 CC -----  
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 CC -----  
 CC EMBL; M88097; AAA29743.1; --  
 CC Malaria; Receptor; Signal; Transmembrane.  
 CC SIGNAL 1 17  
 CC CHAIN 18 2869  
 CC FT DOMAIN 18 2807  
 CC FT TRANSMEM 2808 2826  
 CC FT DOMAIN 2827 2869  
 CC FT SITE 1030 1032  
 CC FT SITE 2599 2601  
 CC SQ SEQUENCE 2869 AA; 330213 MW; B9DBE442205EBCFF CRC64;  
 CC  
 CC Query Match 100.0%; Score 28; DB 1; Length 2869;  
 CC Best Local Similarity 100.0%; Pred. No. 5.7e+02;  
 CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC QY 1 LKEKAK 6  
 CC |||||  
 CC Db 1623 LKEKAK 1628  
 CC  
 CC RESULT 25  
 CC VB02\_VACCC STANDARD; PRT; 219 AA.  
 CC ID VB02\_VACCC  
 CC AC P20599;  
 CC DT 01-FEB-1991 (Rel. 17, Created)  
 CC DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 CC DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 CC GN B2R.  
 CC OS Vaccinia virus (strain Copenhagen).  
 CC OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
 CC OC Orthopoxvirus.  
 CC OX NCBI\_TaxID=10249;  
 CC RN [1]  
 CC RP SEQUENCE FROM N.A.  
 CC RX MEDLINE=91021027; PubMed=2219722;  
 CC RA Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,  
 CC RA Paolletti E.;  
 CC RT "The complete DNA sequence of vaccinia virus";  
 CC RL Virology 179:247-266(1990).  
 CC RN [2]  
 CC RP COMPLETE GENOME.  
 CC RA Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,  
 CC RA Paolletti E.;  
 CC RT "Appendix to 'The complete DNA sequence of vaccinia virus'";  
 CC RL Virology 179:517-563(1990).  
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 CC -----  
 CC EMBL; M35027; AAA48196.1; --  
 CC PIR; A42526; A42526.  
 CC SQ SEQUENCE 219 AA; 24628 MW; EEDE3BB44C8F2A23 CRC64;  
 CC  
 CC Query Match 92.9%; Score 26; DB 1; Length 219;  
 CC Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
 CC Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC QY 1 LKEKAK 6  
 CC :|||  
 CC Db 141 IKEKAK 146

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CC -----
CC EMBL; M31660; AAA31577.1; -.
CC PIR; A40143; A40143.
CC PDB; 1F6F; 20-DEC-00.
CC InterPro; IPR001400; Somatotropin.
CC Pfam; PF00103; hormone; 1.
CC PRINTS; PR00836; SOMATOTROPIN.
CC PROSITE; PS00266; SOMATOTROPIN_1; 1.
CC PROSITE; PS00338; SOMATOTROPIN_2; 1.
CC KW Hormone; Placenta; Signal; 3D-structure.
CC FT SIGNAL 1 36 POTENTIAL.
CC FT CHAIN 37 236 PLACENTAL LACTOGEN.
CC FT DISULFID 97 212 BY SIMILARITY.
CC FT DISULFID 229 234 BY SIMILARITY.
CC SQ SEQUENCE 236 AA; 26695 MW; E6223AFE2FF9BB35 CRC64;

Query Match 92.9%; Score 26; DB 1; Length 236;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
Db 158 IREKAK 163

RESULT 28
LPSA_PASHA
ID LPSA_PASHA STANDARD; PRT; 263 AA.
AC Q05770;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Lipooligosaccharide biosynthesis protein lpsa (EC 2.---.-).
GN LPSA.
OS Pasteurella haemolytica.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Mannheimia.
OX NCBI_TaxID=75985;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Serotype A1;
RX MEDLINE=95301198; PubMed=7781993;
RA Potter M.D., Lo R.Y.C.;
RT "Cloning and characterization of a gene from Pasteurella haemolytica
RT A1 involved in lipopolysaccharide biosynthesis.";
RL FEMS Microbiol. Lett. 129:75-81(1995).
RN [2]
RP SEQUENCE OF 189-263 FROM N.A.
RC STRAIN=Serotype A1;
RX MEDLINE=91358346; PubMed=1885539;
RA Abdullah K.M., Lo R.Y.C., Mellors A.;
RT "Cloning, nucleotide sequence, and expression of the Pasteurella
RT haemolytica A1 glycoprotease gene.";
RL J. Bacteriol. 173:5597-5603(1991).
CC -!- FUNCTION: INVOLVED IN THE BIOSYNTHESIS OF A MOIETY ON THE CORE
CC -!- OF THE LIPOLYSACCHARIDE MOLECULE. ASSEMBLE AT THE INNER SURFACE
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC. ASSEMBLE AT THE INNER SURFACE
CC OF THE CYTOPLASMIC MEMBRANE (POTENTIAL).
CC -!- SIMILARITY: Belongs to the glycosyltransferase family 25.
CC -----
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CC -----
CC EMBL; U15958; AAA80283.1; -.
CC InterPro; IPR002654; Glyco.trans.25.
CC Pfam; PF01755; Glyco.transf.25; 1.
CC Lipopolysaccharide biosynthesis; Transferase; Glycosyltransferase.
CC KW
```

```
CC RESULT 26
CC VB02_VACCV STANDARD; PRT; 219 AA.
CC ID Q01225;
CC DT 01-APR-1993 (Rel. 25, Created)
CC DT 01-APR-1993 (Rel. 25, Last sequence update)
CC DT 01-APR-1993 (Rel. 25, Last annotation update)
CC DE Protein B2.
CC GN B2R.
CC OS Vaccinia virus (strain WR).
CC OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
CC Orthopoxvirus.
CC OX NCBI_TaxID=10254;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE=91259063; PubMed=2045793;
CC RA Smith G.L., Chan Y.S., Howard S.T.;
CC RT "Nucleotide sequence of 42 kbp of vaccinia virus strain WR from near
CC the right inverted terminal repeat.";
CC J. Gen. Virol. 72:1349-1376(1991).
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CC -----
CC EMBL; D11079; BAA01832.1; -.
CC PIR; JQ1796; JQ1796.
CC SQ SEQUENCE 219 AA; 24625 MW; 67D5099D4C9357B2 CRC64;

Query Match 92.9%; Score 26; DB 1; Length 219;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
Db 141 IREKAK 146

RESULT 27
PLL SHEEP
ID PLL SHEEP STANDARD; PRT; 236 AA.
AC P16038;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Placental lactogen precursor.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90114213; PubMed=2608069;
RA Colosi P., Thordarson G., Hellmiss R., Singh K., Forsyth I.A.,
RA Gluckman P., Wood W.I.;
RT "Cloning and expression of ovine placental lactogen.";
RL Mol. Endocrinol. 3:1462-1469(1989).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the somatotropin/prolactin family.
CC -----
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SQ SEQUENCE 263 AA; 30871 MW; B07C39EC1DA603A7 CRC64;  
 Query Match 92.9%; Score 26; DB 1; Length 263;  
 Best Local Similarity 83.3%; Pred. No. 1.8e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
 :|||||  
 DB 40 IREKAK 45

RESULT 29  
 FEN\_THAC  
 ID\_FEN\_THAC STANDARD; PRT; 336 AA.  
 AC Q9HJD4;  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE Flap structure-specific endonuclease (EC 3.-.-.-).  
 GN FEN OR TAL035.  
 OS Thermoplasma acidophilum.  
 OC Archaea; Euryarchaeota; Thermoplasmatia; Thermoplasmatiales;  
 OC Thermoplasmataceae; Thermoplasma.  
 OX NCBI\_TaxID=2303;  
 RN [1]

SEQUENCE FROM N.A.  
 RC STRAIN=DSM 1728;  
 RX MEDLINE=20479972; PubMed=11029001;  
 RA Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,  
 RA Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;  
 RT "The genome sequence of the thermoacidophilic scavenger Thermoplasma  
 acidophilum.";  
 RL Nature 407:508-513 (2000).  
 CC -!- FUNCTION: Endonuclease that cleave the 5'overhanging flap  
 CC structure that is generated by displacement synthesis when DNA  
 CC polymerase encounters the 5'end of a downstream Okazaki fragment.  
 CC Has 5'endo-/exonuclease and 5'pseudo-Y-endonuclease activities.  
 CC Cleaves the junction between single and double-stranded regions of  
 CC flap DNA (by similarity).  
 CC -!- COFACTOR: Binds 2 magnesium ions per subunit (By similarity).  
 CC -!- SIMILARITY: Belongs to the XPG/RAD2 endonuclease family. FEN1  
 CC subfamily.

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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

EMBL; AL45066; CAC12164.1; -;  
 DR HSP; Q58839; 1A76. -;  
 DR HAMAP; MF\_00614; -; 1.  
 DR InterPro; IPR008918; 5\_3\_exo\_C.  
 DR InterPro; IPR000513; Exo N I.  
 DR InterPro; IPR006086; XPG I.  
 DR InterPro; IPR006085; XPG N.  
 DR InterPro; IPR006084; XPG\_Rad.  
 DR Pfam; PF00867; XPG I; 1.  
 DR Pfam; PF00752; XPG N; 1.  
 DR PRINTS; PR00853; XPG\_Rad.  
 DR SMART; SM00279; Hh2; 1.  
 DR SMART; SM00484; XPGI; 1.  
 DR SMART; SM00485; XPGN; 1.  
 DR PROSITE; PS00841; XPG 1; FALSE NEG.  
 KW Hydroxylase; Nuclease; Endonuclease; Magnesium; Metal-binding;  
 KW Complete proteome.  
 FT METAL 153 153 MAGNESIUM 1 (BY SIMILARITY).  
 SQ SEQUENCE 336 AA; 38772 MW; 88EPD91DC80A78B CRC64;

Query Match 92.9%; Score 26; DB 1; Length 336;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
 :|||||  
 DB 97 MKEKAK 102

RESULT 30  
 GDF3\_MOUSE  
 ID\_GDF3\_MOUSE STANDARD; PRT; 366 AA.  
 AC Q07104;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DE Growth/differentiation factor 3 precursor (GDF-3) (VG-1-related  
 protein 2).  
 GN GDF3 OR GDF-3 OR VGR-2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93155193; PubMed=8429021;  
 RA McPherron A.C., Lee S.-J.;  
 RT "GDF-3 and GDF-9: two new members of the transforming growth  
 RT factor-beta superfamily containing a novel pattern of cysteines.";  
 RL J. Biol. Chem. 268:3444-3449 (1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93125570; PubMed=1480182;  
 RA Jones C.M., Simon-Chazottes D., Guenet J.-L., Hogan B.L.;  
 RT "Isolation of Vgr-2, a novel member of the transforming growth  
 RT factor-beta-related gene family.";  
 RL Mol. Endocrinol. 6:1961-1968 (1992).  
 CC -!- SUBUNIT: HOMODIMER OR HETERODIMER (POTENTIAL). BUT, IN CONTRAST TO  
 CC -!- SURCELLULAR LOCATION: Secreted (Probable).  
 CC -!- TISSUE SPECIFICITY: PRIMARILY IN ADULT BONE MARROW, SPLEEN, THYMUS  
 CC AND ADIPOSE TISSUE.  
 CC -!- SIMILARITY: Belongs to the TGF-beta family.

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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

EMBL; L06443; AAA53034.1; -;  
 DR EMBL; S52658; AAB24876.1; -;  
 DR PIR; A45402; A45402.  
 DR PIR; A46607; A46607.  
 DR HSP; P12643; 3BMP.  
 DR MGD; MGI:95686; Gdf3.  
 DR InterPro; IPR002400; GF\_cysknot.  
 DR InterPro; IPR002405; Inhibin\_alpha.  
 DR InterPro; IPR001839; TGFb.  
 DR InterPro; IPR001111; TGFb N.  
 DR Pfam; PF00019; TGF-beta; 1.  
 DR Pfam; PF00688; TGFb\_propeptide; 1.  
 DR PRINTS; PR00438; GPCYSKNOT.  
 DR PRINTS; PR00669; INHIBINA.  
 DR ProDom; PD000357; TGFb; 1.  
 DR SMART; SM00204; TGFb; 1.  
 DR PROSITE; PS00250; TGF\_BETA\_1; 1.  
 KW Signal; Growth factor; Cytokine; Glycoprotein.  
 FT SIGNAL 1 22 POTENTIAL.  
 FT PROPEP 23 252  
 FT CHAIN 253 366 GROWTH/DIFFERENTIATION FACTOR 3.  
 FT DISULFID 266 331 BY SIMILARITY.  
 FT DISULFID 295 363 BY SIMILARITY.

FT DISULFID 299 365 BY SIMILARITY.  
 FT CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 308 308 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 165 165 G -> R (IN REF. 2).  
 FT CONFLICT 167 168 LL -> FV (IN REF. 2).  
 FT CONFLICT 313 313 A -> R (IN REF. 2).  
 SQ SEQUENCE 366 AA; 41527 MW; EB2D7CBB4FA63E71 CRC64;

Query Match 92.9%; Score 26; DB 1; Length 366;  
 Best Local Similarity 83.3%; Pred. No. 2.4e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
 Db 117 IKEKAK 122

RESULT 31  
 PUR8\_BACSU  
 ID PUR8\_BACSU STANDARD; PRT; 431 AA.  
 AC P12047;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Adenylosuccinate lyase (EC 4.3.2.2) (Adenylosuccinase) (ASL)  
 DE (Glutamyl-tRNA synthetase regulatory factor).  
 GN PURB OR PURE OR BSU06440.  
 OS Bacillus subtilis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OC NCBI\_TaxID=1423;  
 RN [1]\_TaxID=1423;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87250425; PubMed=3036807;  
 RA Ebbols D.J., Zalkin H.;  
 RT "Cloning and characterization of a 12-gene cluster from Bacillus  
 RT subtilis encoding nine enzymes for de novo purine nucleotide  
 RT synthesis";  
 RL J. Biol. Chem. 262:8274-8287(1987).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=168;  
 RX MEDLINE=980404033; PubMed=9384377;  
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,  
 RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,  
 RA Borriello R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,  
 RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,  
 RA Choi S.K., Codani J.J., Conneron I.F., Cummings N.J., Daniel R.A.,  
 RA Denisot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,  
 RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,  
 RA Fritsch C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,  
 RA Ghim S.Y., Glaeser P., Goffeau A., Gollightly E.J., Grandi G.,  
 RA Guiseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,  
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,  
 RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,  
 RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,  
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,  
 RA Lee S.M., Levine A., Liu H., Maeda S., Macl C., Medigue C.,  
 RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,  
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,  
 RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,  
 RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,  
 RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,  
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,  
 RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,  
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,  
 RA Takeda M., Takakoshi A., Tanaka T., Terpstra P., Tognoni A.,  
 RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,  
 RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegeer T.,  
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,  
 RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,  
 RT "The complete genome sequence of the Gram-positive bacterium Bacillus  
 RT subtilis";  
 RL Nature 390:249-256(1997).

RN [3]  
 RP SEQUENCE OF 1-30.  
 RC STRAIN=168 / BGSCIAL;  
 RX MEDLINE=92302248; PubMed=1608947;  
 RA Gendron N., Breton R., Champagne N., Lapointe J.;  
 RA "Adenylosuccinate lyase of Bacillus subtilis regulates the activity  
 RT of the glutamyl-tRNA synthetase";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:5389-5392(1992).  
 RN [4]  
 RP X-RAY CRYSTALLOGRAPHY (3.25 ANGSTROMS).  
 RX MEDLINE=20384863; PubMed=10926519;  
 RA Toth E.A., Worby C., Dixon J.E., Goedken E.R., Marqusee S.,  
 RA Yeates T.O.;  
 RT "The crystal structure of adenylosuccinate lyase from Pyrobaculum  
 RT aerophilum reveals an intracellular protein with three disulfide  
 RT bonds";  
 RL J. Mol. Biol. 301:433-450(2000).  
 CC -|- FUNCTION: INFLUENCES THE AFFINITY OF GLUTAMYL-TRNA SYNTHETASE FOR  
 CC ITS SUBSTRATES AND INCREASES ITS THERMOSTABILITY.  
 CC -|- CATALYTIC ACTIVITY: N(6)-(1,2-dicarboxyethyl)AMP = fumarate + AMP.  
 CC -|- CATALYTIC ACTIVITY: (S)-2-[5-amino-1-(5-phospho-D-  
 CC ribosyl)imidazole-4-carboxamido]succinate = fumarate + 5-amino-1-  
 CC (5-phospho-D-ribose)imidazole-4-carboxamide.  
 CC -|- PATHWAY: De novo purine biosynthesis; eighth step.  
 CC -|- SIMILARITY: Belongs to the lyase 1 family. Adenylosuccinate lyase  
 CC subfamily.  
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 CC -----  
 DR EMBL; J02732; AAA22676.1; -;  
 DR EMBL; 299107; CAB12464.1; -;  
 DR PIR; C29326; WZBSDS  
 DR PDB; 1FIO; 10-JAN-01.  
 DR Subtilist; BG10702; purB.  
 DR InterPro; IPR000362; Fumarate lyase.  
 DR InterPro; IPR008948; L-Aspartase-like.  
 DR InterPro; IPR004769; Pur lyase.  
 DR Pfam; PF00206; lyase 1; 1.  
 DR PRINTS; PR00149; FUMRATLYASE.  
 DR TIGRFAMs; TIGR00928; purB; 1.  
 DR PROSITE; PS00163; FUMARATE LYASES; 1.  
 KW Purine biosynthesis; Lyase; Complete proteome; 3D-structure.  
 FT ACT\_SITE 68 68 ACID (BY SIMILARITY).  
 FT ACT\_SITE 141 141 BASE (BY SIMILARITY).  
 FT CONFLICT 5 5 Y -> K (IN REF. 3).  
 SQ SEQUENCE 431 AA; 49484 MW; 89D2ED7F7F6D46A2 CRC64;

Query Match 92.9%; Score 26; DB 1; Length 431;  
 Best Local Similarity 83.3%; Pred. No. 2.8e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
 Db 124 IKEKAK 129

RESULT 32  
 PFL\_LACLA  
 ID PFL\_LACLA STANDARD; PRT; 787 AA.  
 AC O32797;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Formate acetyltransferase (EC 2.3.1.54) (Pyruvate formate-lyase).  
 GN PFL OR LJ0664.  
 OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.

```

OX NCBI_TaxID=1360;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=DE1341;
RX MEDLINE=97440141; PubMed=9294449;
RA Arnau J., Joergensen F., Madsen S.M., Vrang A., Israelsen H.;
RT "Cloning, expression, and characterization of the Lactococcus lactis
RT pfl gene, encoding pyruvate formate-lyase.";
RL J. Bacteriol. 179:5884-5891 (1997).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=IL1403;
RX MEDLINE=21235186; PubMed=11337471;
RA Bolotin A., Wincker P., Mauer S., Jaillon O., Malarne K.,
RA Weissenbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
RT lactis spp. lactis IL1403.";
RL Genome Res. 11:731-753 (2001).
CC -1- CATALYTIC ACTIVITY: Acetyl-CoA + formate = CoA + pyruvate.
CC -1- PATHWAY: Glucose metabolism (nonoxidative conversion).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: STRONG, TO OTHER PYRUVATE FORMATE-LYASES.
CC
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CC
CC EMBL; AJ000326; CA03993.1; -.
CC HSP; P09373; ICM5.
CC InterPro; IPR005949; Form_actrans.
CC InterPro; IPR001150; Form_actrans GR.
CC InterPro; IPR004184; Pyr_Form_lyase.
CC Pfam; PF01228; Gly_radical; 1.
CC Pfam; PF02901; PFL; 1.
CC TIGRFAMs; TIGR01255; pyr_form_ly_1; 1.
CC PROSITE; PS00850; Gly_RADICAL; 1.
CC TRANSFERASE; Acyltransferase; Glucose metabolism; Organic radical;
KW MOD_RES 749 749 FREE RADICAL (BY SIMILARITY).
FT SEQUENCE 787 AA; 89121 MW; BD59BEF6C808C8B8 CRC64;
SQ SEQUENCE 787 AA; 89121 MW; BD59BEF6C808C8B8 CRC64;

Query Match 92.9%; Score 26; DB 1; Length 787;
Best Local Similarity 83.3%; Pred. NO. 4.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
DB 197 MKEKAK 202

RESULT 34
TCOF_HUMAN
ID TCOF_HUMAN STANDARD; PRT; 1411 AA.
AC Q13428; Q99408; Q99860;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Treacle protein (Treacher Collins syndrome protein).
GN TCOF1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=96154183; PubMed=8563749;
RA Dixon J., Edwards S.J., Gladwin A.J., Dixon M.J., Loftus S.K.,
RA Bonner C.A., Koprivnikar K., Wasmuth J.J.;
RT "Positional cloning of a gene involved in the pathogenesis of
RT Treacher Collins syndrome.";
RL Nat. Genet. 12:130-136 (1996).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=97228900; PubMed=9074926;
RA Dixon J., Edwards S.J., Anderson I., Brass A., Scambler P.J.,
RA Dixon M.J.;
RT "Identification of the complete coding sequence and genomic
RT organization of the Treacher Collins syndrome gene.";
RL Genome Res. 7:223-234 (1997).
RN [3]
RN SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RX MEDLINE=97250498; PubMed=9096354;
RA Wise C.A., Chiang L.C., Paznekas W.A., Sharma M., Musy M.M.,

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RA Arnau J., Joergensen F., Madsen S.M., Vrang A., Israelsen H.;
RT "Cloning, expression, and characterization of the Lactococcus lactis
RT pfl gene, encoding pyruvate formate-lyase.";
RL J. Bacteriol. 179:5884-5891 (1997).
CC -1- CATALYTIC ACTIVITY: Acetyl-CoA + formate = CoA + pyruvate.
CC -1- PATHWAY: Glucose metabolism (nonoxidative conversion).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: STRONG, TO OTHER PYRUVATE FORMATE-LYASES.
CC
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CC
CC EMBL; AJ000325; CA03991.1; -.
CC HSP; P09373; ICM5.
CC InterPro; IPR005949; Form_actrans.
CC InterPro; IPR001150; Form_actrans GR.
CC InterPro; IPR004184; Pyr_Form_lyase.
CC Pfam; PF01228; Gly_radical; 1.
CC Pfam; PF02901; PFL; 1.
CC TIGRFAMs; TIGR01255; pyr_form_ly_1; 1.
CC PROSITE; PS00850; Gly_RADICAL; 1.
CC TRANSFERASE; Acyltransferase; Glucose metabolism; Organic radical.
KW MOD_RES 749 749 FREE RADICAL (BY SIMILARITY).
FT SEQUENCE 787 AA; 89106 MW; 66537F0868C82E7E CRC64;
SQ SEQUENCE 787 AA; 89106 MW; 66537F0868C82E7E CRC64;

Query Match 92.9%; Score 26; DB 1; Length 787;
Best Local Similarity 83.3%; Pred. NO. 4.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
DB 197 MKEKAK 202

RESULT 34
TCOF_HUMAN
ID TCOF_HUMAN STANDARD; PRT; 1411 AA.
AC Q13428; Q99408; Q99860;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Treacle protein (Treacher Collins syndrome protein).
GN TCOF1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=96154183; PubMed=8563749;
RA Dixon J., Edwards S.J., Gladwin A.J., Dixon M.J., Loftus S.K.,
RA Bonner C.A., Koprivnikar K., Wasmuth J.J.;
RT "Positional cloning of a gene involved in the pathogenesis of
RT Treacher Collins syndrome.";
RL Nat. Genet. 12:130-136 (1996).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=97228900; PubMed=9074926;
RA Dixon J., Edwards S.J., Anderson I., Brass A., Scambler P.J.,
RA Dixon M.J.;
RT "Identification of the complete coding sequence and genomic
RT organization of the Treacher Collins syndrome gene.";
RL Genome Res. 7:223-234 (1997).
RN [3]
RN SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RX MEDLINE=97250498; PubMed=9096354;
RA Wise C.A., Chiang L.C., Paznekas W.A., Sharma M., Musy M.M.,

```

RA Ashley J.A., Lovett M., Jabs E.W.;  
 RT "TCOF1 gene encodes a putative nucleolar phosphoprotein that exhibits  
 RT mutations in Treacher Collins syndrome throughout its coding  
 RT region."; Treacher Collins syndrome  
 RN Proc. Natl. Acad. Sci. U.S.A. 94:3110-3115(1997).  
 RN [4]  
 RP VARIANTS LEU-439; VAL-810; VAL-1313 AND GLY-1355, AND VARIANT TCS  
 RP ARG-53.  
 RX MEDLINE=97195537; PubMed=9042910;  
 RA Edwards S.J., Gladwin A.J., Dixon M.J.;  
 RT "The mutational spectrum in Treacher Collins syndrome reveals a  
 RT predominance of mutations that create a premature-termination  
 RT codon";  
 RL Am. J. Hum. Genet. 60:515-524(1997).  
 CC -!- DISEASE: Defects in TCOF1 are the cause of Treacher Collins  
 CC syndrome (TCS) [MIM:154500]. TCS is an autosomal dominant disorder  
 CC of craniofacial development that occurs with an incidence of  
 CC 1/50,000 live births. The clinical features of TCS are bilaterally  
 CC symmetrical and include: (1) abnormalities of the external ears,  
 CC atresia of the external ear canals, and malformation of the middle  
 CC ear ossicles, which may result in conductive hearing loss; (2)  
 CC lateral downward sloping of palpebral fissures, frequently with  
 CC colobomas of the lower eyelids; (3) hypoplasia of the mandible and  
 CC zygomatic complex; (4) cleft palate.  
 CC -!- SIMILARITY: Contains 1 Lish domain.  
 CC -----  
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 CC -----  
 DR EMBL; U40847; AAC50903.1; -;  
 DR EMBL; U76366; AAC51181.1; -;  
 DR EMBL; U84664; AAC51185.1; -;  
 DR EMBL; U84640; AAC51185.1; JOINED.  
 DR EMBL; U84641; AAC51185.1; JOINED.  
 DR EMBL; U84642; AAC51185.1; JOINED.  
 DR EMBL; U84643; AAC51185.1; JOINED.  
 DR EMBL; U84644; AAC51185.1; JOINED.  
 DR EMBL; U84645; AAC51185.1; JOINED.  
 DR EMBL; U84646; AAC51185.1; JOINED.  
 DR EMBL; U84647; AAC51185.1; JOINED.  
 DR EMBL; U84648; AAC51185.1; JOINED.  
 DR EMBL; U84649; AAC51185.1; JOINED.  
 DR EMBL; U84650; AAC51185.1; JOINED.  
 DR EMBL; U84651; AAC51185.1; JOINED.  
 DR EMBL; U84652; AAC51185.1; JOINED.  
 DR EMBL; U84653; AAC51185.1; JOINED.  
 DR EMBL; U84654; AAC51185.1; JOINED.  
 DR EMBL; U84655; AAC51185.1; JOINED.  
 DR EMBL; U84656; AAC51185.1; JOINED.  
 DR EMBL; U84657; AAC51185.1; JOINED.  
 DR EMBL; U84658; AAC51185.1; JOINED.  
 DR EMBL; U84659; AAC51185.1; JOINED.  
 DR EMBL; U84660; AAC51185.1; JOINED.  
 DR EMBL; U84661; AAC51185.1; JOINED.  
 DR EMBL; U84662; AAC51185.1; JOINED.  
 DR EMBL; U84663; AAC51185.1; JOINED.  
 DR EMBL; U79659; AAB40722.1; -;  
 DR EMBL; U79645; AAB40722.1; JOINED.  
 DR EMBL; U79646; AAB40722.1; JOINED.  
 DR EMBL; U79647; AAB40722.1; JOINED.  
 DR EMBL; U79648; AAB40722.1; JOINED.  
 DR EMBL; U79649; AAB40722.1; JOINED.  
 DR EMBL; U79650; AAB40722.1; JOINED.  
 DR EMBL; U79651; AAB40722.1; JOINED.  
 DR EMBL; U79652; AAB40722.1; JOINED.  
 DR EMBL; U79653; AAB40722.1; JOINED.  
 DR EMBL; U79654; AAB40722.1; JOINED.  
 DR EMBL; U79655; AAB40722.1; JOINED.

DR EMBL; U79656; AAB40722.1; JOINED.  
 DR EMBL; U79657; AAB40722.1; JOINED.  
 DR EMBL; U79658; AAB40722.1; JOINED.  
 DR Genew; HGNC:11654; TCOF1.  
 DR MIM; 606847; -;  
 DR MIM; 154500; -;  
 DR GO; GO:0005730; C:nucleolus; TAS.  
 DR GO; GO:0005215; F:transporter activity; TAS.  
 DR GO; GO:0001501; P:skeletal development; TAS.  
 DR InterPro; IPR006594; Lish.  
 DR InterPro; IPR003993; treacle.  
 DR Pfam; PF03546; treacle; 3.  
 DR PRINTS; PR01503; TREACLE.  
 DR SMART; SMD0667; Lish; 1.  
 DR PROSITE; PS50896; Lish; 1.  
 KW Disease mutation; Polymorphism.  
 FT DOMAIN 6 38 LISH.  
 FT DOMAIN 89 97 POLY-GLU.  
 FT DOMAIN 204 207 POLY-SER.  
 FT DOMAIN 616 619 POLY-SER.  
 FT DOMAIN 919 924 POLY-SER.  
 FT DOMAIN 1285 1289 POLY-LYS.  
 FT DOMAIN 1375 1386 POLY-LYS.  
 FT DOMAIN 1398 1405 POLY-LYS.  
 FT VARIANT 53 53 W -> R (in TCS).  
 FT VARIANT 439 439 P -> L.  
 FT VARIANT 810 810 A -> V.  
 FT VARIANT 1313 1313 A -> V (in dbSNP:15251).  
 FT VARIANT 1355 1355 D -> G.  
 FT CONFLICT 1312 1312 K -> Q (in REF. 2).  
 SQ SEQUENCE 1411 AA; 144312 MW; 3880203D985C2699 CRC64;  
 Query Match 92.9%; Score 26; DB 1; Length 1411;  
 Best Local Similarity 83.3%; Pred. No. 8e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LKEKAK 6  
 Db 121 MKEKAK 126  
 :|||||  
 RESULT 35  
 ID DMN HUMAN STANDARD; PRT; 1565 AA.  
 AC O15061.  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Desmuslin.  
 GN DMN OR KIAA0353.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 2), AND DESMIN AND ALPHA-DYSTROBREVIN  
 RP BINDING.  
 RC TISSUE=Skeletal muscle;  
 RX MEDLINE=21267385; PubMed=11353857;  
 RA Mizuno Y., Thompson T.G., Guyon J.R., Lidov H.G.W., Brosius M.,  
 RA Imamura M., Ozawa E., Watkins S.C., Kunzel L.M.;  
 RT "Desmuslin, an intermediate filament protein that interacts with  
 RT alpha-dystrobrevin and desmin";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:6156-6161(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Brain;  
 RN Nagase T., Kikuno R., Yamakawa H., Ohara O.;

Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.

[3]  
 RN SEQUENCE OF 192-1565 FROM N.A. (ISOFORM 1).  
 RP TISSUE=Brain;  
 RX MEDLINE=97349984; PubMed=9205841;  
 RA Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N.,  
 RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;  
 RT "Prediction of the coding sequences of unidentified human genes. VII.  
 RT The complete sequences of 100 new cDNA clones from brain which can  
 RT code for large proteins in vitro.";  
 RL DNA Res. 4:141-150(1997).  
 RN [4]  
 RP VARIANTS VAL-272; ILE-330; TRP-338; LEU-567; ALA-612; LEU-761;  
 RP TRP-946; ARG-976; LEU-1059; PRO-1067 AND LEU-1077.  
 RX PubMed=11454237;  
 RA Mizuno Y., Puca A.A., O'Brien K.F., Beggs A.H., Kunkel L.M.;  
 RT "Genomic organization and single-nucleotide polymorphism map of  
 RT desmuslin, a novel intermediate filament protein on chromosome  
 RT 15q26.3.";  
 RL BMC Genet. 2:8-8(2001).  
 CC -!- FUNCTION: Desmuslin is a type-VI intermediate filament which may  
 CC function as a mechanical support to the muscle fibers by making a  
 CC linkage between the extracellular matrix via the dystrophin-  
 CC associated protein complex (DAPC) and the Z-disk.  
 CC -!- SUBUNIT: Interacts with desmin and alpha-dystrobrevin.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable). There are at least  
 CC two distinct DMN subpopulations, one in which DMN interacts with  
 CC desmin within the Z-lines, and another in which it interacts with  
 CC both alpha-dystrobrevin and desmin at the costamere.  
 CC -!- ALTERNATIVE PRODUCTS;  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1;  
 CC IsoId=O15061-1; Sequence=Displayed;  
 CC Note=No experimental confirmation available;  
 CC Name=2;  
 CC IsoId=O15061-2; Sequence=VSP\_002465;  
 CC -!- TISSUE SPECIFICITY: Expressed in heart and muscle. Some expression  
 CC in brain which may be due to tissue-specific isoforms.  
 CC -!- SIMILARITY: Belongs to the intermediate filament family.  
 CC -----  
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 CC -----  
 DR EMBL; AF359284; AK57487.1; -;  
 DR EMBL; AB020351; BAA20810.2; ALT\_INIT.  
 DR MIM; 606087; -;  
 DR GO; GO:0005882; C:intermediate filament; NAS.  
 DR GO; GO:0005515; F:protein binding; IPI.  
 DR GO; GO:0008307; F:structural constituent of muscle; NAS.  
 DR InterPro; IPR001664; IF.  
 DR Pfam; PF00038; filament; 1.  
 DR PROSITE; PS00226; IF; 1.  
 KW Intermediate filament; Coiled coil; Polymorphism;  
 KW Alternative splicing.  
 FT DOMAIN 1 10 HEAD.  
 FT DOMAIN 11 300 ROD.  
 FT DOMAIN 301 1565 TAIL.  
 FT COIL 1A.  
 FT LINKER 1.  
 FT COIL 1B.  
 FT COIL 1C.  
 FT LINKER 1/2.  
 FT COIL 2.  
 FT MISSING (in isoform 2).  
 FT VARSPLIC 1152 1463 /FTId=VSP\_002465.  
 FT VARIANTS 272 272 A -> V.  
 FT VARIANTS 330 330 /FTId=VAR\_012295.  
 FT VARIANTS 330 330 V -> I.  
 FT /FTId=VAR\_012296.

FT VARIANTS 338 338 R -> W.  
 FT /FTId=VAR\_012297.  
 FT VARIANTS 567 567 P -> L.  
 FT /FTId=VAR\_012298.  
 FT VARIANTS 612 612 E -> A.  
 FT /FTId=VAR\_012299.  
 FT VARIANTS 761 761 P -> L.  
 FT /FTId=VAR\_012300.  
 FT VARIANTS 946 946 R -> W.  
 FT /FTId=VAR\_012301.  
 FT VARIANTS 976 976 Q -> R.  
 FT /FTId=VAR\_012302.  
 FT VARIANTS 1059 1059 P -> L.  
 FT /FTId=VAR\_012303.  
 FT VARIANTS 1067 1067 R -> P.  
 FT /FTId=VAR\_012304.  
 FT VARIANTS 1077 1077 S -> L.  
 FT /FTId=VAR\_012305.  
 FT VARIANTS 1386 1386 G -> E (in dbSNP:2292288).  
 FT /FTId=VAR\_012306.  
 FT VARIANTS 1462 1462 F -> C (in dbSNP:2292287).  
 FT /FTId=VAR\_012307.  
 FT CONFLICT 355 355 R -> W (IN REF. 2).  
 FT CONFLICT 462 462 G -> S (IN REF. 2).  
 SQ SEQUENCE 1565 AA; 172767 MW; 18D19000D3CEAS37 CRC64;  
 Query Match 92.9%; Score 26; DB 1; Length 1565;  
 Best Local Similarity 83.3%; Pred. No. 8.8e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LKEKAK 6  
 Db 557 MKEKAK 562  
 RESULT 36  
 POLG\_HCVA STANDARD; PRT; 3898 AA.  
 ID POLG\_HCVA  
 AC P19712;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Genome polypeptide.  
 OS Hog cholera virus (strain Alfort) (Swine fever virus).  
 OC Viruses; SSRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 OC Pestivirus.  
 OX NCBI\_TaxID=11097;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89348014; PubMed=2763466;  
 RA Meyers G., Ruemenapf T., Thiel H.-J.;  
 RT "Molecular cloning and nucleotide sequence of the genome of hog  
 RT cholera virus";  
 RL Virology 171:555-567(1989).  
 RN [2]  
 RP REVISION TO 2731.  
 RA Meyers G.;  
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: PESTIVIRUS P80 (P125) MAY BE A BIFUNCTIONAL PROTEIN  
 CC WITH HELICASE AND PROTEASE ACTIVITY.  
 CC -!- SUBCELLULAR LOCATION: THE GP51-GP54 PROTEIN IS ANCHORED TO THE  
 CC VIRAL ENVELOPE.  
 CC -!- SIMILARITY: TO BOVINE DIARRHEA VIRUS GENOME POLYPROTEIN.  
 CC -----  
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 CC -----



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DR EMBL; J044358; AAA43844.2; -.
DR HSSP; P27958; 1A1V.
DR MEROPS; C53.001; -.
DR INTERPRO; IPR001410; DEAD.
DR INTERPRO; IPR002166; HCV RdRp.
DR INTERPRO; IPR001650; Helicase_C.
DR INTERPRO; IPR008751; Peptidase_C53.
DR INTERPRO; IPR000280; Peptidase_S31.
DR INTERPRO; IPR007095; RNA_pol_DS_PS.
DR INTERPRO; IPR007094; RNA_pol_PSVir.
DR INTERPRO; IPR001568; RNase_T2.
DR PFAM; PF00271; helicase_C; 1.
DR PFAM; PF05550; Peptidase_C53; 1.
DR PFAM; PF05578; Peptidase_S31; 1.
DR PFAM; PF00998; Viral RdRp; 1.
DR PRINTS; PR00729; CDVENDOPTASE.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
DR PROSITE; PS00531; RNASE_T2_2; UNKNOWN_1.
KW Polypeptidein; Glycoprotein; Transmembrane; Hydrolase; Serine protease;
FT CHAIN ?1 7267 CAPSID PROTEIN C (POTENTIAL).
FT CHAIN 7268 7500 GP44-E2 (E2) (POTENTIAL).
FT CHAIN 7501 7689 GP33 (E3) (POTENTIAL).
FT CHAIN 7690 71060 GP55 (ENVELOPE PROTEIN E1).
FT CHAIN 71611 72111 P80 (POTENTIAL).
FT TRANSMEM 1032 1048 POTENTIAL.
FT ACT_SITE 1658 1658 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 1695 1695 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 1752 1752 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 269 269 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 278 278 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 362 362 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 367 367 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 410 410 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 425 425 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 500 500 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 594 594 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 805 805 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 810 810 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 874 874 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 918 918 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 949 949 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 986 986 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1713 1713 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2134 2134 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2217 2217 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2494 2494 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2787 2787 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2815 2815 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2891 2891 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 3211 3211 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 3316 3316 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 3689 3689 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 3698 3698 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 3794 3794 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARIANT 387 387 T -> A.
FT VARIANT 3542 3542 R -> S.
FT SEQUENCE 3898 AA; 438570 MW; 2C1F17B8A359D0F6 CRC64;
Query Match 92.9%; Score 26; DB 1; Length 3898;
Best Local Similarity 83.3%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKEKAK 6
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Db 3152 IKEKAK 3157

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RESULT 37
POLG_HCVB STANDARD; PRT; 3898 AA.
ID POLG_HCVB
AC P21530;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Genome polyprotein.
OS Hog cholera virus (strain Brescia) (Swine fever virus).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Pestivirus.
OX NCBI_TaxID=11098;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90281581; PubMed=2162104;
RA Moormann R.J.M., Warmerdam P.A.M., van der Meer B., Schaaper W.M.M.,
RA Wensvoort G., Hulst M.M.;
RT "Molecular cloning and nucleotide sequence of hog cholera virus
RT strain Brescia and mapping of the genomic region encoding envelope
RT protein E1";
RT Virolology 177:184-198(1990).
RL -!- FUNCTION: PESTIVIRUS P80 (P125) MAY BE A BIFUNCTIONAL PROTEIN
CC WITH HELICASE AND PROTEASE ACTIVITY.
CC -!- SUBCELLULAR LOCATION: THE GP51-GP54 PROTEIN IS ANCHORED TO THE
CC VIRAL ENVELOPE.
CC -!- SIMILARITY: TO BOVINE VIRAL DIARRHEA VIRUS GENOME POLYPROTEIN.
CC -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S31.
CC
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CC -----
CC EMBL; M31768; AAA43843.1; -.
CC PIR; A35317; GNWVHB.
CC HSSP; P27958; 1A1V.
CC MEROPS; C53.001; -.
CC MEROPS; S31.001; -.
CC InterPro; IPR001410; DEAD.
CC InterPro; IPR002166; HCV RdRp.
CC InterPro; IPR001650; Helicase_C.
CC InterPro; IPR008751; Peptidase_C53.
CC InterPro; IPR000280; Peptidase_S31.
CC InterPro; IPR007095; RNA_pol_DS_PS.
CC InterPro; IPR007094; RNA_pol_PSVir.
CC InterPro; IPR001568; RNase_T2.
CC PFAM; PF00271; helicase_C; 1.
CC PFAM; PF05550; Peptidase_C53; 1.
CC PFAM; PF05578; Peptidase_S31; 1.
CC PFAM; PF00998; Viral RdRp; 1.
CC PRINTS; PR00729; CDVENDOPTASE.
CC SMART; SM00487; DEXDC; 1.
CC SMART; SM00490; HELIC; 1.
CC PROSITE; PS00531; RNASE_T2_2; UNKNOWN_1.
KW Polypeptidein; Glycoprotein; Transmembrane; Hydrolase; Serine protease;
KW Helicase.
FT CHAIN ?1 7267 CAPSID PROTEIN C (POTENTIAL).
FT CHAIN 7268 7500 GP42 (E2) (POTENTIAL).
FT CHAIN 7501 7689 GP31 (E3) (POTENTIAL).
FT CHAIN 7690 71060 GP51-GP54 (ENVELOPE PROTEIN E1).
FT CHAIN 71611 72111 P80 (POTENTIAL).
FT TRANSMEM 1032 1048 POTENTIAL.
FT ACT_SITE 1658 1658 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 1695 1695 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 1752 1752 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 269 269 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 278 278 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 362 332 N-LINKED (GLCNAC. .) (POTENTIAL).

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FT CARBOHYD 362 362 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 410 410 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 425 425 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 500 500 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 594 594 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 805 805 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 810 810 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 874 874 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 918 918 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 949 949 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1713 1713 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 2134 2134 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 2217 2217 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 2419 2419 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 2494 2494 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 2787 2787 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 2815 2815 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 2891 2891 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 3103 3103 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 3211 3211 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 3316 3316 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 3689 3689 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 3698 3698 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 3794 3794 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 3898 AA; 438423 MW; EC6EB207A09D59FD CRC64;  
 Query Match 92.9%; Score 26; DB 1; Length 3898;  
 Best Local Similarity 83.3%; Pred. No. 2e+03;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LKEKAK 6  
 DB 3152 IREKAK 3157  
 RESULT 38  
 Y112\_METNA  
 ID Y112\_METNA STANDARD; PRT; 115 AA.  
 AC Q8Q0M4;  
 DT 10-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Hypothetical protein MM0112.  
 GN MM0112.  
 OS Methanosarcina mazei (Methanosarcina frisia).  
 OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;  
 OC Methanosarcinaceae; Methanosarcina.  
 OX NCBI\_TaxID=2209;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Goel / G01 / ATCC BAA-199 / DSM 3647 / OCM 88;  
 RX MEDLINE=22120827; PubMed=12125824;  
 RA Deppenmeier U., Johann A., Hartsch T., Merkl R., Schmitz R.A.,  
 RA Martinez-Arias R., Heme A., Wierzer A., Baeumer S., Jacobi C.,  
 RA Bruggemann H., Lienard T., Christmann A., Boemcke M., Steckel S.,  
 RA Bhattacharyya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,  
 RA Fritz H.-J., Gottschalk G.;  
 RT "The genome of Methanosarcina mazei: evidence for lateral gene  
 RT transfer between Bacteria and Archaea";  
 RL J. Mol. Microbiol. Biotechnol. 4:453-461(2002).  
 CC -!- SIMILARITY: Belongs to the UPF0099 family.  
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 CC -----  
 CC EMBL; AE0113231; AM29808.1; ALT\_INIT.  
 DR HAMAP; MF\_00628; -; 1.  
 DR InterPro; IPR002833; UPF0099.  
 QY 1 LKEKAK 6  
 DB 3152 IREKAK 3157

DR Pfam; PF01981; UPF0099; 1.  
 DR ProDom; PD010667; UPF0099; 1.  
 DR TIGRFAMs; TIGR00283; TIGR00283; 1.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 115 AA; 12612 MW; 029A469B7683947A CRC64;  
 Query Match 89.3%; Score 25; DB 1; Length 115;  
 Best Local Similarity 83.3%; Pred. No. 1.4e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LKEKAK 6  
 DB 65 LAEKAR 70  
 RESULT 39  
 YW69\_METAC  
 ID YW69\_METAC STANDARD; PRT; 115 AA.  
 AC Q8TKX4;  
 DT 10-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Hypothetical protein MA3269.  
 GN MA3269.  
 OS Methanosarcina acetivorans.  
 OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;  
 OC Methanosarcinaceae; Methanosarcina.  
 OX NCBI\_TaxID=2214;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C2A / ATCC 35395 / DSM 2834;  
 RX MEDLINE=21929760; PubMed=11932238;  
 RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,  
 RA FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,  
 RA Allen N., Naylor J., Stange-Thomann N., DeArelano K., Johnson R.,  
 RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,  
 RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,  
 RA Hedderich R., Ingram-Smith C., Kuettnner H.C., Krzycki J.A.,  
 RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,  
 RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,  
 RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,  
 RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,  
 RA Metcalf W.W., Birren B.;  
 RT "The genome of Methanosarcina acetivorans reveals extensive metabolic  
 RT and physiological diversity";  
 RL Genome Res. 12:532-542(2002).  
 CC -!- SIMILARITY: Belongs to the UPF0099 family.  
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 CC -----  
 CC EMBL; AE011031; AM06640.1; -;  
 DR HAMAP; MF\_00628; -; 1.  
 DR InterPro; IPR002833; UPF0099.  
 DR Pfam; PF01981; UPF0099; 1.  
 DR TIGRFAMs; TIGR00283; TIGR00283; 1.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 115 AA; 12644 MW; 06B690968ADF81A6 CRC64;  
 Query Match 89.3%; Score 25; DB 1; Length 115;  
 Best Local Similarity 83.3%; Pred. No. 1.4e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LKEKAK 6  
 DB 65 LAEKAR 70

```

RESULT 40
Y941 STAEF
ID Y941 STAEF STANDARD; PRT; 155 AA.
AC Q8CST6;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical UPF0090 protein SE0941.
GN SE0941.
OS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1282;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 12228;
RX PubMed=12950928;
RA Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,
RA Qin Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z.,
RA Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.;
RT "Genome-based analysis of virulence genes in a non-biofilm-forming
RT Staphylococcus epidermidis strain (ATCC 12228).";
RL Mol. Microbiol. 49:1577-1593(2003).
CC -!- SIMILARITY: Belongs to the UPF0090 family.
CC
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CC
CC EMBL; AE016747; AAC04538.1; -.
CC HAMAP; MF_01077; -; 1.
CC InterPro; IPR003728; DUF150.
CC Pfam; PF02576; DUF150; 1.
CC Hypothetical protein; Complete proteome.
KW SEQUENCE 155 AA; 17638 MW; ACS621AF10637DA7 CRC64;
SQ
Query Match 89.3%; Score 25; DB 1; Length 155;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKEKAK 6
DB 130 VKEKAK 135
:|||||
:|||||

RESULT 41
PTGA_BUCAP
ID PTGA_BUCAP STANDARD; PRT; 167 AA.
AC Q8KAS1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE PTS system, glucose-specific IIA component (EIIA-Glc) (Glucose-
DE permease IIA component) (Phosphotransferase enzyme II, A component)
DE (EC 2.7.1.69) (EII-Glc).
GN CRP OR BUSG060.
OS Buchnera aphidicola (subsp. Schizaphis graminum).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=98794;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=22084549; PubMed=12089438;
RA Tamas I., Klasson L., Canbaeck B., Naeslund A.K., Eriksson A.-S.,
RA Werngren J.J., Sandstrom J.P., Moran N.A., Andersson S.G.E.;
RA "50 million years of genomic stasis in endosymbiotic bacteria.";
RL Science 296:2376-2379(2002).
CC -!- FUNCTION: This is a component of the phosphoenolpyruvate-dependent
CC sugar phosphotransferase system (PTS), a major carbohydrate active
CC -transport system. The IICD domains contain the sugar binding site

```

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CC and the transmembrane channel; the IIA domain contains the primary
CC phosphorylation site (the donor is phospho-HPr); IIA transfers its
CC phosphoryl group to the IIB domain which finally transfers it to
CC the sugar (By similarity).
CC -!- CATALYTIC ACTIVITY: Protein N-phosphohistidine + sugar = protein
CC histidine + sugar phosphate.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Contains 1 PTS EIIA domain.
CC
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CC
CC EMBL; AE014081; AAM67631.1; -.
CC InterPro; IPR001127; PTS_EIIA.
CC Pfam; PF00358; PTS_EIIA.1; 1.
CC ProDom; PD002243; PTS_EIIA; 1.
CC TIGRFAMs; TIGR00830; PTBA; 1.
CC PROSITE; PS00371; PTS_EIIA.1; 1.
CC Phosphotransferase system; Sugar transport; Transferase;
KW Phosphorylation; Complete proteome.
FT ACT_SITE 74 74 IMPORTANT FOR PHOSPHO-DONOR ACTIVITY (BY
FT SIMILARITY).
FT MOD_RES 89 89 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 167 AA; 18338 MW; 9C71B05BC7907551 CRC64;
Query Match 89.3%; Score 25; DB 1; Length 167;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKEKAK 6
DB 126 LKEKAR 131
:|||||
:|||||

RESULT 42
YJ00 AQUAE
ID YJ00 AQUAE STANDARD; PRT; 168 AA.
AC Q67738;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein AQ_1900.
GN AQ_1900.
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Snead M.A., Keller M., Anjay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RA "The complete genome of the hyperthermophilic bacterium Aquifex
RA aeolicus.";
RL Nature 392:353-358(1998).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: STRONG, TO AEBOLICUS AQ_1446.
CC
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CC
CC EMBL; AE000762; AAC07710.1; -.

```

KW Hypothetical protein; Transmembrane; Complete proteome.  
 FT TRANSMEM 4 24 POTENTIAL.  
 FT TRANSMEM 94 114 POTENTIAL.  
 SQ SEQUENCE 168 AA; 20148 MW; 5B1C48B347D11D9 CRC64;

Query Match 89.3%; Score 25; DB 1; Length 168;  
 Best Local Similarity 83.3%; Pred. No. 1.9e+02; Indels 0; Gaps 0;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
 Db 148 LREKAK 153  
 |:|:|:|

RESULT 43  
 DEF STABP STANDARD; PRT; 183 AA.  
 AC O8CPN4;  
 DT 10-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DE Peptide deformylase (BC 3.5.1.88) (PDF) (Polypeptide deformylase).  
 GN DEF OR SE0789.  
 OS Staphylococcus epidermidis.  
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
 OX NCBI\_TaxID=1282;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 12228;  
 RX PubMed=12950922;  
 RA Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,  
 RA Qin Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z.,  
 RA Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.;  
 RT "Genome-based analysis of virulence genes in a non-biofilm-forming  
 RT Staphylococcus epidermidis strain (ATCC 12228).";  
 RL Mol Microbiol. 49:1577-1593(2003).  
 CC -!- FUNCTION: Removes the formyl group from the N-terminal Met of  
 CC newly synthesized proteins. Requires at least a dipeptide for an  
 CC efficient rate of reaction. N-terminal L-methionine is a  
 CC prerequisite for activity but the enzyme has broad specificity at  
 CC other positions (By similarity).  
 CC -!- CATALYTIC ACTIVITY: Formyl-L-methionyl peptide + H(2)O = formate +  
 CC methionyl peptide.  
 CC -!- COFACTOR: Binds 1 iron(II) ion (By similarity).  
 CC -!- SIMILARITY: Belongs to the polypeptide deformylase family.  
 CC  
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 CC  
 CC EMBL; A5016746; AAC04386.1; -;  
 DR HAMAP; MF\_00163; -; 1.  
 DR InterPro; IPR000181; Pep deformylase.  
 DR Pfam; PF01327; Pep deformylase; 1.  
 DR PRINTS; PR01576; PDEFORMYLASE.  
 DR ProDom; PD003844; Pep deformylase; 1.  
 DR TrIRFAME; TRIGR00079; pep deformyl; 1.  
 KW Protein biosynthesis; Hydrolase; Iron; Complete proteome.  
 FT ACT SITE 155 155 BY SIMILARITY.  
 FT METAL 111 111 IRON (BY SIMILARITY).  
 FT METAL 154 154 IRON (BY SIMILARITY).  
 FT METAL 158 158 IRON (BY SIMILARITY).  
 SQ SEQUENCE 183 AA; 20810 MW; 7DC71BF7DC264147 CRC64;

Query Match 89.3%; Score 25; DB 1; Length 183;  
 Best Local Similarity 83.3%; Pred. No. 2.1e+02; Indels 0; Gaps 0;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6

Db |:|:|:|  
 15 LREKAK 20

RESULT 44  
 DPL\_HUMAN STANDARD; PRT; 185 AA.  
 AC Q00765; Q04198; Q9BWH9;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Polypois locus protein 1 (TB2 protein).  
 GN DPL OR TB2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91330307; PubMed=1678319;  
 RA Joslyn G., Carlson M., Thliveris A., Albertsen H., Gelbert L.,  
 RA Samowitz W., Groden J., Stevens J., Spirio L., Robertson M.,  
 RA Sargeant L., Krapcho K., Wolff E., Burt R., Hughes J.P.,  
 RA Warington J., McPherson J.D., Wasmuth J.J., le Paslier D.,  
 RA Abderrahim H., Cohen D., Leppert M., White R.;  
 RT "Identification of deletion mutations and three new genes at the  
 RT familial polyposis locus.";  
 RL Cell 66:601-613(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9133510; PubMed=1651562;  
 RA Kinzler K.W., Nilbert M.C., Su L.K., Vogelstein B., Bryan T.M.,  
 RA Levy D.B., Smith K.J., Preisinger A.C., Hedge P., McKechnie D.,  
 RA Finnick R., Markham A., Groffen J., Boguski M.S., Altschul S.F.,  
 RA Horii A.K., Ando H., Miyoshi Y., Miki Y., Nishisho I., Nakamura Y.;  
 RT "Identification of FAP locus genes from chromosome 5q21.";  
 RL Science 253:661-665(1991).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Eye;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ussin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smaluk D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -!- SIMILARITY: TO C.ELEGANS T19C3.4.  
 CC  
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 CC  
 CC EMBL; M73547; AAA60136.1; -;

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DR EMBL; M74090; AAG6351.1; ALT INIT.
DR EMBL; BC000232; AAH00232.1; -.
DR PIR; A39658; A39658.
DR MIM; 125265; -.
DR GO; GO:0016021; C:integral to membrane; NAS.
DR InterPro; IPR004345; TB2_DPI_HVA22.
DR Pfam; PF03134; TB2_DPI_HVA22; 1.
KW Transmembrane.
FT TRANSMEM 31 51 POTENTIAL.
FT TRANSMEM 86 106 POTENTIAL.
FT CONFLICT 111 111 M -> I (IN REF. 2).
FT CONFLICT 159 159 A -> S (IN REF. 1).
SQ SEQUENCE 185 AA; 21132 MW; E36B961DA56D2BA0 CRC64;

Query Match
Best Local Similarity 89.3%; Score 25; DB 1; Length 185;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
DB 155 LKDKAK 160

RESULT 45
YE46 AQUAE
ID YE46 AQUAE STANDARD; PRT; 185 AA.
AC 067433;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein AQ_1446.
GN AQ_1446.
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Aujay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus.";
RL Nature 392:353-358(1998).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: STRONG, TO A.AEOLICUS AQ_1900.
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CC -----
DR EMBL; AB000741; AAC07402.1; -.
DR PIR; G70425; G70425.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 1 21 POTENTIAL.
FT TRANSMEM 111 131 POTENTIAL.
SQ SEQUENCE 185 AA; 22670 MW; EDA145E48ED739C9 CRC64;

Query Match
Best Local Similarity 89.3%; Score 25; DB 1; Length 185;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
DB 165 LREKAK 170

RESULT 46

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RS4 CHLPN
ID RS4 CHLPN STANDARD; PRT; 209 AA.
AC Q9Z7H2; Q9ZQF0;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 30S ribosomal protein S4.
GN RPSD OR RS4 OR CPN0733 OR CP0013 OR CPB0761.
OS Chlamydia pneumoniae (Chlamydophila pneumoniae).
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
OX NCBI_TaxID=83558;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CWL029;
RX MEDLINE=99206606; PubMed=10192388;
RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
RL Nat. Genet. 21:385-389(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT pneumoniae AR39.";
RL Nucleic Acids Res. 28:1397-1406(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RT from Japan and CML029 from USA.";
RL Nucleic Acids Res. 28:2311-2314(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=TW-183;
RX Geng M.M., Schumacher A., Muehldorfer I., Bensch K.W., Schaefer K.P.,
RA Schneider S., Pohl T., Essig A., Marre R., Melchers K.;
RT "The genome sequence of Chlamydia pneumoniae TW183 and comparison with
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: One of the primary rRNA binding proteins, it binds
CC directly to 16S rRNA where it nucleates assembly of the body of
CC the 30S subunit (By similarity).
CC -!- FUNCTION: With S5 and S12 plays an important role in translational
CC accuracy (By similarity).
CC -!- SUBUNIT: Part of the 30S ribosomal subunit. Contacts protein S5.
CC Of translational fidelity (By similarity).
CC -!- SIMILARITY: Contains 1 S4 RNA-binding domain.
CC -!- SIMILARITY: Belongs to the S4P family of ribosomal proteins.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AE001654; AAD18872.1; -.
DR EMBL; AE002165; AAF37909.1; -.
DR EMBL; AP002547; EAA98940.1; -.
DR EMBL; AE017159; AAF98690.1; -.
DR PIR; A72043; A72043.
DR PIR; B86582; B86582.

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DR HSSP; P81288; 1C05.
DR TIGR; CP0013; -.
DR HAMAP; MF_01306; -.
DR InterPro; IPR001912; Ribosomal_S4.
DR InterPro; IPR005709; Ribosomal_S4_b/o.
DR InterPro; IPR002942; S4.
DR Pfam; PF00163; Ribosomal_S4; 1.
DR SMART; SM00363; S4; 1.
DR TIGRPFAMS; TIGR01017; rpsd bact; 1.
DR PROSITE; PS00632; RIBOSOMAL_S4; FALSE_NEG.
DR PROSITE; PS50889; S4; 1.
KW Ribosomal protein; RNA-binding; Complete proteome.
FT DOMAIN 93 153 S4 RNA-BINDING.
SQ SEQUENCE 209 AA; 24004 MW; 85D95258603D717F CRC64;

Query Match 89.3%; Score 25; DB 1; Length 209;
Best Local Similarity 83.3%; Pred.No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
DB 142 LKEKSK 147

RESULT 47
RS4 CHLTR STANDARD; PRT; 209 AA.
AC O84631;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S4.
GN RPSD OR RS4 OR CT626.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=D/UN-3/Cx;
RX MEDLINE=99000809; PubMed=9784136;
RA Stephens R.S., Kaiman S., Lammel C.J., Fan J., Marathe R., Aravind L., Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V., Davis R.W.;
RA "Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis.";
RT Science 282:754-759(1998).
CC -!- FUNCTION: One of the primary rRNA binding proteins, it binds directly to 16S rRNA where it nucleates assembly of the body of the 30S subunit (By similarity).
CC -!- FUNCTION: With S5 and S12 plays an important role in translational accuracy (By similarity).
CC -!- SUBUNIT: Part of the 30S ribosomal subunit. Contacts protein S5. The interaction surface between S4 and S5 is involved in control of translational fidelity (By similarity).
CC -!- SIMILARITY: Contains 1 S4 RNA-binding domain.
CC -!- SIMILARITY: Belongs to the S4P family of ribosomal proteins.
CC -----
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CC -----
CC EMBL; AE001333; AAC68230.1; -.
CC PIR; C71491; C71491.
CC HSSP; P81288; 1C05.
CC HAMAP; MF_01306; -.
CC InterPro; IPR001912; Ribosomal_S4.
CC InterPro; IPR005709; Ribosomal_S4_b/o.
CC InterPro; IPR002942; S4.

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DR Pfam; PF00163; Ribosomal_S4; 1.
DR SMART; SM00363; S4; 1.
DR TIGRPFAMS; TIGR01017; rpsd bact; 1.
DR PROSITE; PS00632; RIBOSOMAL_S4; FALSE_NEG.
DR PROSITE; PS50889; S4; 1.
KW Ribosomal protein; RNA-binding; Complete proteome.
FT DOMAIN 93 154 S4 RNA-BINDING.
SQ SEQUENCE 209 AA; 23687 MW; 839142405EDC75DE CRC64;

Query Match 89.3%; Score 25; DB 1; Length 209;
Best Local Similarity 83.3%; Pred.No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
DB 142 LKEKSK 147

RESULT 48
FRHG METTH STANDARD; PRT; 235 AA.
AC P19498; O27357;
DT 01-FEB-1991 (Rel. 17, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Coenzyme F420 hydrogenase gamma subunit (EC 1.12.98.1) (8-hydroxy-5-deazaflavin-reducing hydrogenase gamma subunit) (FRH).
GN FRHG OR MTH1298.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=187420;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-30.
RX STRAIN=Delta H;
RX MEDLINE=91002562; PubMed=2207102;
RA Alex L.A., Reeve J.N., Orme-Johnson W.H., Walsh C.T.;
RT "Cloning, sequence determination, and expression of the genes encoding the subunits of the nickel-containing 8-hydroxy-5-deazaflavin reducing hydrogenase from Methanobacterium thermoautotrophicum delta H.";
RT Biochemistry 29:7237-7244(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=Delta H;
RX MEDLINE=98037514; PubMed=9371463;
RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J., Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwan N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics.";
RX J. Bacteriol. 179:7135-7155(1997).
RN [3]
RP SEQUENCE OF 1-14.
RX STRAIN=Delta H;
RX MEDLINE=88024932; PubMed=3663585;
RA Fox J.A., Livingston D.J., Orme-Johnson W.H., Walsh C.T.;
RT "8-hydroxy-5-deazaflavin-reducing hydrogenase from Methanobacterium thermoautotrophicum: 1. Purification and characterization.";
RX Biochemistry 26:4219-4227(1987).
CC -!- FUNCTION: REDUCES THE PHYSIOLOGICAL LOW-POTENTIAL TWO-ELECTRON ACCEPTOR COENZYME F420, AND THE ARTIFICIAL ONE-ELECTRON ACCEPTOR METHYLVIOLGEN.
CC -!- CATALYTIC ACTIVITY: H(2) + coenzyme F420 = reduced coenzyme F420.
CC -!- COFACTOR: FRH contains nickel, iron-sulfur, and FAD cofactors. There are 12-13 Fe atoms/(alpha(1)beta(1)gamma(1)) unit of the FRH.
CC -!- SUBUNIT: HETEROCOMPLEX OF THE FORM (ALPHA(1)BETA(1)GAMMA(1))(8).

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CC -!- SIMILARITY: TO THE SMALL SUBUNITS OF OTHER NI-CONTAINING  
CC HYDROGENASES.

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CC -----  
CC EMBL; J02914; AAA72189.1; -;  
CC EMBL; A800895; AAB85778.1; ALT\_INIT.

DR PIR; C35620; C35620.

DR InterPro; IPR001450; 4Fe4S\_ferredoxin.

DR InterPro; IPR006137; Oxidored\_g6.

DR Pfam; PF00037; fer4; 2.

DR Pfam; PF01058; oxidored\_g6; 1.

DR PROSITE; P500198; 4Fe4S\_FERREDOXIN; 1.

KW Oxidoreductase; Iron-sulfur; 4Fe-4S; Electron transport;

KW Complete proteome.

FT INIT\_MET 0 0

FT METAL 180 180 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).

FT METAL 183 183 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).

FT METAL 186 186 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).

FT METAL 190 190 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).

FT METAL 209 209 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).

FT METAL 212 212 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).

FT METAL 215 215 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).

FT METAL 219 219 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).

FT CONFLICT 13 13 H -> G (IN REF. 3).

FT CONFLICT 94 94 A -> Q (IN REF. 1).

FT SEQUENCE 235 AA; 25685 MW; 0122DCDD135C9AE0 CRC64;

Query Match 89.3%; Score 25; DB 1; Length 235;

Best Local Similarity 83.3%; Pred. No. 2.6e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6

DB 79 LREKAK 84

RESULT 49

YDFB-SCHPO

ID YDFB-SCHPO STANDARD; PRT; 240 AA.

AC Q10483;

DT 01-OCT-1996 (Rel. 34, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Hypothetical protein C17C9.11c in chromosome I.

GN SPAC17C9.11c.

OS Schizosaccharomyces pombe (fission yeast).

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

OC Schizosaccharomycetales; Schizosaccharomycetaceae;

OC Schizosaccharomycetes.

OX NCBI\_TaxID=4896;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=972;

RX MEDLINE=21848401; PubMed=11859360;

RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,

RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,

RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

RA Mooney P., Moutle S., Mungall K., Murphy L., Niblett D., Odell C.,

RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,

RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,

RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,  
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,  
RA Gabel C., Fuchs M., Fritze C., Holzer E., Moestl D., Hilbert H.,  
RA Borzym K., Langer I., Beck A., Lehrach H., Wambutt R., Pohl T.M.,  
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,  
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,  
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,  
RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,  
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,  
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,  
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,  
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;  
RT "The genome sequence of Schizosaccharomyces pombe.";  
RL Nature 415:871-880 (2002).

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CC -----  
CC EMBL; Z73099; CAA97342.2; -;  
CC GeneDB SPombe; SPAC17C9.11c; -;

DR InterPro; IPR007087; Znf\_C2H2.

DR PROSITE; P500028; ZINC\_FINGER\_C2H2\_1; 1.

KW Hypothetical protein; Zinc-finger.

FT ZN\_FING 3 27 C2H2-TYPE.

FT SEQUENCE 240 AA; 27602 MW; A3131E1D3907D11 CRC64;

Query Match 89.3%; Score 25; DB 1; Length 240;

Best Local Similarity 83.3%; Pred. No. 2.7e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6

DB 52 LREKAK 57

RESULT 50

UT11 YEAST

ID UT11 YEAST STANDARD; PRT; 256 AA.

AC P34247;

DT 01-FEB-1994 (Rel. 28, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE U3 small nucleolar RNA-associated protein 11 (U3 snRNA-associated

DE protein 11).

GN UTP11 OR YKL099C OR YKL449.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

OX NCBI\_TaxID=4932;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=S288c;

RX MEDLINE=94078677; PubMed=8256524;

RA Pallier C., Valens M., Fuzos V., Fukuhara H., Cheret G., Sor F.,

RA Bolotin-Fukuhara M.;

RT "DNA sequence analysis of a 17 kb fragment of yeast chromosome XI

RT physically localizes the MRB1 gene and reveals eight new open reading

RT frames, including a homologue of the KIN1/KIN2 and SNF1 protein

RT kinases.";

RL Yeast 9:1149-1155 (1993).

RN [2]

RP FUNCTION, AND SUBCELLULAR LOCATION.

RX MEDLINE=22082292; PubMed=12068309;

RA Dragon F., Gallagher J.E., Compagnone-Post P.A., Mitchell B.M.,

RA Forwancher K.A., Wenne K.A., Wormley S., Settlege R.E.,

RA Shabanowitz J., Osheim Y., Beyer A.L., Hunt D.F., Baserga S.J.;

RT "A large nuclear U3 ribonucleoprotein required for 18S ribosomal RNA

RT biogenesis.";

```

RL Nature 417:967-970(2002).
CC -!- FUNCTION: Involved in nucleolar processing of pre-18S ribosomal
CC RNA.
CC -!- SUBUNIT: Component of the ribosomal small subunit (SSU)
CC processome.
CC -!- SUBCELLULAR LOCATION: Nuclear; nucleolar.
CC -!- SIMILARITY: Belongs to the UTP11 family.
CC -----
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CC -----
DR EMBL; X71133; CAA50458.1; -.
DR EMBL; Z28099; CAA81939.1; -.
DR PIR; S37926; S37926.
DR GerMOnline; I39855; -.
DR SGD; S0001582; UTP11.
DR GO; GO:0005732; C:small nucleolar ribonucleoprotein complex; NAS.
DR GO; GO:0030515; F:snRNA binding; IPI.
DR GO; GO:0003735; F:structural constituent of ribosome; IMP.
DR GO; GO:0030490; F:processing of 20S pre-rRNA; IMP.
DR GO; GO:0006412; P:protein biosynthesis; IMP.
DR InterPro; IPR007144; Utp11.
DR Pfam; PF03998; Utp11; 1.
DR rRNA processing; Nuclear protein.
KW SEQUENCE 256 AA; 30298 MW; E341224F70603579 CRC64;

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Query Match      89.3%; Score 25; DB 1; Length 256;
Best Local Similarity 83.3%; Pred. NO. 2.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      1 LKEKAK 6
Db      51 LREKAK 56

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Search completed: April 19, 2004, 17:18:40
Job time : 5.3871 secs

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OM protein - protein search, using sw model

Run on: April 19, 2004, 17:08:00 ; Search time 26.8065 Seconds  
(without alignments)  
63.242 Million cell updates/sec

Title: US-10-726-692-14  
Perfect score: 28  
Sequence: 1 LKEKAK 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 50 summaries

Database : A\_Geneseq\_29Jan04.\*  
1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	100.0	60	AAU16596	AAU16596 Human nov
2	28	100.0	60	ABU55665	ABU55665 Human nov
3	28	100.0	66	AAW60937	AAW60937 Streptoco
4	28	100.0	85	AAU18490	AAU18490 Peptide #
5	28	100.0	85	ABB37534	ABB37534 Peptide #
6	28	100.0	85	AAU58191	AAU58191 Human bra
7	28	100.0	85	AAU06079	AAU06079 Peptide #
8	28	100.0	132	ABG40332	ABG40332 Human pep
9	28	100.0	134	AAU30534	AAU30534 Novel hum
10	28	100.0	134	ABG22197	ABG22197 Novel hum
11	28	100.0	139	ABG22196	ABG22196 Novel hum
12	28	100.0	141	AAU16181	AAU16181 Human nov
13	28	100.0	141	ABU55250	ABU55250 Human nov
14	28	100.0	158	AAU92244	AAU92244 Human zrn
15	28	100.0	159	ABR52602	ABR52602 Protein s
16	28	100.0	159	ABU35419	ABU35419 Protein e
17	28	100.0	165	ABB64004	ABB64004 Drosophil
18	28	100.0	174	AAU93855	AAU93855 Human pol
19	28	100.0	174	AAU48958	AAU48958 Human col
20	28	100.0	174	ABO52942	ABO52942 Human spl
21	28	100.0	185	AAU84717	AAU84717 A decorin
22	28	100.0	227	AAU30535	AAU30535 Novel hum
23	28	100.0	237	AAU20709	AAU20709 H. pylori
24	28	100.0	247	ABP73270	ABP73270 Candida a
25	28	100.0	249	AAG08495	AAG08495 Arabidops

26	28	100.0	297	4	ABB11849	ABB11849 Human pre
27	28	100.0	302	3	AAG08494	AAG08494 Arabidops
28	28	100.0	322	4	AAB47595	AAB47595 Human DHD
29	28	100.0	326	3	AAG08493	AAG08493 Arabidops
30	28	100.0	326	5	ABR93289	ABR93289 Herbicida
31	28	100.0	326	5	AAE25947	AAE25947 Arabidops
32	28	100.0	326	6	ABU67344	ABU67344 A. thalia
33	28	100.0	331	3	AAU75726	AAU75726 Neisseria
34	28	100.0	338	6	ABU01490	ABU01490 S. pneumo
35	28	100.0	367	4	AAE96209	AAE96209 Putative
36	28	100.0	374	3	AAU75494	AAU75494 Neisseria
37	28	100.0	374	3	AAU75728	AAU75728 Neisseria
38	28	100.0	374	4	AAU37739	AAU37739 Streptoco
39	28	100.0	377	3	AAU75727	AAU75727 Neisseria
40	28	100.0	377	3	AAU75493	AAU75493 Neisseria
41	28	100.0	377	3	AAU75492	AAU75492 Neisseria
42	28	100.0	377	6	ABP08049	ABP08049 N. gonorr
43	28	100.0	386	7	ADC35104	ADC35104 Human bre
44	28	100.0	391	6	ABU11889	ABU11889 Human ABC
45	28	100.0	391	7	ADE55135	ADE55135 Rat Prote
46	28	100.0	391	7	ADE55144	ADE55144 Rat Prote
47	28	100.0	391	7	ADE55141	ADE55141 Rat Prote
48	28	100.0	391	7	ADE55147	ADE55147 Rat Prote
49	28	100.0	391	7	ADE55138	ADE55138 Rat Prote
50	28	100.0	391	7	ADE55132	ADE55132 Rat Prote

ALIGNMENTS

RESULT 1

AAU16596	AAU16596 standard; protein; 60 AA.
ID	AAU16596 standard; protein; 60 AA.
XX	
AC	AAU16596;
XX	
DT	07-NOV-2001 (first entry)
XX	
DE	Human novel secreted protein, Seq ID 1549.
XX	
KW	Human; immunosuppressive; antiarthritic; antirheumatic; cytostatic;
KW	cardiant; vasotropic; cerebroprotective; nontropic; neuroprotective;
KW	antibacterial; virucide; fungicide; ophthalmological; vulnerary;
KW	secreted protein; rheumatoid arthritis; hyperproliferative disorder;
KW	cardiovascular disorder; cardiac arrest; cerebrovascular disorder;
KW	cerebral ischaemia; angiogenesis; nervous system disorder;
KW	Alzheimer's disease; infection; ocular disorder; corneal infection;
KW	wound healing; epithelial cell proliferation; skin ageing; food additive;
KW	preservative; antiproliferative.
XX	
OS	Homo sapiens.
XX	
PN	WO200155322-A2.
XX	
PD	02-AUG-2001.
XX	
PF	17-JAN-2001; 2001WO-US001341.
XX	
PR	31-JAN-2000; 2000US-0179065P.
PR	04-FEB-2000; 2000US-0180628P.
PR	24-FEB-2000; 2000US-0184664P.
PR	02-MAR-2000; 2000US-0186350P.
PR	16-MAR-2000; 2000US-0189874P.
PR	17-MAR-2000; 2000US-0190076P.
PR	18-APR-2000; 2000US-0198123P.
PR	19-MAY-2000; 2000US-0205515P.
PR	28-JUN-2000; 2000US-0209467P.
PR	28-JUN-2000; 2000US-0214886P.
PR	30-JUN-2000; 2000US-0215135P.
PR	07-JUL-2000; 2000US-0216647P.
PR	11-JUL-2000; 2000US-0216880P.
PR	11-JUL-2000; 2000US-0217487P.
PR	11-JUL-2000; 2000US-0217496P.



CC arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis,  
 CC nervous system disorders e.g. Alzheimer's disease, infections caused by  
 CC bacteria, viruses and fungi and ocular disorders e.g. corneal infection,  
 CC and many other disorders listed in the specification. The polypeptides  
 CC can also be used to aid wound healing and epithelial cell proliferation,  
 CC to prevent skin aging due to sunburn, to maintain organs before  
 CC transplantation, for supporting cell culture of primary tissues, to  
 CC regenerate tissues and in chemotaxis. The polypeptides can also be used  
 CC as a food additive or preservative to increase or decrease storage  
 CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,  
 CC minerals, cofactors and other nutritional components. The present  
 CC sequence represents a novel secreted protein of the invention. Note: The  
 CC sequence data for this patent did not form part of the printed

Query Match 100.0%; Score 28; DB 4; Length 60;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6

Db 47 LKEKAK 52

# RESULT 2

ABUS5665

ID ABUS5665 standard; protein; 60 AA.

AC ABUS5665;

DT 18-MAR-2003 (first entry)

DE Human novel polypeptide #752.

XX Human; neural disorder; immune system disorder; renal disorder;  
 KW muscular disorder; respiratory disease; reproductive disorder;  
 KW gastrointestinal disorder; pulmonary disorder; cardiovascular disorder;  
 KW hyperproliferative disorder; inflammatory disease; allergic reaction;  
 KW blood related disorder; cancer; immunosuppressive; antiinflammatory;  
 KW cardiovascular; nephrotropic; cytostatic; antiallergic; thrombolytic;  
 KW haemostatic; antiarteriosclerotic.

OS Homo sapiens.

PN US2002132753-A1.

XX 19-SEP-2002.

PF 17-JAN-2001; 2001US-00764864.

XX 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 28-JUN-2000; 2000US-0214886P.

PR 07-JUL-2000; 2000US-0216647P.

PR 07-JUL-2000; 2000US-0216680P.

PR 11-JUL-2000; 2000US-0217487P.

PR 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.

PR 26-JUL-2000; 2000US-0220964P.

PR 14-AUG-2000; 2000US-0224518P.

PR 14-AUG-2000; 2000US-0224519P.

PR 14-AUG-2000; 2000US-0225267P.

PR 14-AUG-2000; 2000US-0225268P.

PR 14-AUG-2000; 2000US-0225270P.

PR 14-AUG-2000; 2000US-0225447P.

PR 14-AUG-2000; 2000US-0225757P.

PR 22-AUG-2000; 2000US-0225758P.

PR 30-AUG-2000; 2000US-0228924P.

PR 01-SEP-2000; 2000US-0229287P.

PR 01-SEP-2000; 2000US-0229343P.

PR 01-SEP-2000; 2000US-0229344P.

PR 01-SEP-2000; 2000US-0229345P.

PR 05-SEP-2000; 2000US-0229509P.  
 PR 05-SEP-2000; 2000US-0229513P.  
 PR 08-SEP-2000; 2000US-0231413P.  
 PR 21-SEP-2000; 2000US-0234223P.  
 PR 21-SEP-2000; 2000US-0234274P.  
 PR 25-SEP-2000; 2000US-0234997P.  
 PR 27-SEP-2000; 2000US-023634P.  
 PR 29-SEP-2000; 2000US-0236327P.  
 PR 29-SEP-2000; 2000US-0236367P.  
 PR 29-SEP-2000; 2000US-0236368P.  
 PR 29-SEP-2000; 2000US-0236369P.  
 PR 29-SEP-2000; 2000US-0236370P.  
 PR 02-OCT-2000; 2000US-0236802P.  
 PR 02-OCT-2000; 2000US-0237037P.  
 PR 02-OCT-2000; 2000US-0237038P.  
 PR 02-OCT-2000; 2000US-0237039P.  
 PR 02-OCT-2000; 2000US-0237040P.  
 PR 13-OCT-2000; 2000US-023935P.  
 PR 20-OCT-2000; 2000US-0240960P.  
 PR 20-OCT-2000; 2000US-0241785P.  
 PR 20-OCT-2000; 2000US-0241809P.  
 PR 01-NOV-2000; 2000US-0244617P.  
 PR 17-NOV-2000; 2000US-0249299P.  
 PR 08-DEC-2000; 2000US-0251858P.  
 PR 08-DEC-2000; 2000US-0251868P.  
 PR 08-DEC-2000; 2000US-0251869P.

(ROSE/) ROSEN C A.

PA (RUBE/) RUBEN S M.

PA (BARA/) BARASH S C.

XX Rosen CA, Ruben SM, Barash SC;

XX WPI; 2003-147444/14.

DR N-PSDB; ABX73924.

XX New polypeptides and nucleic acids, useful in gene therapy for treating,  
 PT inhibiting or preventing e.g. neural, immune system, muscular,  
 PT respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or  
 PT renal disorders.

PS Claim 11; SEQ ID NO 1549; 402pp; English.

XX The invention relates to human novel polypeptides and their associated  
 CC polynucleotides. The polypeptides and polynucleotides are useful in gene  
 CC therapy for treating, inhibiting or preventing neural disorders, immune  
 CC system disorders (e.g. systemic lupus erythematosus, rheumatoid arthritis  
 CC and multiple sclerosis), muscular disorders, respiratory diseases (e.g.  
 CC nasal vestibulitis, nasal polyps and sinusitis), reproductive disorders,  
 CC gastrointestinal disorders, pulmonary disorders, cardiovascular disorders  
 CC (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left  
 CC heart syndrome), renal disorders (e.g. acute kidney failure and end-stage  
 CC renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and  
 CC leukaemia), inflammatory diseases (e.g. septic shock, bursitis and  
 CC appendicitis), allergic reactions and conditions (e.g. asthma), blood  
 CC related disorders (e.g. thrombosis, atherosclerosis and myocardial  
 CC infarction) and cancerous diseases. Sequences ABUS4914-ABUS5699 and  
 CC ABUS5748 represent human novel polypeptides of the invention

XX Sequence 60 AA;

Query Match 100.0%; Score 28; DB 6; Length 60;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6

Db 47 LKEKAK 52

RESULT 3

AAW60937

ID AAW60937 standard; protein; 66 AA.

```

XX AAW60937;
XX AC
XX 13-OCT-1998 (first entry)
XX DT
XX DE
XX DE Streptococcus pneumoniae encoded polypeptide.
XX KW coding region; ORF; open reading frame; antibacterial; infection;
XX KW prevention; meningitis.
XX OS Streptococcus pneumoniae.
XX PN WO9819689-A1.
XX PD 14-MAY-1998.
XX PF 27-OCT-1997; 97WO-US019226.
XX PI 01-NOV-1996; 96US-0029930P.
XX PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX PI Black MT, Hodgson JE, Knowles DJC, Lonetto MA, Nicholas RO;
XX PI Reid RH, Zarfos PN;
XX PD WPI; 1998-286586/25.
XX DR N-P8DB; AAV37337.
XX PT New isolated nucleic acids from Streptococcus pneumoniae - useful, e.g.
XX PT for identifying anti-bacterial(s) for treatment and prevention of
XX PT meningitis.
XX PS Claim 11; Page 41; 130pp; English.
XX CC The sequence is that of the polypeptide encoded by a region isolated from
XX CC S. pneumoniae. The protein, or agonists of it, may be useful as an
XX CC antibacterial for treatment or prevention of infection, specifically
XX CC caused by S. pneumoniae (particularly meningitis) but possibly also
XX CC Helicobacter pylori (ulcers and gastric cancer). It may be of particular
XX CC use before insertion of an in-dwelling device or any other invasive
XX CC procedure. The protein, or nucleic acid encoding it, can also be used in
XX CC vaccines to induce a cellular and/or humoral immune response, or to
XX CC screen for other antibacterials. The DNA may also contain flanking
XX CC sequences that are potential sources of control elements for bacterial
XX CC gene expression. Detecting a sequence encoding the protein can be used
XX CC diagnostically, e.g. to detect a mutation for serotyping or classifying
XX CC infectious agents
XX SQ Sequence 66 AA;

Query Match 100.0%; Score 28; DB 2; Length 66;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
DB 33 LKEKAK 38

RESULT 4
AAM18490
ID AAM18490 standard; protein; 85 AA.
XX AC
XX AAM18490;
XX DT 12-OCT-2001 (first entry)
XX DE Peptide #4924 encoded by probe for measuring cervical gene expression.
XX KW Probe; human; microarray; gene expression; cervical epithelial cell;
XX KW cervical cancer.
XX

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OS Homo sapiens.
XX PN WO200157278-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000670.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX PD WPI; 2001-488901/53.
XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
XX PT gene expression in human cervical epithelial cells.
XX PS Claim 27; SEQ ID NO 23316; 487pp; English.
XX CC The present invention relates to human single exon nucleic acid probes
XX CC (SENP; see AAI10068-AAI28459). The present sequence is a peptide encoded
XX CC by one such probe. The SENPs are derived from human HeLa cells. The SENPs
XX CC can be used to produce a single exon microarray, which can be used for
XX CC measuring human gene expression in a sample derived from human cervical
XX CC epithelial cells. By measuring gene expression, the probes are therefore
XX CC useful in grading and/or staging of diseases of the cervix, notably
XX CC cervical cancer. Note: The sequence data for this patent did not form
XX CC part of the printed specification, but was obtained in electronic format
XX CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 85 AA;

Query Match 100.0%; Score 28; DB 4; Length 85;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
DB 28 LKEKAK 33

RESULT 5
ABB37534
ID ABB37534 standard; peptide; 85 AA.
XX AC
XX ABB37534;
XX DT 04-FEB-2002 (first entry)
XX DE Peptide #5040 encoded by human foetal liver single exon probe.
XX KW Human; foetal liver; gene expression; single exon nucleic acid probe.
XX OS Homo sapiens.
XX PN WO200157277-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000669.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.

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PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX WPI; 2001-483447/52.  
 XX Human genome-derived single exon nucleic acid probes useful for analyzing  
 XX gene expression in human fetal liver.  
 PT  
 PT  
 XX Claim 27; SEQ ID NO 30169; 639pp + Sequence Listing; English.  
 XX  
 CC The invention relates to a single exon nucleic acid probe for measuring  
 CC human gene expression in a sample derived from human foetal liver. The  
 CC single exon nucleic acid probes may be used for predicting, measuring and  
 CC displaying gene expression in samples derived from human fetal liver. The  
 CC present sequence is a peptide encoded by a single exon nucleic acid probe  
 CC of the invention. Note: The sequence data for this patent did not form  
 CC part of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://ftp.wipo.int/pub/published_pct_sequences)  
 XX  
 XX Sequence 85 AA;  
 SQ  
 Query Match 100.0%; Score 28; DB 4; Length 85;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LKEKAK 6  
 DB 28 LKEKAK 33  
 RESULT 6  
 AAM58191  
 ID AAM58191 standard; protein; 85 AA.  
 AC AAM58191;  
 XX  
 XX 05-NOV-2001 (first entry)  
 DT  
 XX Human brain expressed single exon probe encoded protein SEQ ID NO: 30296.  
 DE  
 XX Human; brain expressed exon; gene expression analysis; probe; microarray;  
 KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.  
 KW  
 XX Homo sapiens.  
 OS  
 XX WO200157275-A2.  
 PN  
 XX 09-AUG-2001.  
 PD  
 XX 30-JAN-2001; 2001WO-US000667.  
 PF  
 XX 04-FEB-2000; 2000US-0180312P.  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 30-JUN-2000; 2000US-00608408.  
 PR 03-AUG-2000; 2000US-00632366.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 XX (MOLE-) MOLECULAR DYNAMICS INC.  
 PA  
 XX Penn SG, Hanzel DK, Chen W, Rank DR;  
 PI WPI; 2001-483446/52.  
 XX Single exon nucleic acid probes for analyzing gene expression in human  
 PT brains.  
 XX

PS Example 4; SEQ ID NO 30296; 650pp + Sequence Listing; English.  
 XX  
 CC The present invention provides a number of single exon nucleic acid  
 CC probes which are derived from genomic sequences expressed in the human  
 CC brain. They can be used to measure gene expression in brain cell samples,  
 CC which may enable the diagnosis and improved treatment of nervous system  
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, of  
 CC epilepsy and cancers. The present sequence is a protein encoded by one of  
 CC the probes of the invention  
 XX  
 SQ Sequence 85 AA;  
 Query Match 100.0%; Score 28; DB 4; Length 85;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LKEKAK 6  
 DB 28 LKEKAK 33  
 RESULT 7  
 AAM06079  
 ID AAM06079 standard; protein; 85 AA.  
 XX  
 XX AAM06079;  
 AC  
 XX  
 XX 09-OCT-2001 (first entry)  
 DT  
 XX Peptide #4761 encoded by probe for measuring breast gene expression.  
 DE  
 XX Probe; human; breast disease; breast cancer; development disorder;  
 KW inflammatory disease; proliferative breast disease; non-carcinoma tumour.  
 KW  
 XX Homo sapiens.  
 OS  
 XX WO200157270-A2.  
 PN  
 XX 09-AUG-2001.  
 PD  
 XX 29-JAN-2001; 2001WO-US000661.  
 PF  
 XX 04-FEB-2000; 2000US-0180312P.  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 30-JUN-2000; 2000US-00608408.  
 PR 03-AUG-2000; 2000US-00632366.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 XX (MOLE-) MOLECULAR DYNAMICS INC.  
 PA  
 XX Penn SG, Hanzel DK, Chen W, Rank DR;  
 PI WPI; 2001-476286/51.  
 XX Novel single exon nucleic acid probe used to measuring gene expression in  
 XX a human breast.  
 DT  
 XX Claim 27; SEQ ID NO 14819; 322pp; English.  
 PS  
 CC The present invention relates to novel single exon nucleic acid probes  
 CC (see AAI00010-AA110067). The present sequence is a peptide encoded by one  
 CC such probe. The probes are useful for measuring human gene expression in  
 CC a human breast sample, where the probe hybridises at high stringency to a  
 CC nucleic acid expressed in the human breast. The probes are useful for  
 CC predicting, diagnosing, grading, staging, monitoring and prognosing  
 CC diseases of the human breast, particularly those diseases with polygenic  
 CC aetiology. The diseases include: breast cancer, disorders of development,  
 CC inflammatory diseases of the breast, fibrocystic changes, proliferative  
 CC breast disease and non-carcinoma tumours. Note: The sequence data for  
 CC this patent did not form part of the printed specification, but was  
 CC obtained in electronic format directly from WIPO at

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CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 85 AA;
SQ
  Query Match      100.0%; Score 28; DB 4; Length 85;
  Best Local Similarity 100.0%; Pred. No. 2.5e+02;
  Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
DB 28 LKEKAK 33

RESULT 8
ABG40332
ID ABG40332 standard; peptide; 85 AA.
AC ABG40332;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human peptide encoded by genome-derived single exon probe SEQ ID 29997.
XX
KW Human; single exon probe; asthma; lung cancer; COPD; ILD;
KW chronic obstructive pulmonary disease; interstitial lung disease;
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW primary ciliary dyskinesia; pulmonary hypertension;
KW hyaline membrane disease.
XX
OS Homo sapiens.
XX
PN WO200186003-A2.
XX
PD 15-NOV-2001.
XX
PF 30-JAN-2001; 2001WO-US000665.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2002-114183/15.
XX
PT Spatially-addressable set of single exon nucleic acid probes, used to
PT measure gene expression in human lung samples.
XX
PS Claim 27; SEQ ID NO 29997; 634pp; English.
XX
CC The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human lung comprising single exon nucleic acid probes having one of
CC 12614 nucleic acid sequences mentioned in the specification, or their
CC complements or the 12387 open reading frames derived from the 12614
CC probes. Also included are a microarray comprising the novel set of probes
CC ; the novel set of probes which hybridise at high stringency to a nucleic
CC acid expressed in the human lung; measuring gene expression in a sample
CC derived from human lung, comprising (a) contacting the array with a
CC collection of detectably labeled nucleic acids derived from human lung
CC mRNA, and (b) measuring the label detectably bound to each probe of the
CC array; identifying exons in a eukaryotic genome, comprising (a)
CC algorithmically predicting at least one exon from genomic sequences of

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CC the eukaryote; and (b) detecting specific hybridisation of detectably
CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
CC having a fragment identical to the predicted exon, the probe is included
CC in the above mentioned microarray; assigning exons to a single gene,
CC comprising (a) identifying exons from genomic sequence by the method
CC above and (b) measuring the expression of each of the exons in several
CC tissues and/or cell types using hybridisation to a single exon
CC microarrays having a probe with the exon, where a common pattern of
CC expression of the exons in the tissues and/or cell types indicates that
CC the exons should be assigned to a single gene; a peptide comprising one
CC of 12011 sequences, mentioned in the specification, or encoded by the
CC probes/open reading frames (ORF). The probes are used for gene expression
CC analysis, and for identifying exons in a gene, particularly using human
CC lung derived mRNA and for the study of lung diseases such as asthma, lung
CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
CC Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
CC present sequence is a peptide/protein encoded by a single exon probe of
CC the invention. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 85 AA;
  Query Match      100.0%; Score 28; DB 5; Length 85;
  Best Local Similarity 100.0%; Pred. No. 2.5e+02;
  Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
DB 28 LKEKAK 33

RESULT 9
AAU30534
ID AAU30534 standard; protein; 132 AA.
XX
AC AAU30534;
XX
DT 18-DEC-2001 (first entry)
XX
DE Novel human secreted protein #1025.
XX
KW Human; vaccination; gene therapy; nutritional supplement;
KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200179449-A2.
XX
PD 25-OCT-2001.
XX
PF 16-APR-2001; 2001WO-US008656.
XX
PR 18-APR-2000; 2000US-00552929.
XX
PR 26-JAN-2001; 2001US-00770160.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-611725/70.
XX
KW Nucleic acids encoding a range of human polypeptides, useful in genetic
KW vaccination, testing and therapy.
XX
PS Claim 20; Page 307; 765pp; English.
XX

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CC The invention relates to novel human secreted polypeptides. The  
 CC polypeptides and antibodies to the polypeptides are useful for  
 CC determining the presence of or predisposition to a disease associated  
 CC with altered levels of polypeptide. The polypeptides are also useful for  
 CC identifying agents (agonists and antagonists) that bind to them. Cells  
 CC expressing the proteins are useful for identifying a therapeutic agent  
 CC for use in treatment of a pathology related to aberrant expression or  
 CC physiological interactions of the polypeptide. Vectors comprising the  
 CC nucleic acids encoding the polypeptides and cells genetically engineered  
 CC to express them are also useful for producing the proteins. The proteins  
 CC are useful in genetic vaccination, testing and therapy, and can be used  
 CC as nutritional supplements. They may be used to increase stem cell  
 CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon  
 CC and/or nerve tissue growth or regeneration; immune suppression and/or  
 CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.  
 CC AAU29510-AAU33304 represent the amino acid sequences of novel human  
 CC secreted proteins of the invention

XX Sequence 132 AA;

Query Match 100.0%; Score 28; DB 4; Length 132;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
 DB 32 LKEKAK 37  
 |||||

RESULT 10

ABG22197  
 ID ABG22197 standard; protein; 134 AA.

XX AC  
 XX ABG22197;

DT 18-FEB-2002 (first entry)

DE Novel human diagnostic protein #22188.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US008631.

XX 31-MAR-2000; 2000US-00540217.

XX 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX N-PSDB; AAS86384.

XX New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity.

XX Claim 20; SEQ ID NO 52556; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)  
 CC sequences. (I) is useful as hybridisation probes, polymerase chain  
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
 CC and in recombinant production of (II). The polynucleotides are also used  
 CC in diagnostics as expressed sequence tags for identifying expressed  
 CC genes. (I) is useful in gene therapy techniques to restore normal

CC activity of (II) or to treat disease states involving (II). (II) is  
 CC useful for generating antibodies against it, detecting or quantitating a  
 CC polypeptide in tissue, as molecular weight markers and as a food  
 CC supplement. (II) and its binding partners are useful in medical imaging  
 CC of sites expressing (II). (I) and (II) are useful for treating disorders  
 CC involving aberrant protein expression or biological activity. The  
 CC polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic  
 CC amino acid sequences of the invention. Note: The sequence data for this  
 CC patent did not appear in the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 134 AA;

Query Match 100.0%; Score 28; DB 4; Length 134;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
 DB 122 LKEKAK 127  
 |||||

RESULT 11

ABG22196

ID ABG22196 standard; protein; 139 AA.

XX AC  
 XX ABG22196;

DT 18-FEB-2002 (first entry)

DE Novel human diagnostic protein #22187.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US008631.

XX 31-MAR-2000; 2000US-00540217.

XX 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX N-PSDB; AAS86383.

XX New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity.

XX Claim 20; SEQ ID NO 52555; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)  
 CC sequences. (I) is useful as hybridisation probes, polymerase chain  
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
 CC and in recombinant production of (II). The polynucleotides are also used  
 CC in diagnostics as expressed sequence tags for identifying expressed  
 CC genes. (I) is useful in gene therapy techniques to restore normal  
 CC activity of (II) or to treat disease states involving (II). (II) is  
 CC useful for generating antibodies against it, detecting or quantitating a

CC polypeptide in tissue, as molecular weight markers and as a food  
CC supplement. (II) and its binding partners are useful in medical imaging  
CC of sites expressing (II). (I) and (II) are useful for treating disorders  
CC involving aberrant protein expression or biological activity. The  
CC polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic  
CC amino acid sequences of the invention. Note: The sequence data for this  
CC patent did not appear in the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 139 AA;

SQ Query Match 100.0%; Score 28; DB 4; Length 139;

Best Local Similarity 100.0%; Pred. No. 4.1e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6

Db 114 LKEKAK 119

RESULT 12

AAU16181

ID AAU16181 standard; protein; 141 AA.

XX AC AAU16181;

XX 07-NOV-2001 (first entry)

XX Human novel secreted protein, Seq ID 1134.

XX Human; immunosuppressive; antiarthritic; antirheumatic; cytostatic;

KW cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective;

KW antibacterial; virucide; fungicide; ophthalmological; vulnerary;

KW secreted protein; rheumatoid arthritis; hyperproliferative disorder;

KW cardiovascular disorder; cardiac arrest; cerebrovascular disorder;

KW cerebral ischaemia; angiogenesis; nervous system disorder;

KW Alzheimer's disease; infection; ocular disorder; corneal infection;

KW wound healing; epithelial cell proliferation; skin ageing; food additive;

KW preservative; antiproliferative.

XX Homo sapiens.

XX WO200155322-A2.

XX 02-AUG-2001.

XX 17-JAN-2001; 2001WO-US001341.

XX 31-JAN-2000; 2000US-0179065P.

XX 04-FEB-2000; 2000US-0180628P.

XX 24-FEB-2000; 2000US-0184664P.

XX 02-MAR-2000; 2000US-0186350P.

XX 16-MAR-2000; 2000US-0189874P.

XX 17-MAR-2000; 2000US-0190076P.

XX 18-APR-2000; 2000US-0198123P.

XX 19-MAY-2000; 2000US-0205515P.

XX 07-JUN-2000; 2000US-0209467P.

XX 28-JUN-2000; 2000US-0214886P.

XX 30-JUN-2000; 2000US-0215135P.

XX 07-JUL-2000; 2000US-0216647P.

XX 11-JUL-2000; 2000US-0217487P.

XX 11-JUL-2000; 2000US-0217496P.

XX 14-JUL-2000; 2000US-0218290P.

XX 26-JUL-2000; 2000US-0220563P.

XX 14-AUG-2000; 2000US-0224518P.

XX 14-AUG-2000; 2000US-0224519P.

PR 14-AUG-2000; 2000US-0225213P.  
PR 14-AUG-2000; 2000US-0225214P.  
PR 14-AUG-2000; 2000US-0225266P.  
PR 14-AUG-2000; 2000US-0225267P.  
PR 14-AUG-2000; 2000US-0225268P.  
PR 14-AUG-2000; 2000US-0225270P.  
PR 14-AUG-2000; 2000US-0225447P.  
PR 14-AUG-2000; 2000US-0225757P.  
PR 14-AUG-2000; 2000US-0225758P.  
PR 14-AUG-2000; 2000US-0225759P.  
PR 18-AUG-2000; 2000US-0226279P.  
PR 22-AUG-2000; 2000US-0226681P.  
PR 22-AUG-2000; 2000US-0226686P.  
PR 22-AUG-2000; 2000US-0227182P.  
PR 23-AUG-2000; 2000US-0227009P.  
PR 30-AUG-2000; 2000US-0228924P.  
PR 01-SEP-2000; 2000US-0229287P.  
PR 01-SEP-2000; 2000US-0229343P.  
PR 01-SEP-2000; 2000US-0229344P.  
PR 01-SEP-2000; 2000US-0229345P.  
PR 05-SEP-2000; 2000US-0229509P.  
PR 05-SEP-2000; 2000US-0229513P.  
PR 06-SEP-2000; 2000US-0230437P.  
PR 06-SEP-2000; 2000US-0230438P.  
PR 08-SEP-2000; 2000US-0231242P.  
PR 08-SEP-2000; 2000US-0231243P.  
PR 08-SEP-2000; 2000US-0231244P.  
PR 08-SEP-2000; 2000US-0231413P.  
PR 08-SEP-2000; 2000US-0231414P.  
PR 08-SEP-2000; 2000US-0232080P.  
PR 08-SEP-2000; 2000US-0232081P.  
PR 12-SEP-2000; 2000US-0231968P.  
PR 14-SEP-2000; 2000US-0232397P.  
PR 14-SEP-2000; 2000US-0232398P.  
PR 14-SEP-2000; 2000US-0232399P.  
PR 14-SEP-2000; 2000US-0232400P.  
PR 14-SEP-2000; 2000US-0232401P.  
PR 14-SEP-2000; 2000US-0233063P.  
PR 14-SEP-2000; 2000US-0233064P.  
PR 14-SEP-2000; 2000US-0233065P.  
PR 21-SEP-2000; 2000US-0234223P.  
PR 21-SEP-2000; 2000US-0234274P.  
PR 25-SEP-2000; 2000US-0234997P.  
PR 25-SEP-2000; 2000US-0234998P.  
PR 26-SEP-2000; 2000US-0235484P.  
PR 27-SEP-2000; 2000US-0235834P.  
PR 27-SEP-2000; 2000US-0235835P.  
PR 29-SEP-2000; 2000US-0236327P.  
PR 29-SEP-2000; 2000US-0236327P.  
PR 29-SEP-2000; 2000US-0236368P.  
PR 29-SEP-2000; 2000US-0236369P.  
PR 29-SEP-2000; 2000US-0236370P.  
PR 02-OCT-2000; 2000US-0236802P.  
PR 02-OCT-2000; 2000US-0237037P.  
PR 02-OCT-2000; 2000US-0237038P.  
PR 02-OCT-2000; 2000US-0237039P.  
PR 02-OCT-2000; 2000US-0237040P.  
PR 13-OCT-2000; 2000US-0239935P.  
PR 13-OCT-2000; 2000US-0239937P.  
PR 20-OCT-2000; 2000US-0240960P.  
PR 20-OCT-2000; 2000US-0241221P.  
PR 20-OCT-2000; 2000US-0241785P.  
PR 20-OCT-2000; 2000US-0241786P.  
PR 20-OCT-2000; 2000US-0241787P.  
PR 20-OCT-2000; 2000US-0241808P.  
PR 20-OCT-2000; 2000US-0241809P.  
PR 20-OCT-2000; 2000US-0241826P.  
PR 01-NOV-2000; 2000US-0244617P.  
PR 08-NOV-2000; 2000US-0246474P.  
PR 08-NOV-2000; 2000US-0246475P.  
PR 08-NOV-2000; 2000US-0246476P.  
PR 08-NOV-2000; 2000US-0246477P.  
PR 08-NOV-2000; 2000US-0246478P.





PR 25-SEP-2000; 2000US-0234997P.  
 PR 27-SEP-2000; 2000US-0235834P.  
 PR 29-SEP-2000; 2000US-0236327P.  
 PR 29-SEP-2000; 2000US-0236367P.  
 PR 29-SEP-2000; 2000US-0236368P.  
 PR 29-SEP-2000; 2000US-0236369P.  
 PR 29-SEP-2000; 2000US-0236370P.  
 PR 02-OCT-2000; 2000US-0236802P.  
 PR 02-OCT-2000; 2000US-0237037P.  
 PR 02-OCT-2000; 2000US-0237038P.  
 PR 02-OCT-2000; 2000US-0237039P.  
 PR 13-OCT-2000; 2000US-0237040P.  
 PR 20-OCT-2000; 2000US-0239935P.  
 PR 20-OCT-2000; 2000US-0240960P.  
 PR 20-OCT-2000; 2000US-0241785P.  
 PR 20-OCT-2000; 2000US-0241809P.  
 PR 01-NOV-2000; 2000US-0244617P.  
 PR 17-NOV-2000; 2000US-0249299P.  
 PR 08-DEC-2000; 2000US-0251856P.  
 PR 08-DEC-2000; 2000US-0251868P.  
 PR 08-DEC-2000; 2000US-0251869P.  
 XX  
 PA (ROSE/) ROSEN C A.  
 PA (RUBE/) RUBEN S M.  
 PA (BARA/) BARASH S C.  
 XX  
 PI Rosen CA, Ruben SM, Barash SC;  
 XX  
 XX WPI; 2003-147444/14.  
 DR N-PSDB; ABX73509.  
 DR  
 XX  
 XX New polypeptides and nucleic acids, useful in gene therapy for treating,  
 PT inhibiting or preventing e.g. neural, immune system, muscular,  
 PT respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or  
 PT renal disorders.  
 XX  
 PS Claim 11; SEQ ID NO 1134; 402pp; English.  
 XX  
 XX The invention relates to human novel polypeptides and their associated  
 CC polynucleotides. The polypeptides and polynucleotides are useful in gene  
 CC therapy for treating, inhibiting or preventing neural disorders, immune  
 CC system disorders (e.g. systemic lupus erythematosus, rheumatoid arthritis  
 CC and multiple sclerosis), muscular disorders, respiratory diseases (e.g.  
 CC nasal vestibulitis, nasal polyps and sinusitis), reproductive disorders,  
 CC gastrointestinal disorders, pulmonary disorders, cardiovascular disorders  
 CC (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left  
 CC heart syndrome), renal disorders (e.g. acute kidney failure and end-stage  
 CC renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and  
 CC leukaemia), inflammatory diseases (e.g. septic shock, bursitis and  
 CC appendicitis), allergic reactions and conditions (e.g. asthma), blood  
 CC related disorders (e.g. thrombosis, atherosclerosis and myocardial  
 CC infarction) and cancerous diseases. Sequences ABU54914-ABU55699 and  
 CC ABU55748 represent human novel polypeptides of the invention  
 XX  
 SQ Sequence 141 AA;  
 Query Match 100.0%; Score 28; DB 6; Length 141;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LXEKAK 6  
 DB 95 LXEKAK 100  
 |||||  
 RESULT 14  
 AAY92244  
 ID AAY92244 standard; protein; 158 AA.  
 XX  
 AC AAY92244;  
 XX  
 DT 10-AUG-2000 (first entry)  
 XX

DE Human zrnpl (ribonucleoprotein 1).  
 XX  
 KW Zrnpl; ribonucleoprotein; 14q22.2; 14q23.1; mRNA processing;  
 KW connective tissue; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Protein 34..158  
 FT /label= "mature\_protein"  
 FT /note= "putative"  
 FT Domain 59..135  
 FT /label= RNA\_binding\_domain  
 FT Peptide 59..64  
 FT /label= beta-strand\_1  
 FT /note= "RNP-2 motif"  
 FT 60  
 FT Binding-site  
 FT Peptide 70..77  
 FT /label= alpha-helix\_1  
 FT Peptide 83..89  
 FT /label= beta-strand\_2  
 FT Peptide 98..105  
 FT /label= beta-strand\_3  
 FT /note= "RNP consensus octamer"  
 FT 100  
 FT Binding-site  
 FT Peptide 109..117  
 FT /label= alpha-helix\_2  
 FT Peptide 130..135  
 FT /label= beta-strand\_4  
 FT 140..158  
 FT Region  
 FT /label= C-terminal  
 FT /note= "very basic any may interact with repetitive  
 FT structures in RNA and modify the overall strength of the  
 FT RNA binding"  
 XX  
 XX WO200020583-A1.  
 XX  
 PD 13-APR-2000.  
 XX  
 PF 28-SEP-1999; 99WO-US022464.  
 XX  
 PR 08-OCT-1998; 98US-0103513P.  
 PR 15-OCT-1998; 98US-0104381P.  
 XX  
 XX (ZYMO ) ZYMOGENETICS INC.  
 PI Conklin DC, Rixon MW;  
 XX  
 DR WPI; 2000-303771/26.  
 DR N-PSDB; AAA09173, AAA09174.  
 XX  
 XX Novel ribonucleoprotein homolog zrnpl used for mediating mRNA processing  
 XX and for diagnosis and treatment of diseases associated with connective  
 XX tissue.  
 PT  
 XX Claim 14; Page 83; 93pp; English.  
 XX  
 PS The human zrnpl shows homology to ribonucleoproteins. The zrnpl gene was  
 CC localized to chromosome 14q22.2-23.1. Proximal and distal framework  
 CC markers were WI-6253 and WI-5815, respectively. The zrnpl DNA and  
 CC polypeptides are used to mediate mRNA processing. They are also used in  
 CC the treatment and diagnosis of diseases associated with connective  
 CC tissues. They may also be used to identify homologues from other species.  
 CC The zrnpl polynucleotide is a source of probes and primers, which are  
 CC used for chromosome mapping. The polynucleotide may also be used in gene  
 CC therapy protocols, to produce transgenic animals, and to recombinantly  
 CC produce the protein. The polypeptide is used to produce antibodies, which  
 CC can be used therapeutically, and to purify the polypeptide  
 XX  
 SQ Sequence 158 AA;

Query Match 100.0%; Score 28; DB 3; Length 158;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LKEKAK 6  
 DB 12 LKEKAK 17

## RESULT 15

ABR52602  
 ID ABR52602 standard; protein; 159 AA.

XX  
 AC ABR52602;

DT 20-JUN-2003 (first entry)

DE Protein sequence #SEQ ID 69.

KW Multiprotein complex; eukaryote; drug target; diagnosis.

XX OS Saccharomyces cerevisiae.

XX PN EP1258494-A1.

XX PD 20-NOV-2002.

XX PF 20-DEC-2001; 2001EP-00130253.

XX PR 15-MAY-2001; 2001EP-00111774.

XX PA (CELL-) CELLZONE AG.

XX PI Bauer A, Gavin A, Grandi P, Krause R, Kruse UD, Kuester BD;

XX PI Marzioch M, Schultz JD, Superti-Furga GD;

XX DR WPI; 2003-250078/25.

DR N-PSDB; ACC60644.

XX New isolated protein complexes useful for diagnosing a disease or  
 disorder, or as a target for an active agent of a pharmaceutical,  
 PT preferably a drug target in the treatment or prevention of disease or  
 disorder.

PS Disclosure; SEQ ID NO 69; 17pp + Sequence Listing; English.

CC The invention relates to multiprotein complexes from eukaryotes. Proteins  
 of the invention and DNA sequences encoding them are given in records  
 ABR52568-ABR53903 and ACC60610-ACC61944 respectively. The complexes are  
 obtainable by using a protein as a bait and isolating the set of proteins  
 which is attached thereto from cells. Such protein complexes may comprise  
 up to 30 distinct proteins. Protein complexes of the invention are useful  
 for diagnosing a disease or disorder, or as a target for an active agent  
 of a pharmaceutical, preferably a drug target in the treatment or  
 prevention of a disease or disorder. Note: The sequence data for this  
 patent is not represented in the printed specification, but is based on  
 CC sequence information supplied by the European Patent Office. The complete  
 CC document is available on CD-ROM

XX Sequence 159 AA;

Query Match 100.0%; Score 28; DB 6; Length 159;

Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LKEKAK 6

DB 99 LKEKAK 104

## RESULT 16

ABU35419  
 ID ABU35419 standard; protein; 159 AA.

XX

AC ABU35419;

DT 19-JUN-2003 (first entry)

DE Protein encoded by Prokaryotic essential gene #20946.

XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX OS Moraxella catarrhalis.

XX PN WO200277183-A2.

XX PD 03-OCT-2002.

XX PF 21-MAR-2002; 2002WO-US009107.

XX PR 21-MAR-2001; 2001US-00815242.

XX PR 06-SEP-2001; 2001US-00948993.

XX PR 25-OCT-2001; 2001US-0342923P.

XX PR 08-FEB-2002; 2002US-00072851.

XX PR 06-MAR-2002; 2002US-0362699P.

XX PA (ELIT-) ELITRA PHARM INC.

XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen Ku, Zyskind JW;

XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX DR WPI; 2003-029926/02.

DR N-PSDB; ACA39289.

XX New antisense nucleic acids, useful for identifying proteins or screening  
 for homologous nucleic acids required for cellular proliferation to  
 isolate candidate molecules for rational drug discovery programs.

PS Claim 25; SEQ ID NO 63343; 1766pp; English.

CC The invention relates to an isolated nucleic acid comprising any one of  
 the 6213 antisense sequences given in the specification where expression  
 of the nucleic acid inhibits proliferation of a cell. Also included are:  
 CC (1) a vector comprising a promoter operably linked to the nucleic acid  
 encoding a polypeptide whose expression is inhibited by the antisense  
 nucleic acid; (2) a host cell containing the vector; (3) an isolated  
 polypeptide or its fragment whose expression is inhibited by the  
 antisense nucleic acid; (4) an antibody capable of specifically binding  
 the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
 proliferation or the activity of a gene in an operon required for  
 proliferation; (7) identifying a compound that influences the activity of  
 the gene product or that has an activity against a biological pathway  
 required for proliferation, or that inhibits cellular proliferation; (8)  
 identifying a gene required for cellular proliferation or the biological  
 pathway in which a proliferation-required gene or its gene product lies  
 or a gene on which the test compound that inhibits proliferation of an  
 organism acts; (9) manufacturing an antibiotic; (10) profiling a  
 compound's activity; (11) a culture comprising strains in which the gene  
 product is overexpressed or underexpressed; (12) determining the extent  
 to which each of the strains is present in a culture or collection of  
 strains; or (13) identifying the target of a compound that inhibits the  
 proliferation of an organism. The antisense nucleic acids are useful for  
 identifying proteins or screening for homologous nucleic acids required  
 for cellular proliferation to isolate candidate molecules for rational  
 drug discovery programs, or for screening homologous nucleic acids  
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
 CC the target prokaryotic essential genes. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from WIPO at  
 CC ftp:wipo.int/pub/published\_pct\_sequences

XX Sequence 159 AA;

Query Match 100.0%; Score 28; DB 6; Length 159;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
 DB 26 LKEKAK 31

RESULT 17  
 ABB64004  
 ID ABB64004 standard; protein; 165 AA.

XX AC ABB64004;  
 XX DT 26-MAR-2002 (first entry)  
 XX DE Drosophila melanogaster polypeptide SEQ ID NO 18804.  
 XX KW Drosophila; developmental biology; cell signalling; insecticide;  
 KW pharmaceutical.  
 XX OS Drosophila melanogaster.

XX PN WO200171042-A2.  
 XX PD 27-SEP-2001.  
 XX PF 23-MAR-2001; 2001WO-US009231.

XX PR 23-MAR-2000; 2000US-0191637P.  
 XX PR 11-JUL-2000; 2000US-00614150.  
 XX PA (PEXE ) PE CORP NY.

XX PI Venter JC, Adams M, Li PWD, Myers EW;  
 XX DR WPI; 2001-656860/75.  
 XX DR N-PSDB; ABL08107.

XX PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 PT interactions.

XX PS Disclosure; SEQ ID NO 18804; 21pp + Sequence Listing; English.

XX CC The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-  
 CC ABB72072). The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 165 AA;

Query Match 100.0%; Score 28; DB 4; Length 165;  
 Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
 DB 26 LKEKAK 31

RESULT 18  
 AAM93855  
 ID AAM93855 standard; protein; 174 AA.

XX AC AAM93855;  
 XX DT 06-NOV-2001 (first entry)

XX Human polypeptide, SEQ ID NO: 3945.  
 XX DE Human; full length cDNA; cDNA synthesis; oligo-capping.

XX OS Homo sapiens.  
 XX PN EP1130094-A2.  
 XX PD 05-SEP-2001.

XX PF 07-JUL-2000; 2000EP-00114089.  
 XX PR 08-JUL-1999; 99JP-00194486.  
 XX PR 11-JAN-2000; 2000JP-00118774.  
 XX PR 02-MAY-2000; 2000JP-00183765.

XX PA (HELI-) HELIX RES INST.

XX PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
 XX DR WPI; 2001-524255/58.  
 XX DR N-PSDB; AAK94811.

XX PT 830 Primers useful for synthesizing full length cDNA clones and their use  
 PT in genetic manipulation.

XX PS Claim 8; SEQ ID NO 3945; 1380pp + Sequence Listing; English.

XX CC The invention relates to primers for synthesising full length cDNA  
 CC clones. 830 cDNA molecules encoding a human protein have been isolated  
 CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have  
 CC been determined. Primers for synthesising the full length cDNA are useful  
 CC for clarifying the function of the protein encoded by the cDNA. The full  
 CC length clones were obtained by construction of full length enriched cDNA  
 CC libraries that were synthesised by the oligo-capping method. The primers  
 CC enable the production of the full length cDNA easily without any special  
 CC methods. The present sequence is a polypeptide encoded by a full length  
 CC human cDNA of the invention. Note: The sequence data for this patent did  
 CC not form part of the printed specification, but was obtained in CD-ROM  
 CC format directly from EPO

XX SQ Sequence 174 AA;

Query Match 100.0%; Score 28; DB 4; Length 174;  
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
 DB 28 LKEKAK 33

RESULT 19  
 AAM48958  
 ID AAM48958 standard; protein; 174 AA.

XX AC AAM48958;  
 XX DT 19-APR-2002 (first entry)

XX DE Human colon cancer related protein SEQ ID NO: 17.

XX KW Human; colon cancer; cytostatic; drug design; adenomatous polyp;  
 KW colorectal carcinoma; high metastatic potential colon tumour;  
 KW metastatic colon cancer.

XX OS Homo sapiens.  
 XX PN WO200196523-A2.  
 XX PD 20-DEC-2001.

XX 15-JUN-2001; 2001WO-US019313.  
 XX PF  
 XX PR  
 XX PS  
 XX (CHIR ) CHIRON CORP.  
 XX PA  
 XX Kennedy GC, Kang S, Reinhard C, Jefferson AB;  
 XX PI  
 XX WPI; 2002-164362/21.  
 XX DR  
 XX N-PSDB; AAL41604.  
 XX PR  
 XX Detecting a cancerous colon cell, useful for diagnosing colon cancer and  
 XX PT for rational drug and therapy design, comprises detecting at least one  
 XX PT differentially expressed gene product.  
 XX PI  
 XX Claim 38; Page 108-109; 135pp; English.  
 XX PS  
 XX The present invention relates to methods for detecting a cancerous colon  
 XX CC cell involving detecting at least one differentially expressed gene such  
 XX CC as those given in AAL41595-AAL41611. This is useful for diagnosing colon  
 XX CC cancer, in rational drug and therapy design, and for identifying  
 XX CC additional genes linked to the development or inhibition of development  
 XX CC of colon cancer. Examples of colon cancer which can be detected include  
 XX CC adenomatous polyp, colorectal carcinoma, high metastatic potential colon  
 XX CC tumours and metastatic colon cancer. The present sequence is a colon  
 XX CC cancer associated protein  
 XX SQ  
 Query Match 100.0%; Score 28; DB 5; Length 174;  
 Best Local Similarity 100.0%; Pred. NO. 5.1e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LKEKAK 6  
 DB 28 LKEKAK 33  
 RESULT 20  
 ABO52942  
 ID ABO52942 standard; protein; 174 AA.  
 AC ABO52942;  
 DT 09-OCT-2003 (first entry)  
 DE Human spliceosome associated protein (SAP) #46.  
 KW Human; SAP; spliceosome associated protein; ribonucleoprotein;  
 KW RNP complex; RNA affinity substrate; RNP assembly sequence;  
 KW spliceosomal complex; hnRNP complex; mRNA export complex;  
 KW mRNA localisation complex; RNA editing complex; intron complex;  
 KW H complex; telomerase complex; fragile X protein complex;  
 KW reverse transcriptase complex; gene splicing complex.  
 XX OS  
 XX Homo sapiens.  
 XX US2003068803-A1.  
 PN US2003068803-A1.  
 PD 10-APR-2003.  
 XX 14-JAN-2002; 2002US-00047991.  
 XX PF  
 XX 12-JAN-2001; 2001US-0261521P.  
 XX PR  
 XX (REED/) REED R.  
 XX PA (ZHOU/) ZHOU Z.  
 XX PI  
 XX Reed R, Zhou Z;  
 XX WPI; 2003-540885/51.  
 XX DR  
 XX Hanson MS, Mullikin BA, Roberts W, Lathigra R;  
 XX

PT Isolating ribonucleoprotein complex, by contacting RNA affinity substrate  
 PT having ribonucleoprotein assembly sequence and affinity tag, with protein  
 PT mixture, subjecting complex formed to chromatography, affinity selection.  
 XX PS  
 XX Claim 24; Page; 39pp; English.  
 XX CC  
 CC The invention relates to forming (M1) an isolated ribonucleoprotein (RNP)  
 CC complex (C), involves contacting an RNA affinity substrate (S) comprising  
 CC an RNP assembly sequence (AS) and an affinity tag, with a protein mixture  
 CC to permit formation of (C) on AS, subjecting (C) to chromatographic  
 CC separation, and subjecting (C) to affinity selection, where the affinity  
 CC tag (e.g. bacteriophage MS2 coat protein in a fusion protein with E. coli  
 CC maltose binding protein) binds to an affinity matrix. Also included are  
 CC an isolated spliceosome preparation (isolated by (M1)), a RNA comprising  
 CC an RNP complex binding site and at least one phage coat protein  
 CC recognition site, a nucleic acid encoding the RNA, and treating (M2) a  
 CC subject having a disorder associated with abnormal RNP complexes (by  
 CC obtaining a sample of cells from a subject, purifying RNP complexes from  
 CC the cells of the subject by (M1), determining the presence in the  
 CC purified RNP complexes of one or more proteins, and normalising the  
 CC amount of RNPs in the subject. (M1) is useful for forming an isolated RNP  
 CC complex selected from a spliceosomal complex (selected from E, A, B and C  
 CC complex), an hnRNP complex, an mRNA export complex, an mRNA localisation  
 CC complex, an RNA editing complex, an intron complex, or an H complex. (M1)  
 CC is useful in a diagnostic assay for determining whether a subject has  
 CC abnormal RNP complexes, (M2) is useful for treating a subject having a  
 CC disorder associated with abnormal RNP complexes. (M1) is useful for  
 CC forming an isolated RNP complex such as a telomerase complex, a fragile X  
 CC protein complex, a reverse transcriptase complex or a gene splicing  
 CC complex. The present sequence represents a known human spliceosome  
 CC associated protein (SAP) isolated by the methods of the invention. Note:  
 CC The present sequence is not shown in the specification but was obtained  
 CC from Genbank or Swissprot using the information provided in table 1 of  
 CC the specification  
 XX SQ  
 Query Match 100.0%; Score 28; DB 6; Length 174;  
 Best Local Similarity 100.0%; Pred. NO. 5.1e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LKEKAK 6  
 DB 28 LKEKAK 33  
 RESULT 21  
 AAY84717  
 ID AAY84717 standard; protein; 185 AA.  
 AC AAY84717;  
 XX 08-AUG-2000 (first entry)  
 DT  
 XX A decorin binding protein of Borrelia burgdorferi.  
 DE  
 XX Decorin binding protein; DbpA; DbpB; adhesin; infection; Lyme disease;  
 KW spirochete infection; vaccine; passive immunotherapy.  
 XX OS  
 XX Borrelia burgdorferi.  
 XX WO2000021989-A1.  
 PN WO2000021989-A1.  
 PD 20-APR-2000.  
 XX 08-OCT-1999; 99WO-US023481.  
 XX PF  
 XX 09-OCT-1998; 98US-0103728P.  
 XX PR  
 XX (MEDI-) MEDIMUNE INC.  
 XX PA  
 XX Hanson MS, Mullikin BA, Roberts W, Lathigra R;  
 XX PI  
 XX



CC isolated from H. pylori by PCR amplification for recombinant polypeptide  
CC production, e.g., in E. coli hosts

SQ Sequence 237 AA;  
Query Match 100.0%; Score 28; DB 2; Length 237;  
Best Local Similarity 100.0%; Pred. No. 6.9e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
|||||  
Db 203 LKEKAK 208

RESULT 24  
ABP73270  
ID ABP73270 standard; protein; 247 AA.

XX AC ABP73270;

XX 30-JAN-2003 (first entry)

XX Candida albicans essential protein SEQ ID NO 7107.

XX Fungus; yeast; tetracycline; promoter; GRACE strain; biosynthesis;  
KW signal transduction; DNA replication; cell division; growth;  
KW proliferation; Candida albicans; fungicide; antifungal.

XX OS Candida albicans.

XX PN WO200253728-A2.

XX PD 11-JUL-2002.

XX PF 26-DEC-2001; 2001WO-US049486.

XX PR 29-DEC-2000; 2000US-0259128P.

XX PR 20-FEB-2001; 2001US-00792024.

XX PR 22-AUG-2001; 2001US-0314050P.

XX PA (ELIT-) ELITRA PHARM INC.

XX PI Roemer T, Jiang B, Boone C, Bussey H, Ohlsen KL;

XX DR N-PSDB; ABZ31820.

XX Constructing strains for identifying gene products as effective targets  
PT for therapeutic intervention, by inactivating in the strain one allele of  
PT a gene and placing other allele of the gene under conditional expression.

XX Claim 44; SEQ ID NO 7107; 167pp + Sequence Listing; English.

XX The invention relates to constructing (M1) a strain of diploid fungal  
CC cells in which both alleles of a gene are modified, comprising modifying  
CC one allele by insertion or replacement by a cassette having an  
CC expressible selectable marker and modifying other allele by  
CC recombination, of a promoter replacement fragment with a heterologous  
CC promoter, so that expression of the second allele is regulated by the  
CC promoter. (M1) is useful for constructing a strain of diploid fungal  
CC cells in which both alleles of a gene are modified. The diploid fungal  
CC cells having both alleles modified are useful for identifying a gene that  
CC is essential to the survival or growth of a fungus, a gene that  
CC contributes to the virulence and/or pathogenicity of a fungus, a gene  
CC that contributes to the resistance of a diploid fungus to an antifungal  
CC agent, an antifungal agent that inhibits the growth of a diploid fungus  
CC and for identifying a therapeutic agent for treatment of a mammalian  
CC disease. (M1) is useful for identifying a compound which modulates the  
CC activity of a gene product, preferably enzymatic activity, carbon  
CC compound catabolism, biosynthesis, transporter, transcriptional,  
CC translational, signal transduction, DNA replication and cell division  
CC activity. The method is useful for identifying a compound having the  
CC ability to inhibit growth or proliferation of C. albicans cells and for

CC treating infection by C. albicans. The present sequence is that of an  
CC essential Candida albicans protein used in the method of the invention.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification but is based on sequence information supplied to Derwent by  
CC the European Patent Office

XX SQ Sequence 247 AA;

Query Match 100.0%; Score 28; DB 5; Length 247;  
Best Local Similarity 100.0%; Pred. No. 7.2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
|||||  
Db 51 LKEKAK 56

RESULT 25

AAG08495

ID AAG08495 standard; protein; 249 AA.

XX AC AAG08495;

XX 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 6055.

XX Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.

XX OS Arabidopsis thaliana.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-00301439.

XX PR 25-FEB-1999; 99US-0121825P.

XX PR 05-MAR-1999; 99US-0123180P.

XX PR 09-MAR-1999; 99US-0123548P.

XX PR 23-MAR-1999; 99US-0125788P.

XX PR 25-MAR-1999; 99US-0126264P.

XX PR 29-MAR-1999; 99US-0126785P.

XX PR 01-APR-1999; 99US-0127462P.

XX PR 06-APR-1999; 99US-0128234P.

XX PR 08-APR-1999; 99US-0128714P.

XX PR 16-APR-1999; 99US-0129845P.

XX PR 19-APR-1999; 99US-0130077P.

XX PR 21-APR-1999; 99US-0130449P.

XX PR 23-APR-1999; 99US-0130510P.

XX PR 23-APR-1999; 99US-0130891P.

XX PR 28-APR-1999; 99US-0131449P.

XX PR 30-APR-1999; 99US-0132048P.

XX PR 04-MAY-1999; 99US-0132407P.

XX PR 05-MAY-1999; 99US-0132484P.

XX PR 06-MAY-1999; 99US-0132485P.

XX PR 06-MAY-1999; 99US-0132486P.

XX PR 06-MAY-1999; 99US-0132487P.

XX PR 07-MAY-1999; 99US-0132863P.

XX PR 11-MAY-1999; 99US-0134256P.

XX PR 14-MAY-1999; 99US-0134218P.

XX PR 14-MAY-1999; 99US-0134219P.

XX PR 14-MAY-1999; 99US-0134221P.

XX PR 14-MAY-1999; 99US-0134370P.

XX PR 18-MAY-1999; 99US-0134768P.

XX PR 19-MAY-1999; 99US-0134941P.

XX PR 20-MAY-1999; 99US-0135124P.

XX PR 21-MAY-1999; 99US-0135353P.

XX PR 24-MAY-1999; 99US-0135623P.

XX PR 25-MAY-1999; 99US-0136021P.

XX PR 27-MAY-1999; 99US-0136392P.

PR 28-MAY-1999; 99US-0136782P.  
PR 01-JUN-1999; 99US-0137222P.  
PR 03-JUN-1999; 99US-0137528P.  
PR 04-JUN-1999; 99US-0137502P.  
PR 07-JUN-1999; 99US-0137724P.  
PR 08-JUN-1999; 99US-0138094P.  
PR 10-JUN-1999; 99US-0138540P.  
PR 10-JUN-1999; 99US-0138847P.  
PR 14-JUN-1999; 99US-0139111P.  
PR 16-JUN-1999; 99US-0139452P.  
PR 16-JUN-1999; 99US-0139453P.  
PR 17-JUN-1999; 99US-0139492P.  
PR 18-JUN-1999; 99US-0139454P.  
PR 18-JUN-1999; 99US-0139455P.  
PR 18-JUN-1999; 99US-0139456P.  
PR 18-JUN-1999; 99US-0139457P.  
PR 18-JUN-1999; 99US-0139458P.  
PR 18-JUN-1999; 99US-0139459P.  
PR 18-JUN-1999; 99US-0139460P.  
PR 18-JUN-1999; 99US-0139461P.  
PR 18-JUN-1999; 99US-0139462P.  
PR 18-JUN-1999; 99US-0139463P.  
PR 18-JUN-1999; 99US-0139750P.  
PR 18-JUN-1999; 99US-0139763P.  
PR 21-JUN-1999; 99US-0139817P.  
PR 22-JUN-1999; 99US-0139899P.  
PR 23-JUN-1999; 99US-0140353P.  
PR 23-JUN-1999; 99US-0140354P.  
PR 24-JUN-1999; 99US-0140695P.  
PR 24-JUN-1999; 99US-0140823P.  
PR 29-JUN-1999; 99US-0140991P.  
PR 30-JUN-1999; 99US-0141287P.  
PR 01-JUL-1999; 99US-0141842P.  
PR 01-JUL-1999; 99US-0142154P.  
PR 02-JUL-1999; 99US-0142055P.  
PR 06-JUL-1999; 99US-0142390P.  
PR 08-JUL-1999; 99US-0142803P.  
PR 09-JUL-1999; 99US-0142920P.  
PR 12-JUL-1999; 99US-0142977P.  
PR 13-JUL-1999; 99US-0143542P.  
PR 14-JUL-1999; 99US-0143624P.  
PR 15-JUL-1999; 99US-0144005P.  
PR 16-JUL-1999; 99US-0144085P.  
PR 16-JUL-1999; 99US-0144086P.  
PR 19-JUL-1999; 99US-0144325P.  
PR 19-JUL-1999; 99US-0144331P.  
PR 19-JUL-1999; 99US-0144332P.  
PR 19-JUL-1999; 99US-0144333P.  
PR 19-JUL-1999; 99US-0144334P.  
PR 19-JUL-1999; 99US-0144335P.  
PR 20-JUL-1999; 99US-0144352P.  
PR 20-JUL-1999; 99US-0144632P.  
PR 20-JUL-1999; 99US-0144884P.  
PR 21-JUL-1999; 99US-0144814P.  
PR 21-JUL-1999; 99US-0145086P.  
PR 21-JUL-1999; 99US-0145088P.  
PR 22-JUL-1999; 99US-0145085P.  
PR 22-JUL-1999; 99US-0145087P.  
PR 22-JUL-1999; 99US-0145089P.  
PR 22-JUL-1999; 99US-0145192P.  
PR 23-JUL-1999; 99US-0145145P.  
PR 23-JUL-1999; 99US-0145218P.  
PR 23-JUL-1999; 99US-0145224P.  
PR 26-JUL-1999; 99US-0145276P.  
PR 27-JUL-1999; 99US-0145913P.  
PR 27-JUL-1999; 99US-0145918P.  
PR 27-JUL-1999; 99US-0145919P.  
PR 28-JUL-1999; 99US-0145951P.  
PR 02-AUG-1999; 99US-0146386P.  
PR 02-AUG-1999; 99US-0146388P.  
PR 02-AUG-1999; 99US-0146389P.  
PR 03-AUG-1999; 99US-0147038P.  
PR 04-AUG-1999; 99US-0147204P.  
PR 04-AUG-1999; 99US-0147302P.  
PR 05-AUG-1999; 99US-0147192P.  
PR 05-AUG-1999; 99US-0147260P.  
PR 06-AUG-1999; 99US-0147303P.  
PR 06-AUG-1999; 99US-0147416P.  
PR 09-AUG-1999; 99US-0147493P.  
PR 09-AUG-1999; 99US-0147935P.  
PR 10-AUG-1999; 99US-0148171P.  
PR 11-AUG-1999; 99US-0148319P.  
PR 12-AUG-1999; 99US-0148341P.  
PR 13-AUG-1999; 99US-0148565P.  
PR 13-AUG-1999; 99US-0148684P.  
PR 16-AUG-1999; 99US-0149368P.  
PR 17-AUG-1999; 99US-0149175P.  
PR 18-AUG-1999; 99US-0149436P.  
PR 20-AUG-1999; 99US-0149722P.  
PR 20-AUG-1999; 99US-0149723P.  
PR 20-AUG-1999; 99US-0149929P.  
PR 23-AUG-1999; 99US-0149902P.  
PR 23-AUG-1999; 99US-0149930P.  
PR 25-AUG-1999; 99US-0150566P.  
PR 26-AUG-1999; 99US-0150884P.  
PR 27-AUG-1999; 99US-0151065P.  
PR 27-AUG-1999; 99US-0151066P.  
PR 27-AUG-1999; 99US-0151080P.  
PR 30-AUG-1999; 99US-0151303P.  
PR 31-AUG-1999; 99US-0151438P.  
PR 01-SEP-1999; 99US-0151930P.  
PR 07-SEP-1999; 99US-0152363P.  
PR 10-SEP-1999; 99US-0153070P.  
PR 13-SEP-1999; 99US-0153758P.  
PR 15-SEP-1999; 99US-0154018P.  
PR 16-SEP-1999; 99US-0154039P.  
PR 20-SEP-1999; 99US-0154779P.  
PR 22-SEP-1999; 99US-0155139P.  
PR 23-SEP-1999; 99US-0155486P.  
PR 24-SEP-1999; 99US-0155659P.  
PR 28-SEP-1999; 99US-0156458P.  
PR 29-SEP-1999; 99US-0156596P.  
PR 04-OCT-1999; 99US-0157117P.  
PR 05-OCT-1999; 99US-0157553P.  
PR 06-OCT-1999; 99US-0157865P.  
PR 07-OCT-1999; 99US-0158029P.  
PR 08-OCT-1999; 99US-0158232P.  
PR 12-OCT-1999; 99US-0158369P.  
PR 13-OCT-1999; 99US-0159293P.  
PR 13-OCT-1999; 99US-0159294P.  
PR 13-OCT-1999; 99US-0159329P.  
PR 14-OCT-1999; 99US-0159295P.  
PR 14-OCT-1999; 99US-0159330P.  
PR 14-OCT-1999; 99US-0159331P.  
PR 14-OCT-1999; 99US-0159637P.  
PR 14-OCT-1999; 99US-0159638P.  
PR 18-OCT-1999; 99US-0159584P.  
PR 21-OCT-1999; 99US-0160741P.  
PR 21-OCT-1999; 99US-0160767P.  
PR 21-OCT-1999; 99US-0160768P.  
PR 21-OCT-1999; 99US-0160770P.  
PR 21-OCT-1999; 99US-0160814P.  
PR 21-OCT-1999; 99US-0160815P.  
PR 22-OCT-1999; 99US-0160980P.  
PR 22-OCT-1999; 99US-0160981P.  
PR 22-OCT-1999; 99US-0160989P.  
PR 25-OCT-1999; 99US-0161404P.  
PR 25-OCT-1999; 99US-0161405P.  
PR 25-OCT-1999; 99US-0161406P.  
PR 26-OCT-1999; 99US-0161359P.  
PR 26-OCT-1999; 99US-0161360P.  
PR 26-OCT-1999; 99US-0161361P.  
PR 28-OCT-1999; 99US-0161920P.  
PR 28-OCT-1999; 99US-0161992P.  
PR 28-OCT-1999; 99US-0161993P.  
PR 29-OCT-1999; 99US-0162142P.



Query Match 100.0%; Score 28; DB 3; Length 249;  
 Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
 DB 209 LKEKAK 214  
 |||||

RESULT 26  
 ID ABB11849  
 AC ABB11849 standard; peptide; 297 AA.  
 XX ABB11849;  
 DT 11-JAN-2002 (first entry)  
 DE Human preproenkephalin homologue, SEQ ID NO:2219.  
 XX Human; cytokine; cell proliferation; cell differentiation; growth factor;  
 KW haematopoiesis regulation; tissue growth; immunomodulator; activin;  
 KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;  
 KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;  
 KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;  
 KW chronic inflammatory condition; proliferative retinopathy;  
 KW atherosclerosis; coronary heart disease; arterial ischaemia;  
 KW bone disorder; osteoporosis; vascular growth disorder;  
 KW tissue regeneration; wound healing; infection; immune disorder;  
 KW cell culture; drug screening; gene therapy; antiinflammatory;  
 KW cytoskeletal; antiarthritic; haemostatic; antiarteriosclerotic;  
 KW cytoskeletal; osteopathic; vasotropic; cardiant; virucide; antibacterial;  
 KW antifungal; vulnery; antiulcer.  
 XX Homo sapiens.  
 OS  
 XX  
 PN WO200157188-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 05-FEB-2001; 2001WO-US003800.  
 XX  
 PR 03-FEB-2000; 2000US-00496914.  
 PR 27-APR-2000; 2000US-00560875.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Tang YT, Liu C, Drmanac RT;  
 XX  
 XX WPI; 2001-457740/49.  
 DR N-PSDB; ABA09093.  
 XX  
 PT Human proteins and DNA encoding sequences useful for preventing, treating  
 PT or ameliorating a medical condition in a mammalian subject e.g. arthritis  
 PT and cancer.  
 XX  
 PS Claim 20; Page 266; 1963pp; English.  
 XX  
 CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and  
 CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The  
 CC invention also relates to vectors and recombinant host cells comprising a  
 CC nucleotide of the invention, methods of producing the novel polypeptides,  
 CC antibodies against the polypeptides, methods of detecting the nucleotides  
 CC or polypeptides in a sample, and methods of identifying compounds which  
 CC bind to polypeptides of the invention. Although novel, many of the  
 CC polypeptides of the invention have homology to known proteins, thereby  
 CC giving an insight into their probable biological activities, and hence  
 CC potential therapeutic applications. The polypeptides of the invention may  
 CC have various activities, including cytokine, cell proliferation or cell  
 CC differentiation activities; stem cell growth factor activity;  
 CC haematopoiesis regulatory activity; tissue growth activity;  
 CC immunomodulatory activity; activin- or inhibin-related activities;  
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or

CC thrombolytic activities; receptor or ligand activities; or may be  
 CC involved in oncogenesis, cancer cell proliferation or metastasis.  
 CC Depending on their biological activities, polypeptides and nucleotides of  
 CC the invention are useful for preventing, treating or ameliorating medical  
 CC conditions, e.g., by protein or gene therapy. Such conditions include  
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell  
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),  
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,  
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal  
 CC vascular growth. Polypeptides involved with tissue regeneration and  
 CC repair (or nucleic acids encoding them) may be used to promote wound  
 CC healing (e.g., of burns, incisions and ulcers), while those with  
 CC immunomodulatory activities may be used in the treatment of viral,  
 CC bacterial and fungal infections in addition to immune disorders.  
 CC Polypeptides with growth factor activity may be used in cell cultures to  
 CC promote cell growth. For example, such polypeptides may be used to  
 CC manipulate stem cells in culture to give rise to neuroepithelial cells  
 CC that can be used to augment or replace cells damaged by illness,  
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides  
 CC may also be used in the diagnosis of the above conditions, and in drug  
 CC screening techniques. The present sequence represents a novel human  
 CC polypeptide of the invention

XX Sequence 297 AA;

Query Match 100.0%; Score 28; DB 4; Length 297;  
 Best Local Similarity 100.0%; Pred. No. 8.6e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
 DB 228 LKEKAK 233  
 |||||

RESULT 27

AAG08494  
 ID AAG08494 standard; protein; 302 AA.

XX AC  
 XX AAG08494;

DT 17-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 6054.

XX KW Protein identification; signal transduction pathway; metabolic pathway;  
 XX KW hybridisation assay; genetic mapping; gene expression control; promoter;  
 XX KW termination sequence.

XX OS Arabidopsis thaliana.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-00301439.

XX PR 25-FEB-1999; 99US-0121825P.

XX PR 05-MAR-1999; 99US-0123180P.

XX PR 09-MAR-1999; 99US-0123548P.

XX PR 23-MAR-1999; 99US-0125788P.

XX PR 25-MAR-1999; 99US-0126264P.

XX PR 29-MAR-1999; 99US-0126785P.

XX PR 01-APR-1999; 99US-0127462P.

XX PR 06-APR-1999; 99US-0128234P.

XX PR 08-APR-1999; 99US-0128714P.

XX PR 16-APR-1999; 99US-0129845P.

XX PR 21-APR-1999; 99US-0130077P.

XX PR 23-APR-1999; 99US-0130449P.

XX PR 23-APR-1999; 99US-0130510P.

XX PR 28-APR-1999; 99US-0131449P.

XX PR 30-APR-1999; 99US-0132048P.

XX PR 30-APR-1999; 99US-0132407P.

PR 04-MAY-1999; 99US-0132484P.  
PR 05-MAY-1999; 99US-0132485P.  
PR 06-MAY-1999; 99US-0132486P.  
PR 06-MAY-1999; 99US-0132487P.  
PR 07-MAY-1999; 99US-01324863P.  
PR 11-MAY-1999; 99US-01324256P.  
PR 14-MAY-1999; 99US-01324218P.  
PR 14-MAY-1999; 99US-0134219P.  
PR 14-MAY-1999; 99US-0134221P.  
PR 14-MAY-1999; 99US-0134327P.  
PR 18-MAY-1999; 99US-0134768P.  
PR 19-MAY-1999; 99US-0134941P.  
PR 20-MAY-1999; 99US-0135124P.  
PR 21-MAY-1999; 99US-0135353P.  
PR 24-MAY-1999; 99US-0135629P.  
PR 25-MAY-1999; 99US-0136021P.  
PR 27-MAY-1999; 99US-0136392P.  
PR 28-MAY-1999; 99US-0136782P.  
PR 01-JUN-1999; 99US-0137222P.  
PR 03-JUN-1999; 99US-0137528P.  
PR 04-JUN-1999; 99US-0137502P.  
PR 07-JUN-1999; 99US-0137724P.  
PR 08-JUN-1999; 99US-0138094P.  
PR 10-JUN-1999; 99US-0138540P.  
PR 10-JUN-1999; 99US-0138847P.  
PR 14-JUN-1999; 99US-0139119P.  
PR 16-JUN-1999; 99US-0139452P.  
PR 16-JUN-1999; 99US-0139453P.  
PR 17-JUN-1999; 99US-0139492P.  
PR 18-JUN-1999; 99US-0139454P.  
PR 18-JUN-1999; 99US-0139455P.  
PR 18-JUN-1999; 99US-0139456P.  
PR 18-JUN-1999; 99US-0139457P.  
PR 18-JUN-1999; 99US-0139458P.  
PR 18-JUN-1999; 99US-0139459P.  
PR 18-JUN-1999; 99US-0139460P.  
PR 18-JUN-1999; 99US-0139461P.  
PR 18-JUN-1999; 99US-0139462P.  
PR 18-JUN-1999; 99US-0139463P.  
PR 18-JUN-1999; 99US-0139750P.  
PR 18-JUN-1999; 99US-0139763P.  
PR 21-JUN-1999; 99US-0139817P.  
PR 22-JUN-1999; 99US-0139899P.  
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Query Match 100.0%; Score 28; DB 3; Length 302;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
DB 262 LKEKAK 267

RESULT 28
AAB47595
ID AAB47595 standard; protein; 322 AA.
XX
AC AAB47595;
XX
DT 07-JAN-2002 (first entry)
DE Human DHDR-4.
XX
KW Human; dehydrogenase; DHDR; cellular proliferation; CNS; cardiac;
KW muscular; cellular growth; differentiation; migration; neurological;
KW immune system; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= Signal peptide
FT Domain 29..50
FT /label= Transmembrane domain
FT Domain 35..82
FT /label= Shikimate 5-dehydrogenase domain
FT Domain 37..231
FT /label= Oxidoreductase protein dehydrogenase domain
FT Domain 38..226
FT /label= Short chain dehydrogenase domain
FT Domain 170..188
FT /label= Transmembrane domain
FT Domain 208..224
FT /label= Transmembrane domain
FT Domain 237..286
FT /label= Dehydrogenase domain
FT Domain 243..287
FT /label= Glucose-1-dehydrogenase domain
FT Domain 250..280
FT /label= Short chain dehydrogenase/reductase domain
FT Domain 258..275
FT /label= Transmembrane domain
XX
PN WO200172976-A2.
XX
PD 04-OCT-2001.
XX
PF 23-MAR-2001; 2001WO-US009613.
XX

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PR 24-MAR-2000; 2000US-0192002P.
PR 08-AUG-2000; 2000US-00634955.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Meyers R, Cook WJ, Williamson M, Rudolph-Owen LA;
XX
DR WPI; 2001-639228/73.
XX
DR N-PSDB; AAH43563, AAH43567.
XX
PT New human dehydrogenase molecules designated DHDR-1, DHDR-2, DHDR-3 and
PT DHDR-4 for finding treatment for dehydrogenase-associated disorders such
PT as viral and cellular proliferation disorders.
XX
PS Claim 2; Fig 16; 83pp; English.
XX
CC The sequences given in AAH43560-67 encode human dehydrogenase (DHDR)-1-4.
CC Modulators of DHDR activity are used to treat a viral or cellular
CC proliferation disorder. The DHDR proteins can also be used to treat
CC disorders characterized by over or under production of DHDR proteins, for
CC example dehydrogenase-associated disorders such as CNS, cardiac,
CC muscular, cellular growth, differentiation or migration, neurological,
CC immune, humoral or viral disorders. The molecules can be used in
CC pharmacogenetics
XX
SQ Sequence 322 AA;

Query Match 100.0%; Score 28; DB 4; Length 322;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
DB 316 LKEKAK 321

RESULT 29
AAG08493
ID AAG08493 standard; protein; 326 AA.
XX
AC AAG08493;
XX
DT 17-OCT-2000 (first entry)
DE Arabidopsis thaliana protein fragment SEQ ID NO: 6053.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
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PR 08-OCT-1999; 99US-0158232P.  
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Query Match 100.0%; Score 28; DB 3; Length 326;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LXEKAK 6
DB 286 LXEKAK 291

RESULT 30
ABB93289
ID ABB93289 standard; protein; 326 AA.
AC ABB93289;
XX
DT 31-MAY-2002 (first entry)
XX
DE Herbicidally active polypeptide SEQ ID NO 2500.
XX
KW Herbicidal; plant; agriculture; herbicide.
XX
OS Arabidopsis thaliana.
XX
PN WO200210210-A2.
XX
PD 07-FEB-2002.
XX
PF 28-AUG-2001; 2001WO-EP009892.
XX
PR 28-AUG-2001; 2001WO-EP009892.
XX
PA (PARB ) BAYER AG.
XX
PI Tietjen K, Weidler M;
XX
DR WPI; 2002-269010/31.
XX
PT Identifying plant target proteins for herbicidally active compounds,
PT comprising aligning and comparing nucleic acid or amino acid sequences
PT from plant with nucleic acid or amino acid sequences from non-plant
PT organisms.
XX
PS Claim 5; SEQ ID NO 2500; 261pp + Sequence Listing; English.
XX
CC The invention relates to identifying target proteins (ABB90790-ABB94016)
CC for herbicidally active compounds, comprising aligning and comparing
CC nucleic acid or amino acid sequences from plant with nucleic acid or
CC amino acid sequences from non-plant organisms using suitable search
CC parameters, where plant sequences having an E-value greater by a factor
CC of 3 than the E-value of most similar non-plant sequences are selected.
CC The polypeptides or nucleic acids encoding them are useful for
CC identifying modulators. The identified modulators are useful as
CC herbicides

XX SQ Sequence 326 AA;
Query Match 100.0%; Score 28; DB 5; Length 326;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LXEKAK 6
DB 286 LXEKAK 291

RESULT 31
AAE25947
ID AAE25947 standard; protein; 326 AA.
XX
AC AAE25947;
XX
DT 15-NOV-2002 (first entry)
XX
DE Arabidopsis thaliana GPPP synthase-related protein.
XX
KW Geranylgeranyl pyrophosphate synthase; GGPPS; enzyme; transgenic;
KW transgenic plant; carotenoid; herbicide.
XX
OS Arabidopsis thaliana.
XX
PN US6410827-B1.
XX
PD 25-JUN-2002.
XX
PF 01-DEC-1999; 99US-00452238.
XX
PR 02-DEC-1998; 98US-0110592P.
XX
PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI Cahoon RE, Shen JB, Williams ME;
XX
DR WPI; 2002-588898/63.
XX
PT New nucleic acid molecule encoding geranylgeranyl pyrophosphate synthase,
PT useful for producing transgenic plants having altered synthase activity
PT and exhibiting altered amounts of carotenoids.
XX
PS Example 4; Col 83-86; 48pp; English.
XX
CC The invention relates to an isolated polynucleotide comprising a
CC nucleotide sequence encoding a polypeptide having geranylgeranyl
CC pyrophosphate synthase (GGPPS) activity. The invention is useful for
CC transforming a cell and producing a transgenic plant. Nucleic acid
CC fragments of the invention are useful to create transgenic plants in
CC which GGPPS polypeptides are present at higher or lower levels than
CC normal or in cell types or developmental stages in which they are not
CC normally found. Increasing the amount of GGPPS in the plant cell results
CC in increased amounts of carotenoids yielding brighter colours in the
CC flower and the fruit and higher levels of beta-carotene as well as other
CC terpenoids derived from GGPP. GGPPS polypeptides are useful as targets
CC for herbicide discovery. The nucleic acid fragments are also useful as
CC probes for genetically and physically mapping the genes that they are a
CC portion and as markers for traits linked to those genes. The information
CC is useful in plant breeding to develop lines with desired phenotypes. The
CC nucleic acid fragments are also useful as restriction fragment length
CC polymorphism (RFLP) markers for physical mapping and in direct
CC fluorescence in situ hybridisation (FISH) mapping. The present sequence
CC is Arabidopsis thaliana GGPP synthase-related protein
XX
SQ Sequence 326 AA;
Query Match 100.0%; Score 28; DB 5; Length 326;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 LKEKAK 6  
Db 286 LKEKAK 291  
RESULT 32  
ID ABU67344  
XX ABU67344 standard; protein; 326 AA.  
AC ABU67344;  
XX  
XX 28-MAY-2003 (first entry)  
XX  
XX A. thaliana geranylgeranyl pyrophosphate (GGPP) synthase-related protein.  
XX  
XX Enzyme; plant; geranylgeranyl pyrophosphate synthase; GGPP synthase;  
KW geranylgeranyl pyrophosphate; GGPP; corn; rice; soybean; wheat;  
KW geranylgeranyl-diphosphate synthase; farnesyl transferase;  
KW geranylgeranyl synthetase; terpenoid; phytoene; phytoene synthase;  
KW carotenoid; phytohormone; gibberellin; seed germination; stem elongation;  
KW flowering; bolting; leaf senescence; fruit senescence; herbicide;  
KW beta-carotene.  
XX  
XX Arabidopsis thaliana.  
XX  
XX US2002177204-A1.  
XX  
XX 28-NOV-2002.  
XX  
XX 28-MAR-2002; 2002US-00108915.  
XX  
XX 02-DEC-1998; 98US-0110592P.  
XX 01-DEC-1999; 99US-00452238.  
XX  
XX (CAHO/) CAHOON R E.  
XX (SHEN/) SHEN J B.  
XX (WILL/) WILLIAMS M E.  
XX  
XX Cahoon RE, Shen JB, Williams ME;  
XX WPI; 2003-328487/31.  
XX  
XX Novel nucleic acid molecule encoding geranylgeranyl pyrophosphate  
PT synthase useful for producing transgenic plants having altered synthase  
PT activity and exhibiting altered amounts of carotenoids.  
XX  
XX Example 4; Fig 2; 52pp; English.  
XX  
XX The invention discloses an isolated geranylgeranyl pyrophosphate (GGPP)  
CC synthase polypeptide comprising a sequence from corn, rice, soybean,  
CC wheat, or other related protein. GGPP synthase, also known as  
CC geranylgeranyl-diphosphate synthase, farnesyl transferase and  
CC geranylgeranyl synthetase, is a key enzyme in plant terpenoid  
CC biosynthesis. One fate of GGPP is conversion to phytoene by phytoene  
CC synthase, the first committed step in carotenoid biosynthesis. GGPP also  
CC serves as a precursor in the formation of defence-related substances and  
CC a precursor of the phytohormone gibberellin which regulates a variety of  
CC physiological processes that include initiation of seed germination, and  
CC stimulation of stem elongation, stimulation of flowering/bolting and  
CC regulation of leaf/fruit senescence. Also disclosed is a method for  
CC selecting an isolated polynucleotide that affects the level of expression  
CC of a GGPP synthase polypeptide in a plant cell. The polypeptide is useful  
CC for evaluating at least one compound for its ability to inhibit the  
CC activity of GGPP synthase polypeptide and as targets for herbicide  
CC discovery. Nucleic acid fragments of the polypeptide are useful for  
CC creating transgenic plants with an increased amounts of carotenoids  
CC yielding brighter colours in the flower and the fruit and higher levels  
CC of beta-carotene as well as other terpenoids derived from GGPP, as probes  
CC for mapping the genes and as markers for traits linked to those genes.  
XX Such information is useful in plant breeding to develop lines with  
CC desired phenotypes. The sequences presented in ABU67321-ABU67344 are the  
CC plant GGPP synthase and GGPP synthase-related proteins  
XX

SQ Sequence 326 AA;  
Query Match 100.0%; Score 28; DB 6; Length 326;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LKEKAK 6  
Db 286 LKEKAK 291  
RESULT 33  
AAU75726  
ID AAU75726 standard; protein; 331 AA.  
XX  
XX AC AAU75726;  
XX  
XX 12-SEP-2003 (revised)  
DT 21-MAR-2000 (first entry)  
XX  
XX Neisseria gonorrhoeae ORF 957 protein sequence SEQ ID NO:2924.  
DE  
XX  
KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;  
KW antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;  
KW antibacterial; gene therapy.  
XX  
XX Neisseria gonorrhoeae.  
XX  
XX WO9957280-A2.  
XX  
XX 11-NOV-1999.  
XX  
XX 30-APR-1999; 99WO-US009346.  
XX  
XX 01-MAY-1998; 98US-0083758P.  
XX 31-JUL-1998; 98US-0094869P.  
XX 02-SEP-1998; 98US-0098994P.  
XX 02-SEP-1998; 98US-0099062P.  
XX 09-OCT-1998; 98US-0103749P.  
XX 09-OCT-1998; 98US-0103794P.  
XX 09-OCT-1998; 98US-0103796P.  
XX 25-FEB-1999; 99US-0121528P.  
XX  
XX (CHIR ) CHIRON CORP.  
XX (GENO-) INST GENOMIC RES.  
XX  
XX Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;  
PI Petersen J, Pizza M, Rappuoli R, Ratti G, Scalato E, Scarselli M;  
PI Tettelin H, Venter JC;  
XX  
XX WPI: 2000-062150/05.  
XX N-PSDB; AAZ54488.  
XX  
XX Novel Neisserial polypeptides predicted to be useful antigens for  
PT vaccines and diagnostics.  
XX  
XX Claim 2; Page 1367; 1453pp; English.  
XX  
XX AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAU74253 to AAU75941  
CC represent novel Neisseria meningitidis and N. gonorrhoeae polynucleotides  
CC and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ55473 represent  
CC PCR primers used in the exemplification of the present invention. The  
CC polypeptides, the polynucleotides, antibodies and compositions of the  
CC invention can be used as vaccines, as diagnostic reagents, and as  
CC immunogenic compositions. The polypeptides can be used in the manufacture  
CC of medicaments for treating or preventing infection due to Neisserial  
CC bacteria (e.g. meningitis and septicaemia), to detect the presence of  
CC Neisseria bacteria, or to raise antibodies. They may also be used to  
CC screen for agonists or antagonists, which may themselves have use as  
CC antibacterial agents. The polynucleotides of the invention may also be  
XX used in gene therapy protocols. (Updated on 12-SEP-2003 to standardise OS  
XX field)

SQ Sequence 331 AA;  
 Query Match 100.0%; Score 28; DB 3; Length 331;  
 Best Local Similarity 100.0%; Pred. No. 9.6e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LKEKAK 6  
 |||||  
 DB 102 LKEKAK 107

RESULT 34  
 ABU01490  
 ID ABU01490 standard; protein; 338 AA.  
 XX  
 AC ABU01490;  
 DT 23-OCT-2003 (revised)  
 DT 11-FEB-2003 (first entry)  
 XX  
 DE S. pneumoniae type 4 strain protein from coding region #1066.  
 XX  
 KW Bacterial meningitis; pneumonia; sepsis; otitis media; ear infection;  
 KW antiinflammatory; antibacterial; immunostimulant; auditory; respiratory;  
 KW gene therapy; vaccine.  
 XX  
 OS Streptococcus pneumoniae; type 4 strain.  
 XX  
 PN WO200277021-A2.  
 XX  
 PD 03-OCT-2002.  
 XX  
 PF 27-MAR-2002; 2002WO-IB002163.  
 XX  
 PR 27-MAR-2001; 2001GB-00007658.  
 XX  
 PA (CHIR-) CHIRON SPA.  
 PA (GENO-) INST GENOMIC RES.  
 XX  
 PI Masignani V, Tettelin H, Fraser C;  
 XX  
 DR WPI: 2003-040579/03.  
 DR N-PSDB; ABX06778.  
 XX  
 PT New proteins and nucleic acid molecules from Streptococcus pneumoniae,  
 PT useful as medicaments for treating or preventing a disease or infection  
 PT due to streptococcus bacteria, such as pneumonia, sepsis, otitis media or  
 PT ear infection.  
 XX  
 PS Claim 1; SEQ ID NO 2132; 56pp; English.  
 XX  
 CC The invention relates to a protein comprising or having at least 50%  
 CC identity to any of the 2469 amino acid sequences, identified in the  
 CC specification (available on a computer readable format), or its fragment,  
 CC expressed from 2469 of 2489 identified DNA coding regions from the  
 CC Streptococcus pneumoniae type 4 strain genomic sequence appearing as  
 CC ABS56454. Also included are an antibody which binds one of the proteins,  
 CC treating a patient by administering the protein, DNA or antibody (in a  
 CC composition), a kit comprising first and second primers, which are the  
 CC nucleic acid cited above or fragments between nucleotides 8-100 of a  
 CC sequence not defined in the specification, for amplifying a target  
 CC sequence contained within a Streptococcus nucleic acid sequence, where  
 CC the first primer is substantially complementary to the target sequence  
 CC and the second primer is substantially complementary to the complement of  
 CC the target sequence, and where the parts of the primers having  
 CC substantial complementarity define the termini of the target sequence to  
 CC be amplified, assay comprising contacting a test compound with the  
 CC protein, and determining whether the test compound binds to the protein  
 CC and a Streptococcus pneumoniae bacterium, where one or more genes  
 CC encoding the proteins has been rendered inactive. The proteins, nucleic  
 CC acid molecules, antibody and compositions are useful as medicaments for  
 CC treating or preventing a disease or infection due to streptococcus  
 CC bacteria, particularly S. pneumoniae, such as pneumonia, sepsis, otitis

media or ear infection. They are also useful in developing vaccines,  
 CC diagnostics and antibiotics. The methods are useful for identifying  
 CC immunodominant proteins. The present sequence is one of the 2469 proteins  
 CC expressed by the identified coding regions from the genomic sequence.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences. (Updated on 23-OCT-2003 to  
 CC standardise OS field)  
 XX  
 SQ Sequence 338 AA;  
 Query Match 100.0%; Score 28; DB 6; Length 338;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LKEKAK 6  
 |||||  
 DB 305 LKEKAK 310

RESULT 35  
 AAB96209  
 ID AAB96209 standard; protein; 367 AA.  
 XX  
 AC AAB96209;  
 XX  
 DT 29-OCT-2001 (first entry)  
 XX  
 DE Putative P. abyssi ATPase involved in DNA repair #1.  
 XX  
 KW Hyperthermophilic archaeon; hyperthermophilic protein.  
 XX  
 OS Pyrococcus abyssi.  
 XX  
 PN FR2792651-A1.  
 XX  
 PD 27-OCT-2000.  
 XX  
 PF 21-APR-1999; 99FR-00005034.  
 XX  
 PR 21-APR-1999; 99FR-00005034.  
 XX  
 PA (CNRS) CNRS CENT NAT RECH SCI.  
 PA (IFRE-) IFREMER INST FR RECH EXPL MER.  
 XX  
 PI Forterre P, Thierry JC, Prieur D, Dietrich J, Lecompte O;  
 PI Querellou J, Weissenbach J, Saurin W, Heilig R;  
 XX  
 DR WPI: 2001-126236/14.  
 XX  
 PT New nucleotide sequences isolated from Pyrococcus abyssi encode proteins  
 PT useful in industry.  
 XX  
 PS Claim 7; Page 852-853; 1657pp; French.  
 XX  
 CC The present invention relates to the genomic sequence of Pyrococcus  
 CC abyssi (see AAF86431 and AAH41223-7) and P. abyssi proteins. P. abyssi is  
 CC a hyperthermophilic archaeon, which is isolated from deep-sea  
 CC hydrothermal vents. The present sequence is one such P. abyssi protein.  
 CC The proteins of the present invention have various potential industrial  
 CC uses, since the proteins are stable at very high temperatures, some up to  
 CC 110 degrees centigrade. Note: This patent is in the same patent family as  
 CC WO200005062, which contains additional sequences as shown in AAB99132-  
 CC AAB99143, AAH75903-AAH75920 and AAG66436  
 XX  
 SQ Sequence 367 AA;  
 Query Match 100.0%; Score 28; DB 4; Length 367;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LKEKAK 6  
 |||||

```

Db      167 LKEKAK 172

RESULT 36
AAY75494
ID AAY75494 standard; protein; 374 AA.
XX
AC AAY75494;
XX
DT 21-MAR-2000 (first entry)
XX
DE Neisseria meningitidis ORF 728 protein sequence SEQ ID NO:2462.
XX
KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KW antigenic; diagnosis; Neisseria gonorrhoeae; infection; meningitis; septicaemia;
KW antibacterial; gene therapy.
XX
OS Neisseria meningitidis.
XX
PN WO9957280-A2.
XX
PD 11-NOV-1999.
XX
PF 30-APR-1999; 99WO-US009346.
XX
PR 01-MAY-1998; 98US-0083758P.
PR 31-JUL-1998; 98US-0094869P.
PR 02-SEP-1998; 98US-0098994P.
PR 02-SEP-1998; 98US-0099062P.
PR 09-OCT-1998; 98US-0103749P.
PR 09-OCT-1998; 98US-0103794P.
PR 09-OCT-1998; 98US-0103796P.
PR 09-OCT-1998; 98US-0103796P.
PR 25-FEB-1999; 99US-0121528P.
XX
PA (CHIR ) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
XX
PI Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;
PI Petersen J, Pizzo M, Rappuoli R, Ratti G, Scalato E, Scarselli M;
PI Tettelin H, Venter JC;
XX
WPI; 2000-062150/05.
DR N-PSDB; AA254256.
XX
PT Novel Neisserial polypeptides predicted to be useful antigens for
PT vaccines and diagnostics.
XX
PS Claim 2; Page 1176; 1453pp; English.
XX
CC AA253015 to AA254536, AA254577 to AA254615, and AAY74253 to AAY75941
CC represent novel Neisseria meningitidis and N. gonorrhoeae polynucleotides
CC and polypeptides. AA254537 to AA254576 and AA254616 to AA255473 represent
CC PCR primers used in the exemplification of the present invention. The
CC polypeptides, the polynucleotides, antibodies and compositions of the
CC invention can be used as vaccines, as diagnostic reagents, and as
CC immunogenic compositions. The polypeptides can be used in the manufacture
CC of medicaments for treating or preventing infection due to Neisserial
CC bacteria (e.g. meningitis and septicaemia), to detect the presence of
CC Neisseria bacteria, or to raise antibodies. They may also be used to
CC screen for agonists or antagonists, which may themselves have use as
CC antibacterial agents. The polynucleotides of the invention may also be
CC used in gene therapy protocols
XX
SQ Sequence 374 AA;

Query Match 100.0%; Score 28; DB 3; Length 374;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
Db 99 LKEKAK 104

RESULT 38

```

```

RESULT 37
AAY75728
ID AAY75728 standard; protein; 374 AA.
XX
AC AAY75728;
XX
DT 21-MAR-2000 (first entry)
XX
DE Neisseria meningitidis ORF 957 protein sequence SEQ ID NO:2928.
XX
KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KW antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
KW antibacterial; gene therapy.
XX
OS Neisseria meningitidis.
XX
PN WO9957280-A2.
XX
PD 11-NOV-1999.
XX
PF 30-APR-1999; 99WO-US009346.
XX
PR 01-MAY-1998; 98US-0083758P.
PR 31-JUL-1998; 98US-0094869P.
PR 02-SEP-1998; 98US-0098994P.
PR 02-SEP-1998; 98US-0099062P.
PR 09-OCT-1998; 98US-0103749P.
PR 09-OCT-1998; 98US-0103794P.
PR 09-OCT-1998; 98US-0103796P.
PR 25-FEB-1999; 99US-0121528P.
XX
PA (CHIR ) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
XX
PI Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;
PI Petersen J, Pizzo M, Rappuoli R, Ratti G, Scalato E, Scarselli M;
PI Tettelin H, Venter JC;
XX
WPI; 2000-062150/05.
DR N-PSDB; AA254490.
XX
PT Novel Neisserial polypeptides predicted to be useful antigens for
PT vaccines and diagnostics.
XX
PS Claim 2; Page 1369; 1453pp; English.
XX
CC AA253015 to AA254536, AA254577 to AA254615, and AAY74253 to AAY75941
CC represent novel Neisseria meningitidis and N. gonorrhoeae polynucleotides
CC and polypeptides. AA254537 to AA254576 and AA254616 to AA255473 represent
CC PCR primers used in the exemplification of the present invention. The
CC polypeptides, the polynucleotides, antibodies and compositions of the
CC invention can be used as vaccines, as diagnostic reagents, and as
CC immunogenic compositions. The polypeptides can be used in the manufacture
CC of medicaments for treating or preventing infection due to Neisserial
CC bacteria (e.g. meningitis and septicaemia), to detect the presence of
CC Neisseria bacteria, or to raise antibodies. They may also be used to
CC screen for agonists or antagonists, which may themselves have use as
CC antibacterial agents. The polynucleotides of the invention may also be
CC used in gene therapy protocols
XX
SQ Sequence 374 AA;

Query Match 100.0%; Score 28; DB 3; Length 374;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
Db 99 LKEKAK 104

RESULT 38

```



```

AAU37739
ID AAU37739 standard; protein; 374 AA.
XX
AC AAU37739;
XX
DT 14-FEB-2002 (first entry)
XX
DE Streptococcus pneumoniae cellular proliferation protein #168.
XX
KW Antisense; prokaryotic cellular proliferation protein; antibiotic;
KW antibacterial; drug design.
XX
OS Streptococcus pneumoniae.
XX
PN WO200170955-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US009180.
XX
PR 21-MAR-2000; 2000US-0191078P.
PR 23-MAY-2000; 2000US-0206948P.
PR 26-MAY-2000; 2000US-0207272P.
PR 23-OCT-2000; 2000US-0242578P.
PR 27-NOV-2000; 2000US-0253625P.
PR 22-DEC-2000; 2000US-0257931P.
PR 16-FEB-2001; 2001US-0269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
DR WPI; 2001-611495/70.
DR N-PSDB; AAS55598.
XX
PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
XX
XX Example 3; SEQ ID NO 13332; 511pp; English.
XX
PS The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 374 AA;
XX
XX Query Match 100.0%; Score 28; DB 4; Length 374;
XX Best Local Similarity 100.0%; Pred. No. 1.1e+03;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 LKEKAK 6
XX Db 341 LKEKAK 346
XX
XX RESULT 39
XX AAU37739
XX
AAU375727 standard; protein; 377 AA.
XX
AC AAU375727;
XX
DT 21-MAR-2000 (first entry)
XX
DE Neisseria meningitidis ORF 957 protein sequence SEQ ID NO:2926.
XX
KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KW antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
KW antibacterial; gene therapy.
XX
OS Neisseria meningitidis.
XX
PN WO9957280-A2.
XX
PD 11-NOV-1999.
XX
PF 30-APR-1999; 99WO-US009346.
XX
PR 01-MAY-1998; 98US-0083758P.
PR 31-JUL-1998; 98US-0094869P.
PR 02-SEP-1998; 98US-0098994P.
PR 02-SEP-1998; 98US-0098062P.
PR 09-OCT-1998; 98US-0103743P.
PR 09-OCT-1998; 98US-0103794P.
PR 09-OCT-1998; 98US-0103796P.
PR 25-FEB-1999; 99US-0121528P.
XX
XX (CHIR ) CHIRON CORP.
XX (GENO-) INST GENOMIC RES.
XX
PI Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;
PI Petersen J, Pizzi M, Rappulli R, Ratti G, Scalato E, Scarselli M;
PI Tettelin H, Venter JC;
XX
DR WPI; 2000-062150/05.
DR N-PSDB; AA254489.
XX
XX Novel Neisserial polypeptides predicted to be useful antigens for
PT vaccines and diagnostics.
PT
XX Claim 2; Page 1367-1368; 1453pp; English.
XX
XX AA253015 to AA254536, AA254577 to AA254615, and AA274253 to AA275941
CC represent novel Neisseria meningitidis and N. gonorrhoeae polynucleotides
CC and polypeptides. AA254537 to AA254576 and AA254616 to AA255473 represent
CC PCR primers used in the exemplification of the present invention. The
CC polypeptides, the polynucleotides, antibodies and compositions of the
CC invention can be used as vaccines, as diagnostic reagents, and as
CC immunogenic compositions. The polypeptides can be used in the manufacture
CC of medicaments for treating or preventing infection due to Neisserial
CC bacteria (e.g. meningitis and septicemia), to detect the presence of
CC Neisseria bacteria, or to raise antibodies. They may also be used to
CC screen for agonists or antagonists, which may themselves have use as
CC antibacterial agents. The polynucleotides of the invention may also be
CC used in gene therapy protocols
XX
XX Sequence 377 AA;
XX
XX Query Match 100.0%; Score 28; DB 3; Length 377;
XX Best Local Similarity 100.0%; Pred. No. 1.1e+03;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 LKEKAK 6
XX Db 102 LKEKAK 107
XX
XX RESULT 40
XX AAU375493
XX ID AAU375493 standard; protein; 377 AA.
XX
XX

```

AC AAY75493;  
 DT 21-MAR-2000 (first entry)  
 XX  
 DE Neisseria meningitidis ORF 728 protein sequence SEQ ID NO:2460.  
 XX  
 DE Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;  
 KW antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;  
 KW antibacterial; gene therapy.  
 XX  
 OS Neisseria meningitidis.  
 XX  
 PN WO9957280-A2.  
 XX  
 PD 11-NOV-1999.  
 XX  
 PF 30-APR-1999; 99WO-US009346.  
 XX  
 PR 01-MAY-1998; 98US-0083758P.  
 PR 31-JUL-1998; 98US-0094869P.  
 PR 02-SEP-1998; 98US-0098994P.  
 PR 02-SEP-1998; 98US-0099062P.  
 PR 09-OCT-1998; 98US-0103749P.  
 PR 09-OCT-1998; 98US-0103794P.  
 PR 09-OCT-1998; 98US-0103796P.  
 PR 25-FEB-1999; 99US-0121528P.  
 XX  
 PA (CHIR ) CHIRON CORP.  
 PA (GENO-) INST GENOMIC RES.  
 XX  
 PI Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;  
 PI Petersen J, Pizsa M, Rappuoli R, Ratti G, Scalato E, Scarselli M;  
 PI Tettelin H, Venter JC;  
 XX  
 DR WPI; 2000-062150/05.  
 DR N-PSDB; AAZ54255.  
 XX  
 XX Novel Neisserial polypeptides predicted to be useful antigens for  
 PT vaccines and diagnostics.  
 PT  
 XX Claim 2; Page 1175; 1453pp; English.  
 XX  
 CC AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941  
 CC represent novel Neisseria meningitidis and N. gonorrhoeae polynucleotides  
 CC and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ5473 represent  
 CC PCR primers used in the exemplification of the present invention. The  
 CC polypeptides, the polynucleotides, antibodies and compositions of the  
 CC invention can be used as vaccines, as diagnostic reagents, and as  
 CC immunogenic compositions. The polypeptides can be used in the manufacture  
 CC of medicaments for treating or preventing infection due to Neisserial  
 CC bacteria (e.g. meningitis and septicaemia), to detect the presence of  
 CC Neisseria bacteria, or to raise antibodies. They may also be used to  
 CC screen for agonists or antagonists, which may themselves have use as  
 CC antibacterial agents. The polynucleotides of the invention may also be  
 CC used in gene therapy protocols  
 XX  
 SQ Sequence 377 AA;  
 Query Match 100.0%; Score 28; DB 3; Length 377;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LKEKAK 6  
 DB 102 LKEKAK 107  
 RESULT 41  
 AAY75492  
 ID AAY75492 standard; protein; 377 AA.  
 XX  
 AC AAY75492;  
 XX

DT 12-SEP-2003 (revised)  
 DT 21-MAR-2000 (first entry)  
 XX  
 DE Neisseria gonorrhoeae ORF 728 protein sequence SEQ ID NO:2458.  
 XX  
 DE Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;  
 KW antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;  
 KW antibacterial; gene therapy.  
 XX  
 OS Neisseria gonorrhoeae.  
 XX  
 PN WO9957280-A2.  
 XX  
 PD 11-NOV-1999.  
 XX  
 PF 30-APR-1999; 99WO-US009346.  
 XX  
 PR 01-MAY-1998; 98US-0083758P.  
 PR 31-JUL-1998; 98US-0094869P.  
 PR 02-SEP-1998; 98US-0098994P.  
 PR 02-SEP-1998; 98US-0099062P.  
 PR 09-OCT-1998; 98US-0103749P.  
 PR 09-OCT-1998; 98US-0103794P.  
 PR 09-OCT-1998; 98US-0103796P.  
 PR 25-FEB-1999; 99US-0121528P.  
 XX  
 PA (CHIR ) CHIRON CORP.  
 PA (GENO-) INST GENOMIC RES.  
 XX  
 PI Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;  
 PI Petersen J, Pizsa M, Rappuoli R, Ratti G, Scalato E, Scarselli M;  
 PI Tettelin H, Venter JC;  
 XX  
 DR WPI; 2000-062150/05.  
 DR N-PSDB; AAZ54254.  
 XX  
 XX Novel Neisserial polypeptides predicted to be useful antigens for  
 PT vaccines and diagnostics.  
 PT  
 XX Claim 2; Page 1174; 1453pp; English.  
 XX  
 CC AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941  
 CC represent novel Neisseria meningitidis and N. gonorrhoeae polynucleotides  
 CC and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ55473 represent  
 CC PCR primers used in the exemplification of the present invention. The  
 CC polypeptides, the polynucleotides, antibodies and compositions of the  
 CC invention can be used as vaccines, as diagnostic reagents, and as  
 CC immunogenic compositions. The polypeptides can be used in the manufacture  
 CC of medicaments for treating or preventing infection due to Neisserial  
 CC bacteria (e.g. meningitis and septicaemia), to detect the presence of  
 CC Neisseria bacteria, or to raise antibodies. They may also be used to  
 CC screen for agonists or antagonists, which may themselves have use as  
 CC antibacterial agents. The polynucleotides of the invention may also be  
 CC used in gene therapy protocols. (Updated on 12-SEP-2003 to standardise OS  
 CC field)  
 XX  
 SQ Sequence 377 AA;  
 Query Match 100.0%; Score 28; DB 3; Length 377;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LKEKAK 6  
 DB 102 LKEKAK 107  
 RESULT 42  
 ABP80849  
 ID ABP80849 standard; protein; 377 AA.  
 XX  
 AC ABP80849;  
 XX



CC The present invention relates to high throughput screening assays for  
 CC agents capable of modulating the activity of ATP-binding cassette  
 CC transporter 1 (ABCA1, also called cholesterol efflux regulating protein  
 CC (CERP)). The method comprises determining the activity of an ABCA1  
 CC polypeptide in the presence of an ABCA1-interacting protein (AIP) that  
 CC has been contacted with an agent. The method is useful for identifying  
 CC modulators of ABCA1 biological activity, particularly for identifying  
 CC agents that modulate cholesterol or phospholipid levels in an animal. The  
 CC method is useful for treating disorders of lipid metabolism, especially  
 CC for reducing elevated plasma phospholipid or cholesterol levels in  
 CC patients, or for preventing elevated phospholipid or cholesterol levels  
 CC in a patient at risk of developing disorders such as cardiovascular  
 CC disease (CVD), coronary artery disease (CAD), cerebrovascular disease,  
 CC coronary stenosis, and peripheral vascular disease. The present  
 CC sequence represents a human AIP polypeptide

XX Sequence 391 AA;  
 SQ Query Match 100.0%; Score 28; DB 6; Length 391;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
 DB 146 LKEKAK 151  
 |||||

RESULT 45  
 ADE55135  
 ID ADE55135 standard; protein; 391 AA.

XX ADE55135;

XX 29-JAN-2004 (first entry)

XX Rat Protein AF062594, SEQ ID NO 940.

XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
 KW Chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX Rattus norvegicus.

XX WO2003016475-A2.

XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

XX 01-NOV-2001; 2001US-0346382P.

XX 26-NOV-2001; 2001US-0333347P.

XX (GEO ) GEN HOSPITAL CORP.

XX (FARB ) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;

XX WPI; 2003-268312/26.

XX GENBANK; AF062594.

XX New composition comprising two or more isolated polypeptides, useful for

XX preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat  
 CC or human polynucleotides or a polynucleotide which represents a fragment,  
 CC derivative or allelic variation of the nucleic acid sequence. Also  
 CC claimed are a vector comprising the novel polynucleotide, a host cell  
 CC comprising the vector, a method for identifying a nucleotide sequence  
 CC which is differentially regulated in an animal subjected to pain and a  
 CC kit to perform the method, an array, a method for identifying an agent  
 CC that increases or decreases the expression of the polynucleotide sequence

CC that is differentially expressed in neuronal tissue of a first animal  
 CC subjected to pain, a method for identifying a compound which regulates  
 CC the expression of a polynucleotide sequence which is differentially  
 CC expressed in an animal subjected to pain, a method for identifying a  
 CC compound that regulates the activity of one or more of the  
 CC polynucleotides, a method for producing a pharmaceutical composition, a  
 CC method for identifying a compound or small molecule that regulates the  
 CC activity in an animal of one or more of the polypeptides given in the  
 CC specification, a method for identifying a compound useful in treating  
 CC pain and a pharmaceutical composition comprising the one or more  
 CC polypeptides or their antibodies. The polynucleotide or the compound that  
 CC modulates its activity is useful for preparing a medicament for treating  
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of  
 CC the specification) which is differentially expressed during pain. Note:  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic form directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 391 AA;

Query Match 100.0%; Score 28; DB 7; Length 391;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
 DB 146 LKEKAK 151  
 |||||

RESULT 46  
 ADE55144  
 ID ADE55144 standard; protein; 391 AA.

XX ADE55144;

XX 29-JAN-2004 (first entry)

XX Rat Protein AF062594, SEQ ID NO 949.

XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
 KW Chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX Rattus norvegicus.

XX WO2003016475-A2.

XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

XX 01-NOV-2001; 2001US-0346382P.

XX 26-NOV-2001; 2001US-0333347P.

XX (GEO ) GEN HOSPITAL CORP.

XX (FARB ) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;

XX WPI; 2003-268312/26.

XX GENBANK; AF062594.

XX New composition comprising two or more isolated polypeptides, useful for

XX preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat

comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

Sequence 391 AA;

Query Match 100.0%; Score 28; DB 7; Length 391;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
Db 146 LKEKAK 151

RESULT 47

AD55141 ID ADE55141 standard; protein; 391 AA.

XX AC ADE55141;

XX DT 29-JAN-2004 (first entry)

XX DE Rat Protein AF062594, SEQ ID NO 946.

XX KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
XX KM chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX OS Rattus norvegicus.

XX PN WO2003016475-A2.

XX PD 27-FEB-2003.

XX PF 14-AUG-2002; 2002WO-US025765.

XX PR 14-AUG-2001; 2001US-0312147P.

XX PR 01-NOV-2001; 2001US-0346382P.

XX PR 26-NOV-2001; 2001US-0333347P.

XX PA (GHEO ) GEN HOSPITAL CORP.

XX PA (FARB ) BAYER AG.

XX PI Woolf C, D'urso D, Befort K, Costigan M;

XX DR WPI; 2003-268312/26.

XX DR GENBANK; AF062594.

XX PT New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.

XX PS Claim 1; Page; 1017pp; English.

XX

The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

Sequence 391 AA;

Query Match 100.0%; Score 28; DB 7; Length 391;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
Db 146 LKEKAK 151

RESULT 48

AD55147 ID ADE55147 standard; protein; 391 AA.

XX AC ADE55147;

XX DT 29-JAN-2004 (first entry)

XX DE Rat Protein AF062594, SEQ ID NO 952.

XX KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
XX KM chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX OS Rattus norvegicus.

XX PN WO2003016475-A2.

XX PD 27-FEB-2003.

XX PF 14-AUG-2002; 2002WO-US025765.

XX PR 14-AUG-2001; 2001US-0312147P.

XX PR 01-NOV-2001; 2001US-0346382P.

XX PR 26-NOV-2001; 2001US-0333347P.

XX PA (GHEO ) GEN HOSPITAL CORP.

XX PA (FARB ) BAYER AG.

XX PI Woolf C, D'urso D, Befort K, Costigan M;

XX DR WPI; 2003-268312/26.

XX DR GENBANK; AF062594.

XX PT New composition comprising two or more isolated polypeptides, useful for

PT preparing a medicament for treating pain in an animal.  
XX  
XX  
PS Claim 1; Page; 1017pp; English.  
XX  
XX The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a rat protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX Sequence 391 AA;  
SQ  
Query Match 100.0%; Score 28; DB 7; Length 391;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LKEKAK 6  
Db 146 LKEKAK 151  
RESULT 49  
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ID ADE55138 standard; protein; 391 AA.  
XX  
XX ADE55138;  
XX  
DT 29-JAN-2004 (first entry)  
DE  
DE Rat Protein AF062594, SEQ ID NO 943.  
XX  
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.  
XX  
XX Rattus norvegicus.  
OS  
XX WO2003016475-A2.  
XX  
XX 27-FEB-2003.  
XX  
XX 14-AUG-2002; 2002WO-US025765.  
PF  
XX 14-AUG-2001; 2001US-0312147P.  
PR  
XX 01-NOV-2001; 2001US-0346382P.  
PR  
XX 26-NOV-2001; 2001US-0333347P.  
XX  
XX (GEO ) GEN HOSPITAL CORP.  
PA  
XX (FARB ) BAYER AG.  
XX  
XX Woolf C, D'urso D, Befort K, Costigan M;  
PI  
XX

DR WPI; 2003-268312/26.  
DR GENEBANK; AF062594.  
XX  
XX New composition comprising two or more isolated polypeptides, useful for  
PT preparing a medicament for treating pain in an animal.  
XX  
XX Claim 1; Page; 1017pp; English.  
XX  
XX The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a rat protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
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XX Sequence 391 AA;  
SQ  
Query Match 100.0%; Score 28; DB 7; Length 391;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LKEKAK 6  
Db 146 LKEKAK 151  
RESULT 50  
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ID ADE55132 standard; protein; 391 AA.  
XX  
XX ADE55132;  
XX  
DT 29-JAN-2004 (first entry)  
DE  
DE Rat Protein AF062594, SEQ ID NO 937.  
XX  
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.  
XX  
XX Rattus norvegicus.  
OS  
XX WO2003016475-A2.  
XX  
XX 27-FEB-2003.  
XX  
XX 14-AUG-2002; 2002WO-US025765.  
PF  
XX 14-AUG-2001; 2001US-0312147P.  
PR  
XX 01-NOV-2001; 2001US-0346382P.  
PR  
XX 26-NOV-2001; 2001US-0333347P.  
XX  
XX (GEO ) GEN HOSPITAL CORP.  
PA

PA (PARE ) BAYER AG.  
XX  
PI Woolf C, D'urso D, Befort K, Costigan M;  
XX  
DR WPI: 2003-268312/26.  
DR GENBANK; AF062594.  
XX  
PT New composition comprising two or more isolated polypeptides, useful for  
XX preparing a medicament for treating pain in an animal.  
XX  
XX Claim 1; Page; 1017pp; English.  
XX  
XX The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a rat protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 391 AA;

Query Match 100.0%; Score 28; DB 7; Length 391;  
Best Local Similarity 100.0%; Pred. NO. 1.1e+03;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 LKEKAK 6  
Db |||||  
146 LKEKAK 151

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Job time : 29.8065 secs

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OM protein - protein search, using sw model

Run on: April 19, 2004, 17:22:11 ; Search time 20.0323 Seconds  
(without alignments)  
82.569 Million cell updates/sec

Title: US-10-726-692-14

Perfect score: 28

Sequence: 1 LKEKAK 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1124875 seqs, 275673149 residues

Total number of hits satisfying chosen parameters: 1124875

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : Published Applications AA.\*

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- 17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	100.0	60	9 US-09-764-864-1549	Sequence 1549, Ap
2	28	100.0	63	12 US-10-424-599-232705	Sequence 232705,
3	28	100.0	82	12 US-10-424-599-163245	Sequence 163245,
4	28	100.0	85	9 US-09-864-761-43162	Sequence 43162, A
5	28	100.0	96	12 US-10-424-599-143746	Sequence 143746,
6	28	100.0	141	9 US-09-764-864-1134	Sequence 1134, Ap
7	28	100.0	159	12 US-10-282-122A-63343	Sequence 63343, A
8	28	100.0	174	9 US-09-840-787-27	Sequence 27, Appl
9	28	100.0	175	10 US-09-883-152-17	Sequence 17, Appl
10	28	100.0	205	12 US-10-424-599-263529	Sequence 263529,
11	28	100.0	236	12 US-10-335-977-6032	Sequence 6032, Ap
12	28	100.0	237	12 US-10-335-977-6033	Sequence 6033, Ap
13	28	100.0	247	14 US-10-032-585-7107	Sequence 7107, Ap
14	28	100.0	290	12 US-10-335-977-6834	Sequence 6834, Ap
15	28	100.0	297	12 US-10-276-774-2219	Sequence 2219, Ap

16	28	100.0	308	12	US-10-335-977-6835	Sequence 6835, Ap
17	28	100.0	322	9	US-09-838-561-11	Sequence 11, Appl
18	28	100.0	322	9	US-09-816-760-11	Sequence 11, Appl
19	28	100.0	322	14	US-10-172-585-11	Sequence 11, Appl
20	28	100.0	326	13	US-10-108-915-46	Sequence 46, Appl
21	28	100.0	374	9	US-09-815-242-13332	Sequence 13332, A
22	28	100.0	386	14	US-10-146-473-70	Sequence 70, Appl
23	28	100.0	386	14	US-10-156-761-9922	Sequence 9922, Ap
24	28	100.0	404	15	US-10-023-634-40	Sequence 40, Appl
25	28	100.0	406	9	US-09-925-301-1320	Sequence 1320, Ap
26	28	100.0	406	14	US-10-106-698-4620	Sequence 4620, Ap
27	28	100.0	432	12	US-10-425-114-53665	Sequence 53665, Ap
28	28	100.0	442	12	US-10-282-122A-76831	Sequence 76831, A
29	28	100.0	452	15	US-10-023-634-36	Sequence 36, Appl
30	28	100.0	452	15	US-10-023-634-38	Sequence 38, Appl
31	28	100.0	455	15	US-10-023-634-97	Sequence 97, Appl
32	28	100.0	492	15	US-10-108-260A-4337	Sequence 4337, Ap
33	28	100.0	560	9	US-09-864-761-37938	Sequence 37938, A
34	28	100.0	572	9	US-09-864-761-34546	Sequence 34546, A
35	28	100.0	629	15	US-10-023-634-96	Sequence 96, Appl
36	28	100.0	797	10	US-09-999-314A-2	Sequence 2, Appl
37	28	100.0	797	12	US-10-377-097-121	Sequence 121, Appl
38	28	100.0	890	15	US-10-104-047-2992	Sequence 2992, Ap
39	28	100.0	913	15	US-10-334-143-40	Sequence 40, Appl
40	28	100.0	1042	12	US-10-282-122A-58014	Sequence 58014, A
41	28	100.0	1080	15	US-10-023-634-42	Sequence 42, Appl
42	28	100.0	1525	12	US-09-839-479-68	Sequence 68, Appl
43	28	100.0	1525	12	US-10-702-148-68	Sequence 68, Appl
44	28	100.0	1525	12	US-10-376-537-69	Sequence 69, Appl
45	28	100.0	1527	12	US-09-839-479-27	Sequence 27, Appl
46	28	100.0	1527	12	US-10-702-148-27	Sequence 27, Appl
47	28	100.0	1527	12	US-10-376-537-27	Sequence 27, Appl
48	28	100.0	1531	12	US-09-839-479-29	Sequence 29, Appl
49	28	100.0	1531	12	US-10-702-148-29	Sequence 29, Appl
50	28	100.0	1531	12	US-10-376-537-29	Sequence 29, Appl

#### ALIGNMENTS

RESULT 1  
US-09-764-864-1549  
; Sequence 1549, Application US/09764864  
; Patent No. US20020132753A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PT223  
; CURRENT APPLICATION NUMBER: US/09/764,864  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 1792  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1549  
; LENGTH: 60  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (33)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-764-864-1549

Query Match 100.0%; Score 28; DB 9; Length 60;  
Best Local Similarity 100.0%; Pred.No.1.6e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LKEKAK 6  
DB 47 LKEKAK 52  
RESULT 2

US-10-424-599-232705

; Sequence 232705, Application US/10424599

; Publication No. US20040031072A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J

; APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua

; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 232705

; LENGTH: 63

; TYPE: PRT

; ORGANISM: Glycine max

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)..(63)

; OTHER INFORMATION: unsure at all Xaa locations

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_52157C.1.pcp

US-10-424-599-232705

Query Match 100.0%; Score 28; DB 12; Length 63;

Best Local Similarity 100.0%; Pred. No. 1.7e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6

DB 36 LKEKAK 41

RESULT 3

US-10-424-599-163245

; Sequence 163245, Application US/10424599

; Publication No. US20040031072A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J

; APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua

; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 163245

; LENGTH: 82

; TYPE: PRT

; ORGANISM: Glycine max

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_118429C.1.pcp

US-10-424-599-163245

Query Match 100.0%; Score 28; DB 12; Length 82;

Best Local Similarity 100.0%; Pred. No. 2.2e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6

DB 4 LKEKAK 9

RESULT 4

US-09-864-761-43162

; Sequence 43162, Application US/09864761

; Patent No. US20020048763A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharron G.

; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: Aecmica-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 43162  
; LENGTH: 85  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AL122057.1  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.96  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.8  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1  
; OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 1.6  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7  
; OTHER INFORMATION: EST HUMAN HIT: BF701492.1, EVALUE 2.00e-42  
; OTHER INFORMATION: SWISSPROT HIT: Q9Y5S9, EVALUE 2.00e-43  
US-09-864-761-43162

Query Match 100.0%; Score 28; DB 9; Length 85;

Best Local Similarity 100.0%; Pred. No. 2.2e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6

DB 28 LKEKAK 33

RESULT 5

US-10-424-599-143746

; Sequence 143746, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT

FILE REFERENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 143746

LENGTH: 96

TYPE: PRT

ORGANISM: Glycine max

FEATURE:

OTHER INFORMATION: Clone ID: PAT\_MRT3847\_100816C.1.pap

US-10-424-599-143746

Query Match 100.0%; Score 28; DB 12; Length 96;

Best Local Similarity 100.0%; Pred. No. 2.5e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6

DB 23 LKEKAK 28

RESULT 6

US-09-764-864-1134

Sequence 1134, Application US/09764864

Patent No. US20020132753A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PT223

CURRENT APPLICATION NUMBER: US/09/764,864

Prior application date: 2001-01-17

Number of SEQ ID NOS removed - consult PALM or file wrapper

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1134

LENGTH: 141

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SITE

LOCATION: (105)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-764-864-1134

Query Match 100.0%; Score 28; DB 9; Length 141;

Best Local Similarity 100.0%; Pred. No. 3.6e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6

DB 95 LKEKAK 100

RESULT 7

US-10-282-122A-63343

Sequence 63343, Application US/10282122A

Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu

APPLICANT: Zamudio, Carlos

APPLICANT: Malone, Cheryl

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Kari

APPLICANT: Zyskind, Judith

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John

APPLICANT: Carr, Grant

APPLICANT: Yamamoto, Robert

APPLICANT: Forsyth, R.

APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELTRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

Prior application number: 60/191,078

Prior filing date: 2000-03-21

Prior application number: 60/206,848

Prior filing date: 2000-05-23

Prior application number: 60/207,727

Prior filing date: 2000-05-26

Prior application number: 60/230,335

Prior filing date: 2000-09-06

Prior application number: 60/230,347

Prior filing date: 2000-09-09

Prior application number: 60/242,578

Prior filing date: 2000-10-23

Prior application number: 60/253,625

Prior filing date: 2000-11-27

Prior application number: 60/257,931

Prior filing date: 2000-12-22

Prior application number: 60/267,636

Prior filing date: 2001-02-09

Prior application number: 60/269,308

Prior filing date: 2001-02-16

Remaining prior application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 78614

SOFTWARE: PatentIn version 3.1

SEQ ID NO 63343

LENGTH: 159

TYPE: PRT

ORGANISM: Moraxella catarrhalis

US-10-282-122A-63343

Query Match 100.0%; Score 28; DB 12; Length 159;

Best Local Similarity 100.0%; Pred. No. 4e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6

DB 26 LKEKAK 31

RESULT 8

US-09-840-787-27

Sequence 27, Application US/09840787

Patent No. US20020058264A1

GENERAL INFORMATION:

APPLICANT: Lal, Preeti

Hillman, Jennifer L.

Bandman, Olga

Shah, Purvi

Au-Young, Janice

Yue, Henry

Guegler, Karl J.

Corley, Neil C.

TITLE OF INVENTION: HUMAN REGULATORY MOLECULES

NUMBER OF SEQUENCES: 98

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

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; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA: US/09/840,787
; FILING DATE: 23-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/518,865
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0356 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LNCNOT03
; CLONE: 1574624
; SEQUENCE DESCRIPTION: SEQ ID NO: 27 :
US-09-840-787-27
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Query Match 100.0%; Score 28; DB 9; Length 174;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 LKEKAK 6
   |||||
Db 28 LKEKAK 33
```

```
RESULT 9
US-09-883-152-17
; Sequence 17, Application US/09883152
; Publication No. US2003008284A1
; GENERAL INFORMATION:
; APPLICANT: Kennedy, Giulia
; APPLICANT: Kang, Sanmao
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne Bennett
; TITLE OF INVENTION: POLYNUCLEOTIDES RELATED TO COLON CANCER
; FILE REFERENCE: 2300-1663
; CURRENT APPLICATION NUMBER: US/09/883,152
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/211,835
; PRIOR FILING DATE: 2000-06-15
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 174
; TYPE: PRT
; ORGANISM: H. sapiens
US-09-883-152-17
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Query Match 100.0%; Score 28; DB 10; Length 174;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 LKEKAK 6
   |||||
Db 28 LKEKAK 33
```

```
RESULT 10
US-10-424-599-263529
; Sequence 263529, Application US/10424599
; Publication No. US20040031072A1
```

```
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yinua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 263529
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_79989C.1.pap
US-10-424-599-263529

Query Match 100.0%; Score 28; DB 12; Length 205;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
   |||||
Db 18 LKEKAK 23

RESULT 11
US-10-335-977-6032
; Sequence 6032, Application US/10335977
; Publication No. US20040052799A1
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; RELATING TO HELICOBACTER PYLORI FOR
; DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 10031
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Windows NT 4.0
; SOFTWARE: UNIX
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/335,977
; FILING DATE: 30-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/993,002
; FILING DATE: 17-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: GTN-018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 6032:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Helicobacter pylori
; FEATURE:
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; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...236
; SEQUENCE DESCRIPTION: SEQ ID NO: 6032:
US-10-335-977-6032
Query Match 100.0%; Score 28; DB 12; Length 236;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
   |||||
Db 202 LKEKAK 207

RESULT 12
US-10-335-977-6033
; Sequence 6033, Application US/10335977
; Publication No. US20040052799A1
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; RELATING TO HELICOBACTER PYLORI FOR
; DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 10031
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Windows NT 4.0
; SOFTWARE: UNIX
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/335,977
; FILING DATE: 30-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/993,002
; FILING DATE: 17-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: GTN-018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 6033:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 237 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Helicobacter pylori
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...237
; SEQUENCE DESCRIPTION: SEQ ID NO: 6033:
US-10-335-977-6033
Query Match 100.0%; Score 28; DB 12; Length 237;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
   |||||
Db 203 LKEKAK 208

RESULT 13
US-10-032-585-7107
; Sequence 7107, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jiang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bussey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
; FILE REFERENCE: 10182-005-999
; CURRENT APPLICATION NUMBER: US/10/032,585
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 7107
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Candida albicans
; US-10-032-585-7107
Query Match 100.0%; Score 28; DB 14; Length 247;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
   |||||
Db 51 LKEKAK 56

RESULT 14
US-10-335-977-6834
; Sequence 6834, Application US/10335977
; Publication No. US20040052799A1
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; RELATING TO HELICOBACTER PYLORI FOR
; DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 10031
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Windows NT 4.0
; SOFTWARE: UNIX
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/335,977
; FILING DATE: 30-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/993,002
; FILING DATE: 17-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: GTN-018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 6834:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 290 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
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; ORGANISM: Helicobacter pylori
;
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...290
; SEQUENCE DESCRIPTION: SEQ ID NO: 6834:
US-10-335-977-6834
Query Match 100.0%; Score 28; DB 12; Length 290;
Best Local Similarity 100.0%; Pred. No. 7.1e+02; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

QY 1 LKEKAK 6
Db 73 LKEKAK 78

RESULT 15
US-10-276-774-2219
; Sequence 2219, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NO. US20040053245A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 2219
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(297)
; OTHER INFORMATION: Xaa = any amino acid or nothing
US-10-276-774-2219
Query Match 100.0%; Score 28; DB 12; Length 297;
Best Local Similarity 100.0%; Pred. No. 7.3e+02; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

QY 1 LKEKAK 6
Db 228 LKEKAK 233

RESULT 16
US-10-335-977-6835
; Sequence 6835, Application US/10335977
; Publication No. US20040052799A1
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 10031
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Windows NT 4.0

; ORGANISM: Helicobacter pylori
;
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...308
; SEQUENCE DESCRIPTION: SEQ ID NO: 6835:
US-10-335-977-6835
Query Match 100.0%; Score 28; DB 12; Length 308;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
Db 91 LKEKAK 96

RESULT 17
US-09-838-561-11
; Sequence 11, Application US/09838561
; Patent No. US20020042371A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel
; APPLICANT: Cook, William James
; APPLICANT: Williamson, Mark
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Gimeno, Ruth
; TITLE OF INVENTION: 32142, 21481, 25964, 21686, NOVEL DEHYDROGENASE
; TITLE OF INVENTION: MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-134CP2
; CURRENT APPLICATION NUMBER: US/09/838,561
; CURRENT FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 09/816,760
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 09/634,955
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/192,002
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-838-561-11
Query Match 100.0%; Score 28; DB 9; Length 322;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
Db 11 LKEKAK 11
```

Db 316 LKEKAK 321

RESULT 18

US-09-816-760-11  
; Sequence 11, Application US/09816760  
; Patent No. US20020052032A1  
; GENERAL INFORMATION:  
; APPLICANT: Meyers, Rachel  
; APPLICANT: Cook, William James  
; APPLICANT: Williams, Mark  
; APPLICANT: Rudolph-Owen, Laura A.  
; TITLE OF INVENTION: 32142, 21481, 25964, 21686, NOVEL HUMAN DEHYDROGENASE  
; TITLE OF INVENTION: MOLECULES AND USES THEREFOR  
; FILE REFERENCE: MNI-134CP  
; CURRENT APPLICATION NUMBER: US/09/816,760  
; CURRENT FILING DATE: 2001-03-23  
; PRIOR APPLICATION NUMBER: 09/634,955  
; PRIOR FILING DATE: 2000-08-08  
; PRIOR APPLICATION NUMBER: 60/192,002  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 322  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-816-760-11

Query Match 100.0%; Score 28; DB 9; Length 322;

Best Local Similarity 100.0%; Pred. No. 7.9e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6

Db 316 LKEKAK 321

RESULT 19

US-10-172-585-11  
; Sequence 11, Application US/10172585  
; Publication No. US20030166200A1  
; GENERAL INFORMATION:  
; APPLICANT: Meyers, Rachel  
; APPLICANT: Cook, William James  
; TITLE OF INVENTION: 32142, 21481, 25964, 21686, NOVEL HUMAN DEHYDROGENASE  
; TITLE OF INVENTION: MOLECULES AND USES THEREFOR  
; FILE REFERENCE: MNI-134  
; CURRENT APPLICATION NUMBER: US/10/172,585  
; CURRENT FILING DATE: 2002-06-14  
; PRIOR APPLICATION NUMBER: US/09/634,955  
; PRIOR FILING DATE: 2000-08-08  
; PRIOR APPLICATION NUMBER: 60/192,002  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: FastSeq for Windows Version 4.  
; SEQ ID NO 11  
; LENGTH: 322  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-172-585-11

Query Match 100.0%; Score 28; DB 14; Length 322;

Best Local Similarity 100.0%; Pred. No. 7.9e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6

Db 316 LKEKAK 321

RESULT 20

US-10-108-915-46

; Sequence 46, Application US/10108915  
; Publication No. US20020177204A1  
; GENERAL INFORMATION:  
; APPLICANT: Cahoon, Rebecca E.  
; APPLICANT: Shen, Jennie  
; APPLICANT: Williams, Mark  
; TITLE OF INVENTION: Geranylgeranyl Pyrophosphate Synthases  
; FILE REFERENCE: BB1286 US NA  
; CURRENT APPLICATION NUMBER: US/10/108,915  
; CURRENT FILING DATE: 2002-03-28  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/452,238  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-01  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/110,592  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-December-02  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 46  
; LENGTH: 326  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-10-108-915-46

Query Match 100.0%; Score 28; DB 13; Length 326;

Best Local Similarity 100.0%; Pred. No. 8e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6

Db 286 LKEKAK 291

RESULT 21

US-09-815-242-13332  
; Sequence 13332, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13332  
; LENGTH: 374  
; TYPE: PRT  
; ORGANISM: Streptococcus pneumoniae  
US-09-815-242-13332

Query Match

Best Local Similarity 100.0%; Score 28; DB 9; Length 374;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6

Db 341 LKEKAK 346

RESULT 22

US-10-146-473-70  
; Sequence 70, Application US/10146473  
; Publication No. US20030108888A1  
; GENERAL INFORMATION:  
; APPLICANT: Scanlan, Matthew  
; APPLICANT: Gout, Ivan  
; APPLICANT: Stockert, Elisabeth  
; APPLICANT: Gure, Ali  
; APPLICANT: Chen, Yao-Tsang  
; APPLICANT: Old, Lloyd  
; TITLE OF INVENTION: Breast Cancer Antigens  
; FILE REFERENCE: L00461/70130(JRV)  
; CURRENT APPLICATION NUMBER: US/10/146,473  
; CURRENT FILING DATE: 2002-05-15  
; PRIOR APPLICATION NUMBER: US 60/291,150  
; PRIOR FILING DATE: 2001-05-15  
; NUMBER OF SEQ ID NOS: 82  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 70  
; LENGTH: 386  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-146-473-70

Query Match 100.0%; Score 28; DB 14; Length 386;

Best Local Similarity 100.0%; Pred. No. 9.4e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6

Db 146 LKEKAK 151

RESULT 23

US-10-156-761-9922  
; Sequence 9922, Application US/10156761  
; Publication No. US20030119018A1  
; GENERAL INFORMATION:  
; APPLICANT: OMURA, SATOSHI  
; APPLICANT: IKEDA, HARUO  
; APPLICANT: ISHIKAWA, JUN  
; APPLICANT: HORIKAWA, HIROSHI  
; APPLICANT: SHIBA, TADAYOSHI  
; APPLICANT: SAKAKI, YOSHIYUKI  
; APPLICANT: HATTORI, MASAHIRA  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-262  
; CURRENT APPLICATION NUMBER: US/10/156,761  
; CURRENT FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: JP 2001-204089  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: JP 2001-272697  
; PRIOR FILING DATE: 2001-08-02  
; NUMBER OF SEQ ID NOS: 15109  
; SEQ ID NO 9922  
; LENGTH: 386  
; TYPE: PRT  
; ORGANISM: Streptomyces avermitilis  
US-10-156-761-9922

Query Match 100.0%; Score 28; DB 14; Length 386;

Best Local Similarity 100.0%; Pred. No. 9.4e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6

Db 181 LKEKAK 186

RESULT 24

US-10-023-634-40  
; Sequence 40, Application US/10023634  
; Publication No. US20030236389A1  
; GENERAL INFORMATION:  
; APPLICANT: Shinkets, Richard A  
; APPLICANT: Colman, Steven D  
; APPLICANT: Spytek, Kimberly A  
; APPLICANT: Ballinger, Robert A  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Tchernev, Velizar T  
; APPLICANT: Shenoy, Suresh G  
; APPLICANT: Li, Li  
; APPLICANT: Ellerman, Karen  
; APPLICANT: Zerhusen, Bryan D  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Casman, Stacie J  
; APPLICANT: Boldog, Ferenc  
; APPLICANT: Gusev, Vladimir Y  
; APPLICANT: Burgess, Catherine E  
; APPLICANT: Edinger, Shlomit R  
; APPLICANT: Gangolli, Esha A  
; APPLICANT: Malyankar, Uriel M  
; APPLICANT: Gunther, Erik  
; APPLICANT: Smithson, Glennda  
; APPLICANT: Millet, Isabelle  
; APPLICANT: Gerlach, Valerie  
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of  
; TITLE OF INVENTION: Using the Same  
; FILE REFERENCE: 21402-221  
; CURRENT APPLICATION NUMBER: US/10/023,634  
; CURRENT FILING DATE: 2002-06-28  
; PRIOR APPLICATION NUMBER: 60/256,025  
; PRIOR FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: 60/265,163  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: 60/272,929  
; PRIOR FILING DATE: 2001-03-02  
; PRIOR APPLICATION NUMBER: 60/274,864  
; PRIOR FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/276,688  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,880  
; PRIOR FILING DATE: 2001-03-22  
; PRIOR APPLICATION NUMBER: 60/286,409  
; PRIOR FILING DATE: 2001-04-25  
; PRIOR APPLICATION NUMBER: 60/309,246  
; PRIOR FILING DATE: 2001-07-31  
; PRIOR APPLICATION NUMBER: 60/315,600  
; PRIOR FILING DATE: 2001-08-29  
; NUMBER OF SEQ ID NOS: 132  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 40  
; LENGTH: 404  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-023-634-40

Query Match 100.0%; Score 28; DB 15; Length 404;

Best Local Similarity 100.0%; Pred. No. 9.8e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6

Db 97 LKEKAK 102

RESULT 25

US-09-925-301-1320



; Sequence 1320, Application US/09925301  
; Patent No. US20020052308A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA106  
; CURRENT APPLICATION NUMBER: US/09/925,301  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05882  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 1694  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1320  
; LENGTH: 406  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-925-301-1320

Query Match 100.0%; Score 28; DB 9; Length 406;  
Best Local Similarity 100.0%; Pred. No. 9.8e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LKEKAK 6  
DB 169 LKEKAK 174

RESULT 26  
US-10-106-698-4620  
; Sequence 4620, Application US/10106698  
; Publication No. US20030109690A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide  
; FILE REFERENCE: PA005P1  
; CURRENT APPLICATION NUMBER: US/10/106,698  
; CURRENT FILING DATE: 2002-03-27  
; PRIOR APPLICATION NUMBER: PCT/US00/26524  
; PRIOR FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: US 60/157,137  
; PRIOR FILING DATE: 1999-09-29  
; PRIOR APPLICATION NUMBER: US 60/163,280  
; PRIOR FILING DATE: 1999-11-03  
; NUMBER OF SEQ ID NOS: 8564  
; SOFTWARE: PatentIn Ver. 3.0  
; SEQ ID NO 4620  
; LENGTH: 406  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-106-698-4620

Query Match 100.0%; Score 28; DB 14; Length 406;  
Best Local Similarity 100.0%; Pred. No. 9.8e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LKEKAK 6  
DB 169 LKEKAK 174

RESULT 27  
US-10-425-114-53665  
; Sequence 53665, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E.  
; APPLICANT: Tabaska, Jack E.  
; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 53665  
; LENGTH: 432  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: UC-ZMFLB73088F05\_FLI.pgp  
US-10-425-114-53665

Query Match 100.0%; Score 28; DB 12; Length 432;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LKEKAK 6  
DB 265 LKEKAK 270

RESULT 28  
US-10-282-122A-76831  
; Sequence 76831, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.  
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
; FILE REFERENCE: ELITRA.034A  
; CURRENT APPLICATION NUMBER: US/10/282,122A  
; CURRENT FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/230,335  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR APPLICATION NUMBER: 60/230,347  
; PRIOR FILING DATE: 2000-09-09  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/267,636  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 78614  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 76831  
; LENGTH: 442  
; TYPE: PRT  
; ORGANISM: Ureaplasma urealyticum  
US-10-282-122A-76831

Query Match 100.0%; Score 28; DB 12; Length 442;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
|||||  
DB 105 LKEKAK 110

## RESULT 29

US-10-023-634-36

; Sequence 36, Application US/10023634

; Publication No. US20030236389A1

; GENERAL INFORMATION:

; APPLICANT: Shimkets, Richard A

; APPLICANT: Colman, Steven D

; APPLICANT: Spytek, Kimberly A

; APPLICANT: Ballinger, Robert A

; APPLICANT: Guo, Xiaojia

; APPLICANT: Tchernev, Velizar T

; APPLICANT: Shenoy, Suresh G

; APPLICANT: Li, Li

; APPLICANT: Ellerman, Karen

; APPLICANT: Zerhusen, Bryan D

; APPLICANT: Patturajan, Meera

; APPLICANT: Casman, Stacie J

; APPLICANT: Boldog, Ferenc

; APPLICANT: Gusev, Vladimir Y

; APPLICANT: Burgess, Catherine E

; APPLICANT: Edinger, Shlomit R

; APPLICANT: Gangolli, Esha A

; APPLICANT: Malyankar, Uriel M

; APPLICANT: Gunther, Erik

; APPLICANT: Smithson, Glenda

; APPLICANT: Millet, Isabelle

; APPLICANT: Gerlach, Valerie

; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of

; FILE REFERENCE: 21402-221

; CURRENT APPLICATION NUMBER: US/10/023,634

; CURRENT FILING DATE: 2002-06-28

; PRIOR APPLICATION NUMBER: 60/256,025

; PRIOR FILING DATE: 2000-12-15

; PRIOR APPLICATION NUMBER: 60/265,163

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: 60/272,929

; PRIOR FILING DATE: 2001-03-02

; PRIOR APPLICATION NUMBER: 60/274,864

; PRIOR FILING DATE: 2001-03-09

; PRIOR APPLICATION NUMBER: 60/276,688

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/277,880

; PRIOR FILING DATE: 2001-03-22

; PRIOR APPLICATION NUMBER: 60/286,409

; PRIOR FILING DATE: 2001-04-25

; PRIOR APPLICATION NUMBER: 60/309,246

; PRIOR FILING DATE: 2001-07-31

; PRIOR APPLICATION NUMBER: 60/315,600

; PRIOR FILING DATE: 2001-08-29

; NUMBER OF SEQ ID NOS: 132

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 36

; LENGTH: 452

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-023-634-36

Query Match 100.0%; Score 28; DB 15; Length 452;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
|||||

DB 97 LKEKAK 102

## RESULT 30

US-10-023-634-38

; Sequence 38, Application US/10023634

; Publication No. US20030236389A1

; GENERAL INFORMATION:

; APPLICANT: Shimkets, Richard A

; APPLICANT: Colman, Steven D

; APPLICANT: Spytek, Kimberly A

; APPLICANT: Ballinger, Robert A

; APPLICANT: Guo, Xiaojia

; APPLICANT: Tchernev, Velizar T

; APPLICANT: Shenoy, Suresh G

; APPLICANT: Li, Li

; APPLICANT: Ellerman, Karen

; APPLICANT: Zerhusen, Bryan D

; APPLICANT: Patturajan, Meera

; APPLICANT: Casman, Stacie J

; APPLICANT: Boldog, Ferenc

; APPLICANT: Gusev, Vladimir Y

; APPLICANT: Burgess, Catherine E

; APPLICANT: Edinger, Shlomit R

; APPLICANT: Gangolli, Esha A

; APPLICANT: Malyankar, Uriel M

; APPLICANT: Gunther, Erik

; APPLICANT: Smithson, Glenda

; APPLICANT: Millet, Isabelle

; APPLICANT: Gerlach, Valerie

; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of

; FILE REFERENCE: 21402-221

; CURRENT APPLICATION NUMBER: US/10/023,634

; CURRENT FILING DATE: 2002-06-28

; PRIOR APPLICATION NUMBER: 60/256,025

; PRIOR FILING DATE: 2000-12-15

; PRIOR APPLICATION NUMBER: 60/265,163

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: 60/272,929

; PRIOR FILING DATE: 2001-03-02

; PRIOR APPLICATION NUMBER: 60/274,864

; PRIOR FILING DATE: 2001-03-09

; PRIOR APPLICATION NUMBER: 60/276,688

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/277,880

; PRIOR FILING DATE: 2001-03-22

; PRIOR APPLICATION NUMBER: 60/286,409

; PRIOR FILING DATE: 2001-04-25

; PRIOR APPLICATION NUMBER: 60/309,246

; PRIOR FILING DATE: 2001-07-31

; PRIOR APPLICATION NUMBER: 60/315,600

; PRIOR FILING DATE: 2001-08-29

; NUMBER OF SEQ ID NOS: 132

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 38

; LENGTH: 452

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-023-634-38

Query Match 100.0%; Score 28; DB 15; Length 452;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6

|||||

DB 97 LKEKAK 102

## RESULT 31

US-10-023-634-97

; Sequence 97, Application US/10023634

Publication No. US20030236389A1  
GENERAL INFORMATION:  
APPLICANT: Shimkets, Richard A  
APPLICANT: Colman, Steven D  
APPLICANT: Spytek, Kimberly A  
APPLICANT: Ballinger, Robert A  
APPLICANT: Guo, Xiaojia  
APPLICANT: Tchernev, Velizar T  
APPLICANT: Shenoy, Suresh G  
APPLICANT: Li, Li  
APPLICANT: Ellerman, Karen  
APPLICANT: Zerhusen, Bryan D  
APPLICANT: Patturajan, Meera  
APPLICANT: Casman, Stacie J  
APPLICANT: Boldog, Ferenc  
APPLICANT: Gusev, Vladimir Y  
APPLICANT: Burgess, Catherine E  
APPLICANT: Edinger, Shlomit R  
APPLICANT: Gangolli, Esha A  
APPLICANT: Malyankar, Uriel M  
APPLICANT: Gunther, Erik  
APPLICANT: Smithson, Glennda  
APPLICANT: Millet, Isabelle  
APPLICANT: Gerlach, Valerie  
TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of  
FILE REFERENCE: 21402-221  
CURRENT APPLICATION NUMBER: US/10/023,634  
PRIOR FILING DATE: 2002-06-28  
PRIOR APPLICATION NUMBER: 60/256,025  
PRIOR FILING DATE: 2000-12-15  
PRIOR APPLICATION NUMBER: 60/265,163  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: 60/272,929  
PRIOR FILING DATE: 2001-03-02  
PRIOR APPLICATION NUMBER: 60/274,864  
PRIOR FILING DATE: 2001-03-09  
PRIOR APPLICATION NUMBER: 60/276,688  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/277,880  
PRIOR FILING DATE: 2001-03-22  
PRIOR APPLICATION NUMBER: 60/286,409  
PRIOR FILING DATE: 2001-04-25  
PRIOR APPLICATION NUMBER: 60/309,246  
PRIOR FILING DATE: 2001-07-31  
PRIOR APPLICATION NUMBER: 60/315,600  
PRIOR FILING DATE: 2001-08-29  
NUMBER OF SEQ ID NOS: 132  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 97  
LENGTH: 455  
TYPE: PRT  
ORGANISM: Mus musculus  
US-10-023-634-97

Query Match 100.0%; Score 28; DB 15; Length 455;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
DB 31 LKEKAK 36

RESULT 32  
US-10-108-260A-4337  
Sequence 4337, Application US/10108260A  
Publication No. US20040005560A1  
GENERAL INFORMATION:  
APPLICANT: HELIX RESEARCH INSTITUTE  
TITLE OF INVENTION: NO. US20040005560A1e1 full length cDNA  
FILE REFERENCE: H1-A0106  
CURRENT APPLICATION NUMBER: US/10/108,260A

CURRENT FILING DATE: 2002-03-27  
NUMBER OF SEQ ID NOS: 5458  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4337  
LENGTH: 492  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-108-260A-4337

Query Match 100.0%; Score 28; DB 15; Length 492;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
DB 306 LKEKAK 311

RESULT 33  
US-09-864-761-37938  
Sequence 37938, Application US/09864761  
Patent No. US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wensheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
FILE REFERENCE: Aecmics-X-1  
CURRENT APPLICATION NUMBER: US/09/864,761  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263.6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

SEQ ID NO 37938  
LENGTH: 560  
TYPE: PRT

; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AC005074.1  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.5  
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.8  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.9  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.93  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.99  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3  
; OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 1.8  
; OTHER INFORMATION: EST HUMAN HIT: AW976211.1, EVALUE 2.00e-91  
; OTHER INFORMATION: SWISSPROT HIT: P53935, EVALUE 2.00e-03  
US-09-864-761-37938

Query Match 100.0%; Score 28; DB 9; Length 560;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
|||  
Db 254 LKEKAK 259

RESULT 34  
US-09-864-761-34546  
; Sequence 34546, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
; FILE REFERENCE: Aeonica-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30

; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 34546  
; LENGTH: 572  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AC005089.2  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3  
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 5.4  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4  
; OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 5.6  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.3  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.1  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.7  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.1  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.7  
; OTHER INFORMATION: SWISSPROT HIT: P53935, EVALUE 2.00e-03  
; OTHER INFORMATION: EST\_HUMAN HIT: AW976211.1, EVALUE 2.00e-91  
US-09-864-761-34546

Query Match 100.0%; Score 28; DB 9; Length 572;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
|||  
Db 261 LKEKAK 266

RESULT 35  
US-10-023-634-96  
; Sequence 96, Application US/10023634  
; Publication No. US20030236389A1  
; GENERAL INFORMATION:  
; APPLICANT: Shinketsu, Richard A  
; APPLICANT: Colman, Steven D  
; APPLICANT: Spytek, Kimberly A  
; APPLICANT: Ballinger, Robert A  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Tchernev, Velizar T  
; APPLICANT: Shenoy, Suresh G  
; APPLICANT: Li, Li  
; APPLICANT: Ellerman, Karen  
; APPLICANT: Zerhusen, Bryan D  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Casman, Stacie J  
; APPLICANT: Boldog, Ferenc  
; APPLICANT: Gusev, Vladimir Y  
; APPLICANT: Burgess, Catherine E  
; APPLICANT: Edinger, Shlomit R  
; APPLICANT: Gangolli, Esha A  
; APPLICANT: Malyankar, Uriel M  
; APPLICANT: Gunther, Erik  
; APPLICANT: Smithson, Glennnda  
; APPLICANT: Millet, Isabelle  
; APPLICANT: Gerlach, Valerie  
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of  
; TITLE OF INVENTION: Using the Same  
; FILE REFERENCE: 21402-221  
; CURRENT APPLICATION NUMBER: US/10/023,634  
; CURRENT FILING DATE: 2002-06-28  
; PRIOR APPLICATION NUMBER: 60/256,025  
; PRIOR FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: 60/265,163  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: 60/272,929  
; PRIOR FILING DATE: 2001-03-02  
; PRIOR APPLICATION NUMBER: 60/274,864  
; PRIOR FILING DATE: 2001-03-09

;; PRIOR APPLICATION NUMBER: 60/276,688  
;; PRIOR FILING DATE: 2001-03-16  
;; PRIOR APPLICATION NUMBER: 60/277,880  
;; PRIOR FILING DATE: 2001-03-22  
;; PRIOR APPLICATION NUMBER: 60/286,409  
;; PRIOR FILING DATE: 2001-04-25  
;; PRIOR APPLICATION NUMBER: 60/309,246  
;; PRIOR FILING DATE: 2001-07-31  
;; PRIOR APPLICATION NUMBER: 60/315,600  
;; PRIOR FILING DATE: 2001-08-29  
;; NUMBER OF SEQ ID NOS: 132  
;; SOFTWARE: Patent In Ver. 2.1  
;; SEQ ID NO 96  
;; LENGTH: 629  
;; TYPE: PRT  
;; ORGANISM: Mus musculus  
US-10-023-634-96

Query Match 100.0%; Score 28; DB 15; Length 629;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
DB 264 LKEKAK 269

RESULT 36  
US-09-999-314A-2  
;; Sequence 2, Application US/09999314A  
;; Publication No. US20030040474A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Kapeller-Libermann, Rosana  
;; APPLICANT: Hunter, John J.  
;; APPLICANT: Rudolph-Owen, Laura A.  
;; TITLE OF INVENTION: 32229, A NOVEL HUMAN ACYL-CoA  
;; FILE REFERENCE: 10448-103001  
;; CURRENT APPLICATION NUMBER: US/09/999,314A  
;; CURRENT FILING DATE: 2001-10-22  
;; PRIOR APPLICATION NUMBER: 60/242,211  
;; PRIOR FILING DATE: 2000-10-20  
;; NUMBER OF SEQ ID NOS: 7  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 2  
;; LENGTH: 797  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-999-314A-2

Query Match 100.0%; Score 28; DB 10; Length 797;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
DB 442 LKEKAK 447

RESULT 37  
US-10-377-097-121  
;; Sequence 121, Application US/10377097  
;; Publication No. US20040033509A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Millennium Pharmaceuticals, Inc  
;; APPLICANT: Meyers, Rachel E.  
;; APPLICANT: Williamson, Mark W.  
;; APPLICANT: Kapeller-Libermann, Rosana  
;; APPLICANT: MacBeth, Kyle J.  
;; APPLICANT: Hunter, John J.  
;; APPLICANT: Rudolph-Owen, Laura A.  
;; APPLICANT: Bandaru, Rajasekhar  
;; APPLICANT: Tsai, Fong-Ying

;; TITLE OF INVENTION: NOVEL 13237, 18480, 2245, 16228, 7677,  
;; TITLE OF INVENTION: 26320, 46619, 33166, 16836, 46867, 21617, 55562, 39228,  
;; TITLE OF INVENTION: 62088, 46745, 23155, 21657, 42755, 32229, 22325, 46863 AND  
;; FILE REFERENCE: MPI03-0350WNIM  
;; CURRENT APPLICATION NUMBER: US/10/377,097  
;; CURRENT FILING DATE: 2003-02-28  
;; PRIOR APPLICATION NUMBER: US 09/910,150  
;; PRIOR FILING DATE: 2001-07-18  
;; PRIOR APPLICATION NUMBER: US 60/219,028  
;; PRIOR FILING DATE: 2000-07-18  
;; PRIOR APPLICATION NUMBER: US 10/251,507  
;; PRIOR FILING DATE: 2002-09-20  
;; PRIOR APPLICATION NUMBER: US 09/715,479  
;; PRIOR FILING DATE: 2000-11-17  
;; PRIOR APPLICATION NUMBER: US 60/218,053  
;; PRIOR FILING DATE: 2000-07-13  
;; PRIOR APPLICATION NUMBER: US 09/644,929  
;; PRIOR FILING DATE: 2000-08-23  
;; PRIOR APPLICATION NUMBER: US 60/212,439  
;; PRIOR FILING DATE: 2000-06-16  
;; PRIOR APPLICATION NUMBER: US 09/892,870  
;; PRIOR FILING DATE: 2001-06-26  
;; PRIOR APPLICATION NUMBER: US 60/214,174  
;; PRIOR FILING DATE: 2000-06-26  
;; PRIOR APPLICATION NUMBER: US 09/775,117  
;; PRIOR FILING DATE: 2001-02-01  
;; Remaining Prior Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 156  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 121  
;; LENGTH: 797  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-377-097-121

Query Match 100.0%; Score 28; DB 12; Length 797;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
DB 442 LKEKAK 447

RESULT 38  
US-10-104-047-2992  
;; Sequence 2992, Application US/10104047  
;; Publication No. US20030236392A1  
;; GENERAL INFORMATION:  
;; APPLICANT: HELIX RESEARCH INSTITUTE  
;; TITLE OF INVENTION: No. US20030236392A1el full length cDNA  
;; FILE REFERENCE: HL-A0105  
;; CURRENT APPLICATION NUMBER: US/10/104,047  
;; CURRENT FILING DATE: 2002-03-25  
;; PRIOR APPLICATION NUMBER:  
;; PRIOR FILING DATE:  
;; NUMBER OF SEQ ID NOS: 4096  
;; SOFTWARE: Patent In Ver. 2.1  
;; SEQ ID NO 2992  
;; LENGTH: 890  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-104-047-2992

Query Match 100.0%; Score 28; DB 15; Length 890;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
DB 704 LKEKAK 709

```
RESULT 39
US-10-334-143-40
; Sequence 40, Application US/10334143
; Publication No. US2004009549A1
; GENERAL INFORMATION:
; APPLICANT: GRIGORIEV, IGOR VYACHESLAVOVICH
; TITLE OF INVENTION: METHOD FOR DETECTING REMOTE HOMOLOGUES AND NOVEL
; TITLE OF INVENTION: KINASES IDENTIFIED WITH THE METHOD
; FILE REFERENCE: 038602/1543
; CURRENT APPLICATION NUMBER: US/10/334,143
; CURRENT FILING DATE: 2002-12-31
; PRIOR APPLICATION NUMBER: 60/343,169
; PRIOR FILING DATE: 2001-12-31
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 913
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-334-143-40

Query Match      100.0%; Score 28; DB 15; Length 913;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LKEKAK 6
DB      489 LKEKAK 494

RESULT 40
US-10-282-122A-58014
; Sequence 58014, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16

; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58014
; LENGTH: 1042
; TYPE: PRT
; ORGANISM: Enterococcus faecium
US-10-282-122A-58014

Query Match      100.0%; Score 28; DB 12; Length 1042;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LKEKAK 6
DB      192 LKEKAK 197

RESULT 41
US-10-023-634-42
; Sequence 42, Application US/10023634
; Publication No. US20030236389A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A
; APPLICANT: Colman, Steven D
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Ballinger, Robert A
; APPLICANT: Guo, Xiaojia
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Li, Li
; APPLICANT: Ellerman, Karen
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Patturajan, Meera
; APPLICANT: Casman, Stacie J
; APPLICANT: Boldog, Ferenc
; APPLICANT: Gusev, Vladimir Y
; APPLICANT: Burgess, Catherine E
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Gangolli, Esha A
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Gunther, Erik
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: Gerlach, Valerie
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE REFERENCE: 21402-221
; CURRENT APPLICATION NUMBER: US/10/023,634
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/256,025
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/265,163
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,929
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/274,864
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/276,688
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,880
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/286,409
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 60/309,246
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/315,600
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 1080
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-10-023-634-42

Query Match      100.0%; Score 28; DB 15; Length 1080;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LKEKAK 6
DB      656 LKEKAK 661

RESULT 42
US-09-839-479-68
; Sequence 68, Application US/09839479
; Publication No. US20020039779A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-042002
; CURRENT APPLICATION NUMBER: US/09/839,479
; CURRENT FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: US 09/418,710
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01783
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JP 9/310027
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: JP 9/116570
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 1525
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-839-479-68

Query Match      100.0%; Score 28; DB 12; Length 1525;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LKEKAK 6
DB      558 LKEKAK 563

RESULT 43
US-10-702-148-68
; Sequence 68, Application US/10702148
; Publication No. US20040063145A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-042002
; CURRENT APPLICATION NUMBER: US/10/702,148
; CURRENT FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: US/09/839,479
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: US 09/418,710
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01783
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JP 9/310027
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: JP 9/116570
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 1525
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-839-479-68

Query Match      100.0%; Score 28; DB 12; Length 1525;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LKEKAK 6
DB      558 LKEKAK 563

RESULT 44
US-10-376-537-69
; Sequence 69, Application US/10376537
; Publication No. US20030224405A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-042001
; CURRENT APPLICATION NUMBER: US/10/376,537
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US/09/418,710
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01783
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JP 9/310027
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: JP 9/116570
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69
; LENGTH: 1525
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-376-537-69

Query Match      100.0%; Score 28; DB 12; Length 1525;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LKEKAK 6
DB      558 LKEKAK 563

RESULT 45
US-09-839-479-27
; Sequence 27, Application US/09839479
; Publication No. US20020039779A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-042002
; CURRENT APPLICATION NUMBER: US/09/839,479
; CURRENT FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: US 09/418,710
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01783
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JP 9/310027
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: JP 9/116570
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 1527
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-839-479-27

Query Match      100.0%; Score 28; DB 12; Length 1527;
```

```
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
Db 558 LKEKAK 563

RESULT 46
US-10-702-148-27
; Sequence 27, Application US/10702148
; Publication No. US20040063145A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-042002
; CURRENT APPLICATION NUMBER: US/10/702,148
; CURRENT FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: US/09/839,479
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: US 09/418,710
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01783
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JP 9/310027
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: JP 9/116570
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 1527
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-702-148-27

Query Match 100.0%; Score 28; DB 12; Length 1527;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
Db 558 LKEKAK 563

RESULT 47
US-10-376-537-27
; Sequence 27, Application US/10376537
; Publication No. US20030224405A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-042001
; CURRENT APPLICATION NUMBER: US/10/376,537
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US/09/418,710
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01783
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JP 9/310027
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: JP 9/116570
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 1527
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-376-537-27

Query Match 100.0%; Score 28; DB 12; Length 1527;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
Db 558 LKEKAK 563

RESULT 48
US-09-839-479-29
; Sequence 29, Application US/09839479
; Publication No. US20020039779A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-042002
; CURRENT APPLICATION NUMBER: US/09/839,479
; CURRENT FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: US 09/418,710
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01783
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JP 9/310027
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: JP 9/116570
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 1531
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-839-479-29

Query Match 100.0%; Score 28; DB 12; Length 1531;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6
Db 558 LKEKAK 563

RESULT 49
US-10-702-148-29
; Sequence 29, Application US/10702148
; Publication No. US20040063145A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-042002
; CURRENT APPLICATION NUMBER: US/10/702,148
; CURRENT FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: US/09/839,479
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: US 09/418,710
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01783
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JP 9/310027
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: JP 9/116570
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 1531
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-702-148-29

Query Match 100.0%; Score 28; DB 12; Length 1531;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```



QY 1 LKEKAK 6  
| | | | |  
DB 558 LKEKAK 563

RESULT 50  
US-10-376-537-29  
; Sequence 29, Application US/10376537  
; Publication No. US20030224405A1  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Michael H.  
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR  
; FILE REFERENCE: 06501-042001  
; CURRENT APPLICATION NUMBER: US/10/376,537  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US/09/418,710  
; PRIOR FILING DATE: 1999-10-15  
; PRIOR APPLICATION NUMBER: PCT/JP98/01783  
; PRIOR FILING DATE: 1998-04-17  
; PRIOR APPLICATION NUMBER: JP 9/310027  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: JP 9/116570  
; PRIOR FILING DATE: 1997-04-18  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 29  
; LENGTH: 1531  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-376-537-29

Query Match 100.0%; Score 28; DB 12; Length 1531;  
Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
| | | | |  
DB 558 LKEKAK 563

Search completed: April 19, 2004, 17:46:48  
Job time : 21.0323 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 19, 2004, 17:12:35 ; Search time 6 Seconds  
(without alignments)  
96.192 Million cell updates/sec

Title: US-10-726-692-14

Perfect score: 28  
Sequence: 1 LKEKAK 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 50 summaries

Database : PIR 78.\*

1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	100.0	148	2 C83750	hypothetical prote
2	28	100.0	159	2 S49749	probable membrane
3	28	100.0	173	2 JC7836	RNA-binding motif
4	28	100.0	224	2 E64542	hypothetical prote
5	28	100.0	236	2 E71965	hypothetical prote
6	28	100.0	241	2 D71167	hypothetical prote
7	28	100.0	247	2 S59135	mast cell proteina
8	28	100.0	247	2 S23504	chymase (EC 3.4.21
9	28	100.0	247	2 S64708	chymase (EC 3.4.21
10	28	100.0	254	2 C81846	hypothetical prote
11	28	100.0	260	2 S26043	chymase (EC 3.4.21
12	28	100.0	326	2 T05674	farnesyltransferas
13	28	100.0	338	2 C95124	glycosyl transfera
14	28	100.0	344	2 S16863	gene DN38 protein
15	28	100.0	367	2 A75110	hypothetical prote
16	28	100.0	372	2 A82214	hypothetical prote
17	28	100.0	374	2 H81783	hypothetical prote
18	28	100.0	374	2 E97994	glycosyltransferas
19	28	100.0	374	2 F97866	hypothetical prote
20	28	100.0	377	2 D81206	hypothetical prote
21	28	100.0	391	2 S40510	nucleosome assembl
22	28	100.0	391	2 JS0707	nucleosome assembl
23	28	100.0	431	2 A97225	fKBP-type peptidyl
24	28	100.0	434	2 B72328	conserved hypothet
25	28	100.0	442	2 B82899	conserved hypothet
26	28	100.0	458	2 D70410	cytosolic axial fi
27	28	100.0	508	2 S26979	H+-transporting tw
28	28	100.0	517	2 F64560	CMP-N-acetylneuram
29	28	100.0	545	2 D69679	polyketide synthas

30	28	100.0	590	2 D69722	thiamin biosynthes
31	28	100.0	635	2 H69626	PTS fructose-speci
32	28	100.0	688	2 T27020	hypothetical prote
33	28	100.0	863	2 S06017	neuraxin - rat
34	28	100.0	1231	1 NBHUH	complement factor
35	28	100.0	1451	2 S42167	190K protein - hum
36	28	100.0	2364	2 A56577	microtubule-asoci
37	28	100.0	2829	2 A42771	reticulocyte-bind
38	26	92.9	109	2 A69448	hypothetical prote
39	26	92.9	185	2 D70437	ATP synthase FO su
40	26	92.9	219	2 JQ1796	B2R protein - vacc
41	26	92.9	219	2 A42526	B2R protein - vacc
42	26	92.9	236	2 A40143	placental lactogen
43	26	92.9	337	2 G71869	hypothetical prote
44	26	92.9	342	2 E71101	probable geranylge
45	26	92.9	366	2 A45402	transforming growt
46	26	92.9	366	2 A46607	growth/differentia
47	26	92.9	366	2 T52612	SRP receptor homol
48	26	92.9	373	2 T02470	hypothetical prote
49	26	92.9	431	1 WZBSDS	adenylosuccinate l
50	26	92.9	555	2 D90369	NADH oxidase SSO20

ALIGNMENTS

RESULT 1

C83750  
hypothetical protein BH0803 [imported] - Bacillus halodurans (strain C-125)  
C:Species: Bacillus halodurans  
C:Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 15-Jun-2001  
C:Accession: C83750  
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hir  
Nucleic Acids Res. 28, 4317-4331, 2000  
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and  
A:Reference number: A83650; MUID:20512582; PMID:11058132  
A:Accession: C83750  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-148 <STO>  
A:Cross-references: GB:AP001509; GB:BA000004; NID:g10173176; PIDN:BA04522.1; GSPDB:GNO  
A:Experimental source: strain C-125  
C:Genetics:  
A:Gene: BH0803

Query Match 100.0%; Score 28; DB 2; Length 148;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
|||  
DB 32 LKEKAK 37

RESULT 2

S49749  
probable membrane protein YML030w - Yeast (Saccharomyces cerevisiae)  
C:Species: Saccharomyces cerevisiae  
C:Date: 13-Jan-1995 #sequence\_revision 10-Feb-1995 #text\_change 19-Apr-2002  
C:Accession: S49749  
R:Badcock, K.; Churcher, C.  
Submitted to the EMBL Data Library, November 1994  
A:Reference number: S49741  
A:Accession: S49749  
A:Molecule type: DNA  
A:Residues: 1-159 <BAD>  
A:Cross-references: EMBL:Z46659; NID:g575680; PID:g575689; GSPDB:GN00013; MIPS:YML030w  
C:Genetics:  
A:Gene: MIPS:YML030w  
A:Cross-references: SGD:S0004492  
A:Map position: 13L  
C:Superfamily: Saccharomyces cerevisiae probable membrane protein YML030w  
C:Keywords: transmembrane protein

F:33-49/Domain: transmembrane #status predicted <TM1>  
F:68-94/Domain: transmembrane #status predicted <TM2>

Query Match 100.0%; Score 28; DB 2; Length 159;  
Best Local Similarity 100.0%; Pred. No. 68;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
|||||

Db 99 LKEKAK 104

#### RESULT 3

JC7836

C:Species: RNA-binding motif protein 8, RBM8 - Japanese medaka

C:Date: 09-Dec-2002 #sequence\_revision 09-Dec-2002 #text\_change 31-Mar-2003

C:Accession: JC7836

R:Okubo, K.; Mitani, H.; Naruse, K.; Kondo, M.; Shima, A.; Tanaka, M.; Aida, K.

A:Title: Conserved physical linkage of GnRH-R and RBM8 in the medaka and human genomes.

A:Reference number: JC7836; MUID:22050021; PMID:12054603

A:Accession: JC7836

A:Molecule type: mRNA

A:Residues: 1-173 <OKU>

A:Cross-references: DDBJ:AB069905

C:Comment: This protein, a member of a highly conserved RNA binding motif(RBM) protein family, is expressed in embryonic, breast, and ovarian tumor suppression.

C:Genetics:

A:Gene: rbm8

A:Map position: LG16

A:Introns: 21/1; 41/1; 67/1; 112/3; 158/2

Query Match 100.0%; Score 28; DB 2; Length 173;

Best Local Similarity 100.0%; Pred. No. 74;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6

|||||

Db 26 LKEKAK 31

#### RESULT 4

E64542

hypothetical protein HP0181 - Helicobacter pylori (strain 26695)

C:Species: Helicobacter pylori

C:Date: 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 08-Oct-1999

C:Accession: E64542

R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.

Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.

Nature 388, 539-547, 1997

A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.

A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A:Reference number: A64520; MUID:97394467; PMID:9252185

A:Accession: E64542

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-224 <TOM>

A:Cross-references: GB:AE000538; GB:AE000511; NID:g2313263; PIDN:AAD07253.1; PID:g231327

C:Genetics:

A:Start codon: GTG

Query Match 100.0%; Score 28; DB 2; Length 224;

Best Local Similarity 100.0%; Pred. No. 94;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6

|||||

Db 193 LKEKAK 198

#### RESULT 5

E71965

hypothetical protein jhp0169 - Helicobacter pylori (strain J99)

C:Species: Helicobacter pylori

A:Variety: strain J99

C:Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 08-Oct-1999

C:Accession: E71965

R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;

Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;

Nature 397, 176-180, 1999

A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori

A:Reference number: A71800; MUID:99120557; PMID:9923682

A:Accession: E71965

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-236 <ARN>

A:Cross-references: GB:AE001455; GB:AE001439; NID:g4154678; PIDN:AAD05750.1; PID:g415468

A:Experimental source: strain J99

C:Genetics:

A:Gene: jhp0169

Query Match 100.0%; Score 28; DB 2; Length 236;

Best Local Similarity 100.0%; Pred. No. 99;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6

|||||

Db 202 LKEKAK 207

#### RESULT 6

D71167

hypothetical protein PH0536 - Pyrococcus horikoshii

C:Species: Pyrococcus horikoshii

C:Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 20-Jun-2000

C:Accession: D71167

R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki,

M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi,

DNA Res. 5, 55-76, 1998

A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic bacterium, Pyrococcus horikoshii

A:Reference number: A71000; MUID:98344137; PMID:9679194

A:Accession: D71167

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-241 <KAW>

A:Cross-references: GB:AP000002; NID:g3236129; PIDN:BAA29625.1; PID:g3256942

A:Experimental source: strain OT3

A:Note: this accession replaces an interim accession for a sequence replaced by GenBank

C:Genetics:

A:Gene: PH0536

Query Match 100.0%; Score 28; DB 2; Length 241;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6

|||||

Db 71 LKEKAK 76

#### RESULT 7

S59135

mast cell proteinase 3 (EC 3.4.21.-) precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 15-Feb-1996 #sequence\_revision 01-Mar-1996 #text\_change 20-Jun-2000

C:Accession: S59135

R:Ride, H.; Itoh, H.; Tomita, M.; Murakumo, Y.; Kobayashi, T.; Maruyama, H.; Osada, Y.;

Biochem. J. 311, 675-680, 1995

A:Title: Cloning of the cDNA encoding a novel rat mast-cell proteinase, rMCP-3, and its

A:Reference number: S59135; MUID:96033070; PMID:7487912

A:Accession: S59135

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-247 <IDE>

A:Cross-references: EMBL:D38495; NID:g559376; PIDN:BAA07507.1; PID:g559377  
C:Superfamily: trypsin; trypsin homology  
C:Keywords: hydrolase; serine proteinase  
F:22-240/Domain: trypsin homology <TRY>  
F:66,110,203/Active site: His, Asp, Ser #status predicted

Query Match 100.0%; Score 28; DB 2; Length 247;  
Best Local Similarity 100.0%; Pred. No. 1e+02; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0;

QY 1 LKEKAK 6  
|||||  
DB 116 LKEKAK 121

RESULT 8  
S23504  
chymase (EC 3.4.21.39) 1 precursor - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 22-Nov-1993 #sequence\_revision 03-Aug-1995 #text\_change 22-Jun-1999  
C:Accession: S23504  
R:Chu, W.; Johnson, D.A.; Musich, P.R.  
Biochim. Biophys. Acta 1121, 83-87, 1992  
A:Title: Molecular cloning and characterization of mouse mast cell chymases.  
A:Reference number: S23504; MUID:92287966; PMID:1376147  
A:Accession: S23504  
A:Molecule type: mRNA  
A:Residues: 1-247 <CHU>  
A:Cross-references: EMBL:M68898; NID:g199028; PIDN:AAA39492.1; PID:g199029  
C:Superfamily: trypsin; trypsin homology  
C:Keywords: hydrolase; mast cell; serine proteinase  
F:1-21/Domain: signal sequence #status predicted <SIG>  
F:22-247/Product: chymase #status predicted <MAT>  
F:22-240/Domain: trypsin homology <TRY>  
F:66,110,203/Active site: His, Asp, Ser #status predicted

Query Match 100.0%; Score 28; DB 2; Length 247;  
Best Local Similarity 100.0%; Pred. No. 1e+02; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0;

QY 1 LKEKAK 6  
|||||  
DB 116 LKEKAK 121

RESULT 9  
S64708  
chymase (EC 3.4.21.39) 2 precursor - Mongolian jird  
N:Alternate names: mast cell protease-2 precursor  
C:Species: Meriones unguiculatus (Mongolian jird)  
C>Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 20-Jun-2000  
C:Accession: S64708  
R:Ittoh, H.; Murakumo, Y.; Tomita, M.; Ide, H.; Kobayashi, T.; Maruyama, H.; Horii, Y.; N  
Biochem. J. 314, 923-929, 1996  
A:Title: Cloning of the cDNAs for mast-cell chymases from the jejunum of Mongolian gerbi  
t cells of mice and rats.  
A:Reference number: S64707; MUID:96177868; PMID:8615790  
A:Accession: S64708  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-247 <ITO>  
A:Cross-references: EMBL:D45174; NID:g633079; PIDN:BAA08122.1; PID:g633080  
C:Superfamily: trypsin; trypsin homology  
C:Keywords: hydrolase; serine proteinase  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-21/Domain: propeptide #status predicted <PRO>  
F:22-247/Product: chymase 2 #status predicted <MAT>  
F:22-240/Domain: trypsin homology <TRY>  
F:66,110,203/Active site: His, Asp, Ser #status predicted

Query Match 100.0%; Score 28; DB 2; Length 247;  
Best Local Similarity 100.0%; Pred. No. 1e+02; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0;

QY 1 LKEKAK 6  
|||||  
DB 116 LKEKAK 121

RESULT 10  
C81846  
hypothetical protein NMA1544 [imported] - Neisseria meningitidis (strain Z2491 serogrou  
C:Species: Neisseria meningitidis  
C>Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001  
C:Accession: C81846  
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; More  
; Holroyd, S.; Jagsels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream  
Nature 404, 502-506, 2000  
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.  
A:Reference number: A81775; MUID:20222556; PMID:10761919  
A:Accession: C81846  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-254 <PAR>  
A:Cross-references: GB:ALJ62756; GB:ALI57959; NID:g7380091; PIDN:CAB84771.1; PID:g73801  
A:Experimental source: serogroup A, strain Z2491  
C:Genetics:  
A:Gene: NMA1544

Query Match 100.0%; Score 28; DB 2; Length 254;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0;

QY 1 LKEKAK 6  
|||||  
DB 225 LKEKAK 230

RESULT 11  
S26043  
chymase (EC 3.4.21.39) 5 precursor - mouse  
N:Alternate names: mast cell proteinase MMCP-5; mast cell serine proteinase 5  
C:Species: Mus musculus (house mouse)  
C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 22-Jun-1999  
C:Accession: S26043; A41076; B41076; C35646  
R:Huang, R.; Blom, T.; Hellman, L.  
Eur. J. Immunol. 21, 1611-1621, 1991  
A:Title: Cloning and structural analysis of MMCP-1, MMCP-4 and MMCP-5, three mouse mast  
A:Reference number: S26041; MUID:91285010; PMID:2060576  
A:Accession: S26043  
A:Molecule type: mRNA  
A:Residues: 1-260 <HUA>  
A:Cross-references: EMBL:X68805; NID:g53158; PIDN:CAA48705.1; PID:g53159  
R:McNeil, H.P.; Austen, K.F.; Somerville, L.L.; Gurish, M.F.; Stevens, R.L.  
J. Biol. Chem. 266, 20316-20322, 1991  
A:Title: Molecular cloning of the mouse mast cell protease-5 gene. A novel secretory gr  
A:Reference number: A41076; MUID:92041862; PMID:1939089  
A:Accession: A41076  
A:Molecule type: DNA  
A:Residues: 14-260 <MCI>  
A:Cross-references: GB:M73760  
A:Accession: B41076  
A:Molecule type: mRNA  
A:Residues: 14-260 <MC2>  
A:Cross-references: GB:M73759  
R:Revold, D.S.; Stevens, R.L.; Lane, W.S.; Carr, M.H.; Austen, K.F.; Serafin, W.E.  
Proc. Natl. Acad. Sci. U.S.A. 87, 3230-3234, 1990  
A:Title: Different mouse mast cell populations express various combinations of at least  
A:Reference number: A35646; MUID:90222202; PMID:2326280  
A:Accession: C35646  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 35-40, 'X', 42-63, 'R' <REV>  
C:Genetics:  
A:Introns: 42/2; 92/3; 138/1; 223/1  
C:Superfamily: trypsin; trypsin homology

C;Keywords: hydrolase; mast cell; serine proteinase; zymogen  
 F;1-32/Domain: signal sequence #status predicted <SIG>  
 F;33-34/Domain: activation peptide #status predicted <ACT>  
 F;35-260/Product: chymase 5 #status experimental <MAY>  
 F;35-253/Domain: trypsin homology <TRY>  
 F;79,123,216/Active site: His, Asp, Ser #status predicted

Query Match 100.0%; Score 28; DB 2; Length 260;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02; Indels 0; Gaps 0;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
 |||||  
 Db 129 LKEKAK 134

## RESULT 12

T05674

farnesyltransferase homolog F20M13.20 - Arabidopsis thaliana  
 C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 26-Aug-1999

C;Accession: T05674

R;Bevan, M.; Wedler, H.; Kutzner, M.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.R.  
 submitted to the Protein Sequence Database, February 1999

A;Reference number: Z15420

A;Accession: T05674

A;Molecule type: DNA

A;Residues: 1-326 <BEV>

A;Cross-references: EMBL:AL035540

A;Experimental source: cultivar Columbia; BAC clone F20M13

C;Genetics:

A;Map position: 4

A;Introns: 118/3

A;Note: F20M13.20

C;Superfamily: Geranyltransferase

Query Match 100.0%; Score 28; DB 2; Length 326;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02; Indels 0; Gaps 0;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
 |||||  
 Db 286 LKEKAK 291

## RESULT 13

C95124

glycosyl transferase CpoA SP1075 [imported] - Streptococcus pneumoniae (strain TIGR4)

C;Species: Streptococcus pneumoniae

C;Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 03-Aug-2001

C;Accession: C95124

R;Tetteelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid  
 on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel,  
 on, T.; Hickey, E.K.; Holt, I.E.

Science 293, 498-506, 2001

A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,  
 A.; Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.

A;Reference number: A95000; MUID:21357209; PMID:11463916

A;Accession: C95124

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-338 <KUR>

A;Cross-references: GB:AE005672; PIDN:AAK75188.1; PID:gl14972550; GSPDB:GN00164; TIGR:SP4

A;Experimental source: strain TIGR4

C;Genetics:

A;Gene: SP1075

Query Match 100.0%; Score 28; DB 2; Length 338;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02; Indels 0; Gaps 0;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
 |||||

Db 305 LKEKAK 310

## RESULT 14

S16863

gene DN38 protein - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 05-Nov-1999

C;Accession: S16863

R;Kato, K.

submitted to the EMBL Data Library, August 1991

A;Description: Sequence analysis of twenty mouse brain cDNA clones selected by specific

A;Reference number: S16416

A;Accession: S16863

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-344 <KAT>

A;Cross-references: EMBL:X61449; NID:g50721; PIDN:CAA43689.1; PID:g50722

Query Match 100.0%; Score 28; DB 2; Length 344;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02; Indels 0; Gaps 0;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
 |||||  
 Db 97 LKEKAK 102

## RESULT 15

A75110

hypothetical protein PAB0463 - Pyrococcus abyssi (strain Orsay)

C;Species: Pyrococcus abyssi

C;Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 20-Aug-1999

C;Accession: A75110

R;Anonymous, Genoscope

submitted to the EMBL Data Library, July 1999

A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome str

A;Reference number: A75001

A;Accession: A75110

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-367 <KAW>

A;Cross-references: GB:AJ248285; GB:AL096836; NID:g5458067; PIDN:CAB49594.1; PID:e15154;

A;Experimental source: strain Orsay

C;Genetics:

A;Gene: PAB0463

Query Match 100.0%; Score 28; DB 2; Length 367;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02; Indels 0; Gaps 0;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
 |||||  
 Db 167 LKEKAK 172

## RESULT 16

AH2214

hypothetical protein all3271 [imported] - Nostoc sp. (strain PCC 7120)

C;Species: Nostoc sp. PCC 7120

A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Dec-2002

C;Accession: AH2214

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,

DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An

A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AH2214

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-372 <KUR>

A;Cross-references: GB:BA0000019; PIDN:BAW74970.1; PID:gl17132366; GSPDB:GN00179

A;Experimental source: strain PCC 7120

C;Genetics:

A;Gene: all3271

C;Superfamily: hypothetical protein yxab

Query Match. 100.0%; Score 28; DB 2; Length 372;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6

Db 72 LKEKAK 77

#### RESULT 17

H81783 hypothetical protein NMA2122 [imported] - Neisseria meningitidis (strain Z2491 serogroup

C;Species: Neisseria meningitidis

C;Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001

C;Accession: H81783

R;Parikhill, J.; Achtmann, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel

; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,

Nature 404, 502-506, 2000

A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.

A;Reference number: A81775; MUID:20222556; PMID:10761919

A;Accession: H81783

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-374 <PAR>

A;Cross-references: GB:AL162758; GB:AL157959; NID:g7380672; PIDN:CAB85335.1; PID:g738074

A;Experimental source: serogroup A, strain Z2491

C;Genetics:

A;Gene: NMA2122

C;Superfamily: Neisseria meningitidis hypothetical protein NMB0366

Query Match 100.0%; Score 28; DB 2; Length 374;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6

Db 99 LKEKAK 104

#### RESULT 18

E97994

glycosyltransferase [imported] - Streptococcus pneumoniae (strain R6)

C;Species: Streptococcus pneumoniae

C;Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 22-Oct-2001

C;Accession: E97994

R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E

e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M

y, P.; Sun, P.M.; Winkler, M.E.

J. Bacteriol. 183, 5709-5717, 2001

A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;

A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.

A;Reference number: A97872; MUID:21429245; PMID:11544234

A;Accession: E97994

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-374 <KUR>

A;Cross-references: GB:AE007317; PIDN:AAK99785.1; PID:g15458595; GSPDB:GN00174

C;Genetics:

A;Gene: cpoA

Query Match 100.0%; Score 28; DB 2; Length 374;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6

Db 341 LKEKAK 346

#### RESULT 19

F97866

hypothetical protein pntAA [imported] - Rickettsia conorii (strain Malish 7)

C;Species: Rickettsia conorii

C;Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 17-May-2002

C;Accession: F97866

R;Gyaca, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; R

Science 293, 2093-2098, 2001

A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.

A;Reference number: A97700; MUID:21442074; PMID:11557893

A;Accession: F97866

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-374 <KUR>

A;Cross-references: GB:AE006914; PIDN:AAL03872.1; PID:g15620476; GSPDB:GN00173

C;Genetics:

A;Gene: pntAA

C;Superfamily: alanine dehydrogenase; alanine dehydrogenase homology

Query Match 100.0%; Score 28; DB 2; Length 374;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6

Db 6 LKEKAK 11

#### RESULT 20

D81206

hypothetical protein NMB0366 [imported] - Neisseria meningitidis (strain MC58 serogroup

C;Species: Neisseria meningitidis

C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001

C;Accession: D81206

R;Tetzelin, H.; Saunders, N.J.; Heideberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.

Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.

ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizzi, M.

Science 287, 1809-1815, 2000

A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; V

A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A;Reference number: A81000; MUID:20175755; PMID:10710307

A;Accession: D81206

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-377 <TET>

A;Cross-references: GB:AE002393; GB:AE002098; NID:g7225586; PIDN:AAF40808.1; PID:g72255

A;Experimental source: serogroup B, strain MC58

C;Genetics:

A;Gene: NMB0366

C;Superfamily: Neisseria meningitidis hypothetical protein NMB0366

Query Match 100.0%; Score 28; DB 2; Length 377;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6

Db 102 LKEKAK 107

#### RESULT 21

S40510

nucleosome assembly protein l-like 1 - human

N;Alternate names: NRP protein

C;Species: Homo sapiens (man)

C;Date: 07-Sep-1994 #sequence\_revision 26-May-1995 #text\_change 19-May-2000

C;Accession: S40510; T47171

R;Simon, H.U.; Mills, G.B.; Kozlowski, M.; Hogg, D.; Branch, D.; Ishimi, Y.; Siminovic

Biochem. J. 297, 389-397, 1994

A;Title: Molecular characterization of hNRP, a cDNA encoding a human nucleosome-assembly

A;Reference number: S40510; MUID:94128073; PMID:8297347

A;Accession: S40510

A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-391 <SIM>  
A:Cross-references: EMBL:M86667; NID:g189066; PIDN:AAC37544.1; PID:g189067  
A>Note: In the authors' translation 36-Arg is not shown, consequently, residues 37-65 are  
R:Bloeker, H.; Boecher, M.; Brandt, P.; Mewes, H.W.; Well, B.; Wiemann, S.  
submitted to the Protein Sequence Database, March 2000  
A:Reference number: Z24376  
A:Accession: T47171  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-391 <AAA>  
A:Cross-references: EMBL:AL162068  
A:Experimental source: adult melanoma (MeWo cell line); clone DKF2p762G106  
C:Genetics:  
A:Gene: GDB:NAP1L1; NRP  
A:Cross-references: GDB:307756; OMIM:164060  
A:Map position: 5q13.1-5q13.1  
A>Note: DKF2p762G106.1

Query Match 100.0%; Score 28; DB 2; Length 391;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
|||||  
DB 146 LKEKAK 151

RESULT 22  
JS0707  
nucleosome assembly protein 1 - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 05-Nov-1999  
C:Accession: JS0707  
R:Okuda, A.  
submitted to JIPID, July 1992  
A:Reference number: JS0707  
A:Accession: JS0707  
A>Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-391 <OKU>  
A:Cross-references: DDBJ:D12618; NID:g220495; PIDN:BAA02142.1; PID:d1002632; PID:g220496

Query Match 100.0%; Score 28; DB 2; Length 391;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
|||||  
DB 146 LKEKAK 151

RESULT 23  
A97225  
FKBP-type peptidyl-prolyl cis-trans isomerase (trigger factor) [imported] - Clostridium a  
C:Species: Clostridium acetobutylicum  
C:Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 12-Jun-2003  
C:Accession: A97225  
R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,  
; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001  
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo  
A:Reference number: A96900; MUID:21359325; PMID:21359325  
A:Accession: A97225  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-431 <KUR>  
A:Cross-references: GB:AE001437; PIDN:AAK80588.1; PID:g15025668; GSPDB:GN00168  
A:Experimental source: Clostridium acetobutylicum ATCC824  
C:Genetics:  
A:Gene: CAC2641  
C:Superfamily: FKBP-type peptidyl-prolyl cis-trans isomerase (trigger factor); BKBP-type

Query Match 100.0%; Score 28; DB 2; Length 431;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
|||||  
DB 379 LKEKAK 384

RESULT 24  
B72328  
conserved hypothetical protein - Thermotoga maritima (strain MSB8)  
C:Species: Thermotoga maritima  
C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 21-Jul-2000  
C:Accession: B72328  
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey  
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.,  
C.M.  
Nature 399, 323-329, 1999  
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome se  
A:Reference number: A72200; MUID:99287316; PMID:10360571  
A:Accession: B72328  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-434 <ARN>  
A:Cross-references: GB:AE001750; GB:AE000512; NID:g4981356; PIDN:AAD35912.1; PID:g498135  
A:Experimental source: strain MSB8  
C:Genetics:  
A:Gene: TW0830  
C:Superfamily: conserved hypothetical protein b0835

Query Match 100.0%; Score 28; DB 2; Length 434;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
|||||  
DB 352 LKEKAK 357

RESULT 25  
B82899  
conserved hypothetical ATP/GTP-binding protein UU383 [imported] - Ureaplasma urealyticum  
C:Species: Ureaplasma urealyticum  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Sep-2000  
C:Accession: B82899  
R:Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.  
submitted to GenBank, February 2000  
A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mi  
A:Reference number: B82870  
A:Accession: B82899  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-442 <GLA>  
A:Cross-references: GB:AE002135; GB:AF222894; NID:g68899358; PIDN:AAF30793.1; GSPDB:GN001  
A:Experimental source: serovar 3; biovar 1  
C:Genetics:  
A:Gene: UU383  
A:Genetic code: SGC3  
C:Superfamily: Mycobacterium leprae probable GTP-binding protein; translation elongation  
F,175-296/Domain: translation elongation factor Tu homology <ETU>

Query Match 100.0%; Score 28; DB 2; Length 442;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
|||||  
DB 105 LKEKAK 110

RESULT 26



D70410  
cytosolic axial filament protein - Aquifex aeolicus  
C:Species: Aquifex aeolicus  
C:Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 05-Nov-1999  
C:Accession: D70410  
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Oviatt, D.  
Nature 392, 353-358, 1998  
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.  
A:Reference number: A70300; MUID:98196666; PMID:9537320  
A:Accession: D70410  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-458 <AQF>  
A:Cross-references: GB:AB000732; NID:g2983704; PIDN:AAC07269.1; PID:g2983706; GB:AE00065  
A:Experimental source: strain VF5  
C:Genetics:  
A:Gene: cafa

Query Match 100.0%; Score 28; DB 2; Length 458;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
|||||  
DB 178 LKEKAK 183

## RESULT 27

S26979  
H+-transporting two-sector ATPase (EC 3.6.3.14) alpha chain - kidney bean mitochondrion  
N:Alternate names: ATPase alpha chain  
C:Species: Mitochondrion Phaseolus vulgaris (kidney bean)  
C:Date: 23-Apr-1993 #sequence\_revision 23-Apr-1993 #text\_change 03-Jun-2002  
C:Accession: S26979  
R:Chase, C.D.; Ortega, V.M.  
Curr. Genet. 22, 147-153, 1992  
A:Title: Organization of ATPase coding and 3' flanking sequences associated with cytoplasmic inheritance of H<sup>+</sup>-ATPase in Phaseolus vulgaris.  
A:Reference number: S26979; MUID:93046798; PMID:1423717  
A:Accession: S26979  
A:Molecule type: DNA  
A:Residues: 1-508 <CHA>  
A:Cross-references: EMBL:M64246; NID:g169317; PIDN:AB01582.1; PID:g169318  
A:Note: the authors translated the codon GGG for residue 257 as Cys  
C:Genetics:  
A:Gene: atpa

A:Genome: mitochondrion  
C:Superfamily: H<sup>+</sup>-transporting ATP synthase alpha chain; H<sup>+</sup>-transporting ATP synthase alpha chain  
C:Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; nucleotide-binding motif A (P-loop)  
F:171-178/Region: nucleotide-binding motif A (P-loop)  
F:205-377/Domain: H<sup>+</sup>-transporting ATP synthase alpha chain homology <ATP>  
Query Match 100.0%; Score 28; DB 2; Length 508;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
|||||  
DB 499 LKEKAK 504

## RESULT 28

F64560  
CMP-N-acetylneuraminic acid synthetase - Helicobacter pylori (strain 26695)  
C:Species: Helicobacter pylori  
C:Date: 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 08-Oct-1999  
C:Accession: F64560  
R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, J.; Delcher, A.L.; Kohn, M.; Venter, A.; Adams, J.; Hargrett-Nelson, N.; White, O.; Watthey, L.; Son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.; Nature 388, 539-547, 1997  
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.  
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A:Reference number: A64520; MUID:97394467; PMID:9252185  
A:Accession: F64560  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-517 <TOM>  
A:Cross-references: GB:AE000550; GB:AE000511; NID:g2313417; PIDN:AAD07393.1; PID:g231341.

Query Match 100.0%; Score 28; DB 2; Length 517;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
|||||  
DB 300 LKEKAK 305

## RESULT 29

D69679  
polyketide synthase pksN - Bacillus subtilis  
C:Species: Bacillus subtilis  
C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 15-Oct-1999  
C:Accession: D69679  
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte, C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chhabra, A.P.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.; Nature 390, 249-256, 1997  
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelli, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon, A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. Bacillus subtilis.  
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
A:Reference number: A69580; MUID:98044033; PMID:9384377  
A:Accession: D69679

A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-545 <KUN>  
A:Cross-references: GB:Z99113; GB:AL009126; NID:G2634090; PIDN:CAB13604.1; PID:ell83379  
A:Experimental source: strain 168  
C:Genetics:  
A:Gene: pksN  
Query Match 100.0%; Score 28; DB 2; Length 545;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
|||||  
DB 100 LKEKAK 105

## RESULT 30

D69722  
thiamin biosynthesis protein thia - Bacillus subtilis  
C:Species: Bacillus subtilis  
C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 24-Oct-2000  
C:Accession: D69722; T4417  
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte, C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chhabra, A.P.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.; Nature 390, 249-256, 1997  
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelli, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon, A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. Bacillus subtilis.  
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
A:Reference number: A69580; MUID:98044033; PMID:9384377  
A:Accession: D69679

A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-545 <KUN>  
A:Cross-references: GB:Z99113; GB:AL009126; NID:G2634090; PIDN:CAB13604.1; PID:ell83379  
A:Experimental source: strain 168  
C:Genetics:  
A:Gene: pksN  
Query Match 100.0%; Score 28; DB 2; Length 545;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.  
 A:Authors: Yoshikawa, H.F.; Zumsstein, E.; Yoshikawa, H.; Danchin, A. Bacillus subtilis.  
 A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
 A:Reference number: A69580; MUID:98044033; PMID:9384377  
 A:Accession: D69722  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-590 <KUN>  
 A:Cross-references: GB:Z99108; GB:AL009126; NID:G2633055; PIDN:CAB12707.1; PID:G2633202  
 A:Experimental source: strain 168  
 R:Zhang, Y.; Begley, T.P.  
 submitted to the EMBL Data Library, May 1995  
 A:Description: Cloning and sequencing of thiA: a gene involved in the biosynthesis of th  
 A:Reference number: Z22759  
 A:Accession: T44417  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA  
 A:Residues: 1-139, 'Q', '141-169, 'RLFLP', '175-333, 'L', '335-546, 'G', '548-590 <ZHA>  
 A:Cross-references: EMBL:U26178; PIDN:AAA68243.1  
 A:Experimental source: strain 168  
 C:Genetics:  
 A:Gene: thiA  
 A:Map position: 70 minutes  
 C:Function:  
 A:Description: involved in the biosynthesis of the pyrimidine moiety of thiamin  
 C:Superfamily: thiamin biosynthesis protein thiC  
 C:Keywords: thiamin biosynthesis

Query Match 100.0%; Score 28; DB 2; Length 590;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
 |||||  
 DB 574 LKEKAK 579

RESULT 31  
 H69626  
 PTS fructose-specific enzyme IIBC component fruA - Bacillus subtilis  
 C:Species: Bacillus subtilis  
 C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 20-Jun-2000  
 C:Accession: H69626  
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter  
 C.; Bron, S.; Brouillet, S.; Bruschini, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch  
 A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
 Nature 390, 249-256, 1997  
 A:Authors: Foulger, D.; Fritze, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall  
 iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.  
 Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,  
 A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel  
 Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle  
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,  
 A:Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seron  
 akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama  
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K  
 A:Authors: Yoshikawa, H.F.; Zumsstein, E.; Yoshikawa, H.; Danchin, A.  
 A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
 A:Reference number: A69580; MUID:98044033; PMID:9384377  
 A:Accession: H69626  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-635 <KUN>  
 A:Cross-references: GB:Z99111; GB:AL009126; NID:G2633699; PIDN:CAB13313.1; PID:G2633811  
 A:Experimental source: strain 168  
 C:Genetics:  
 A:Gene: fruA  
 C:Superfamily: phosphotransferase system enzyme II, fructose-specific; phosphotransferas  
 F;20-147/Domain: phosphotransferase system mannitol-specific enzyme II factor III homold

Query Match 100.0%; Score 28; DB 2; Length 635;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LKEKAK 6  
 |||||  
 DB 192 LKEKAK 197

RESULT 32  
 T27020  
 hypothetical protein Y48E1B.9 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 04-Mar-2000  
 C:Accession: T27020  
 R:McMurray, A.  
 submitted to the EMBL Data Library, March 1997  
 A:Reference number: Z20299  
 A:Accession: T27020  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA  
 A:Residues: 1-688 <WIL>  
 A:Cross-references: EMBL:Z93393; PIDN:CAB07697.1; GSPDB:GN00020; CESP:Y48E1B.9  
 A:Experimental source: clone Y48E1B  
 C:Genetics:  
 A:Gene: CESP:Y48E1B.9  
 A:Map position: 2  
 A:Introns: 41/3; 130/2; 141/3; 154/2; 183/1; 293/1; 360/3; 522/3; 594/3  
 C:Superfamily: Caenorhabditis elegans hypothetical protein Y48E1B.9

Query Match 100.0%; Score 28; DB 2; Length 688;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
 |||||  
 DB 480 LKEKAK 485

RESULT 33  
 S06017  
 neuraxin - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 07-Sep-1990 #sequence\_revision 03-Mar-1995 #text\_change 07-Jul-2003  
 C:Accession: S06017  
 R:Pienitz, A.; Grenningloh, G.; Hermans-Borgmeyer, I.; Kirsch, J.; Littauer, U.Z.; Prior  
 EMO J. 8, 2879-2888, 1989  
 A:Title: Neuraxin, a novel putative structural protein of the rat central nervous system  
 A:Reference number: S06017; MUID:90059871; PMID:2555150  
 A:Accession: S06017  
 A:Molecule type: mRNA  
 A:Residues: 1-863 <RIE>  
 A:Cross-references: EMBL:X16623; NID:G57826; PIDN:CRA34620.1; PID:G57827  
 A:Note: the authors translated the codon GCA for residue 723 as His  
 C:Keywords: brain; microtubulin binding; spinal cord; tandem repeat  
 F:258-461/Region: 17-residue repeats  
 F:628-741/Region: arginine/lysine-rich

Query Match 100.0%; Score 28; DB 2; Length 863;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
 |||||  
 DB 634 LKEKAK 639

RESULT 34  
 NBHUH  
 complement factor H precursor, long splice form [validated] - human  
 C:Species: Homo sapiens (man)  
 C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 08-Dec-2000  
 C:Accession: S00254; A60238; A54726; A61565; A26505; I72654; S66298  
 R:Ripoche, J.; Day, A.J.; Harris, T.J.R.; Sim, R.B.  
 Biochem. J. 249, 593-602, 1988

A:Title: The complete amino acid sequence of human complement factor H.  
 A:Reference number: S00254; MUID:88134059; PMID:2963625  
 A:Accession: S00254  
 A:Molecule type: mRNA  
 A:Residues: 1-1231 <RIP>  
 A:Cross-references: EMBL:Y00716; NID:g31964; PIDN:CAA68704.1; PID:g31965  
 A:Note: 402-Tyr was also found  
 A:Note: parts of this sequence, including the amino and carboxyl ends of the mature protein  
 R:Estaller, C.; Schwaeble, W.; Dierich, M.; Weiss, E.H.  
 Eur. J. Immunol. 21, 799-802, 1991  
 A:Title: Human complement factor H: two factor H proteins are derived from alternatively  
 A:Reference number: A60238; MUID:91184292; PMID:1826264  
 A:Accession: A60238  
 A:Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-56;1177-1231 <EST>  
 A:Note: only portions of this 4.3 kilobase mRNA were sequenced  
 R:Day, A.J.; Ripoch, J.; Lyons, A.; McIntosh, B.; Harris, T.J.R.; Sim, R.B.  
 Biosci. Rep. 7, 201-207, 1987  
 A:Title: Sequence analysis of a cDNA clone encoding the C-terminal end of human compleme  
 A:Reference number: A54726; MUID:88025472; PMID:2889480  
 A:Accession: A54726  
 A:Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 'DFRN', 579-1231 <DAY>  
 A:Cross-references: GB:M17517; NID:g180497; PIDN:AAA52016.1; PID:g180498  
 A:Note: parts of this sequence were determined by protein sequencing  
 R:Ripoch, J.; Day, A.J.; Willis, A.C.; Belt, K.T.; Campbell, R.D.; Sim, R.B.  
 Biosci. Rep. 6, 65-72, 1986  
 A:Title: Partial characterization of human complement factor H by protein and cDNA sequ  
 A:Reference number: A61565; MUID:86188123; PMID:2938641  
 A:Accession: A61565  
 A:Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 'METGRNHLNAKI', 1050-1057, 'T', 1059-1102 <RI2>  
 R:Sim, R.B.; Disceplo, R.G.  
 Biochem. J. 205, 285-293, 1982  
 A:Title: Purification and structural studies on the complement-system control protein be  
 A:Reference number: A26505; MUID:83048213; PMID:6215918  
 A:Accession: A26505  
 A:Molecule type: protein  
 A:Residues: 19-20, 'Q', 22-29, 'V', 31-33, 'Q', 35 <SIM>  
 R:Barlow, P.N.; Norman, D.G.; Steinkasserer, A.; Horne, T.J.; Pearce, J.; Driscoll, P.C.  
 Biochemistry 31, 3626-3634, 1992  
 A:Title: Solution structure of the fifth repeat of factor H: A second example of the com  
 A:Reference number: A44551; MUID:92232649; PMID:1533152  
 A:Contents: annotation; NMR structure determination, residues 264-292  
 R:Norman, D.G.; Barlow, P.N.; Baron, M.; Day, A.J.; Sim, R.B.; Campbell, I.D.  
 J. Mol. Biol. 219, 717-725, 1991  
 A:Title: Three-dimensional structure of a complement control protein module in solution.  
 A:Reference number: A49224; MUID:91278097; PMID:1829116  
 A:Contents: annotation; NMR structure determination, residues 927-985  
 R:Estaller, C.; Koistinen, V.; Schwaeble, W.; Dierich, M.P.; Weiss, E.H.  
 J. Immunol. 146, 3190-3196, 1991  
 A:Title: Cloning of the 1.4-kb mRNA species of human complement factor H reveals a novel  
 A:Reference number: I56100; MUID:91201892; PMID:1826708  
 A:Accession: I72654  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1047-1231 <RES>  
 A:Cross-references: GB:M65294; NID:g183766; PIDN:AAA35948.1; PID:g183767  
 R:Carroll, J.A.; Bates, R.C.; Smith, A.I.; Teto, T.; Arellano, A.; Gordon, D.L.; Burns,  
 Biochim. Biophys. Acta 1289, 305-311, 1996  
 A:Title: Factor H co-purifies with thrombospondin isolated from platelet secretate.  
 A:Reference number: S66298; MUID:96205365; PMID:8620012  
 A:Accession: S66298  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 411-419;574-578,580-582 <CAR>  
 C:Comment: Factor H has also been found bound to cell membranes in an unknown manner. HC  
 C:Comment: Alternative transcripts of 4.3, 1.8, and 1.4 kilobases are expressed in liver.  
 C:Genetics: <HF1>

A:Gene: GDB:HF1; HF  
 A:Cross-references: GDB:120041; OMIM:134370  
 A:Map position: 1q32-1q32  
 C:Genetics: <HF2>  
 A:Gene: GDB:HF2; HF  
 A:Cross-references: GDB:129095  
 A:Map position: 1q32-1q32  
 A:Note: the correspondence between the two loci and the sequences indicated is unclear;  
 C:Function:  
 A:Description: a cofactor in the inactivation of C3b by serine proteinase I; also incre  
 he alternative complement pathway  
 A:Pathway: complement alternate pathway  
 C:Superfamily: complement factor H; complement factor H repeat homology  
 C:Keywords: alternative splicing; complement alternate pathway; glycoprotein; plasma  
 F:1-18/Domain: signal sequence #status predicted <SIG>  
 F:19-1229/Product: complement factor H, short splice form #status experimental <MPT>  
 F:21-80/Domain: complement factor H repeat homology <FH01>  
 F:85-141/Domain: complement factor H repeat homology <FH02>  
 F:146-205/Domain: complement factor H repeat homology <FH03>  
 F:210-262/Domain: complement factor H repeat homology <FH04>  
 F:246-248/Region: cell attachment (R-G-D) motif  
 F:267-320/Domain: complement factor H repeat homology <FH05>  
 F:325-385/Domain: complement factor H repeat homology <FH06>  
 F:389-442/Domain: complement factor H repeat homology <FH07>  
 F:448-505/Domain: complement factor H repeat homology <FH08>  
 F:509-564/Domain: complement factor H repeat homology <FH09>  
 F:569-623/Domain: complement factor H repeat homology <FH10>  
 F:630-684/Domain: complement factor H repeat homology <FH11>  
 F:691-744/Domain: complement factor H repeat homology <FH12>  
 F:753-803/Domain: complement factor H repeat homology <FH13>  
 F:811-864/Domain: complement factor H repeat homology <FH14>  
 F:870-926/Domain: complement factor H repeat homology <FH15>  
 F:931-984/Domain: complement factor H repeat homology <FH16>  
 F:989-1043/Domain: complement factor H repeat homology <FH17>  
 F:1048-1102/Domain: complement factor H repeat homology <FH18>  
 F:1109-1163/Domain: complement factor H repeat homology <FH19>  
 F:1167-1228/Domain: complement factor H repeat homology <FH20>  
 F:21-66,52-80,85-129,114-141,146-192,178-205,210-251,237-262,267-309,294-320,325-374,33  
 1-803,811-853,839-864,870-915,901-926,931-973,959-984,989-1032,1018-1043,1048-1091,1077  
 F:217/Binding site: carbohydrate (Asn) (covalent) #status absent  
 F:529,802,823,882,911/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F:718,1029,1095/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 Query Match 100.0%; Score 28; DB 1; Length 1231;  
 Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LKEKAK 6  
 DB 469 LKEKAK 474  
 RESULT 35  
 S42167  
 190K protein - human  
 C:Species: Homo sapiens (man)  
 C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 24-Sep-1999  
 C:Accession: S42167  
 R:Vinkemeier, U.; Obermann, W.; Weber, K.; Fuerst, D.O.  
 J. Cell Sci. 106, 319-330, 1993  
 A:Title: The globular head domain of titin extends into the center of the sarcomeric M  
 A:Reference number: S42166; MUID:94095665; PMID:7505783  
 A:Accession: S42167  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-1451 <VIN>  
 A:Cross-references: EMBL:X69090; NID:g407098; PIDN:CAA48833.1; PID:g407099  
 C:Superfamily: skelemin  
 Query Match 100.0%; Score 28; DB 2; Length 1451;  
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
|||||  
Db 844 LKEKAK 849

## RESULT 36

A56577

microtubule-associated protein MAP 1B - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)  
C>Date: 21-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 16-Feb-1997  
C:Accession: A56577  
R:Zauner, W.; Kratz, J.; Staunton, J.; Feick, P.; Wiche, G.  
Eur. J. Cell Biol. 57, 66-74, 1992  
A:Title: Identification of two distinct microtubule binding domains on recombinant rat  
A:Reference number: A56577; MUID:92347374; PMID:1639092  
A:Accession: A56577  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-2364 <ZAU>  
A:Cross-references: GB:X60550  
A:Experimental source: brain  
A>Note: nucleotide sequence not given; conceptual translation not complete  
C:Superfamily: microtubule-associated protein MAP1B

Query Match 100.0%; Score 28; DB 2; Length 2364;  
Best Local Similarity 100.0%; Pred. No. 9e+02; 0; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0;

QY 1 LKEKAK 6  
|||||  
Db 2135 LKEKAK 2140

## RESULT 37

A42771

reticulocyte-binding protein 1 - Plasmodium vivax

C:Species: Plasmodium vivax  
C>Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 28-Apr-1995  
C:Accession: A42771  
R:Galinski, M.R.; Medina, C.C.; Ingravallo, P.; Barnwell, J.W.  
Cell 69, 1213-1226, 1992  
A:Title: A reticulocyte-binding protein complex of Plasmodium vivax merozoites.  
A:Reference number: A42771; MUID:92315338; PMID:1617731  
A:Accession: A42771  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-2829 <GAL>  
A:Experimental source: Belem strain, merozoites  
A>Note: sequence extracted from NCBI backbone (NCBIN:108114, NCBIP:108115)

Query Match 100.0%; Score 28; DB 2; Length 2829;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
|||||  
Db 1583 LKEKAK 1588

## RESULT 38

A69448

hypothetical protein AF1586 - Archaeoglobus fulgidus

C:Species: Archaeoglobus fulgidus  
C>Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 17-Mar-2000  
C:Accession: A69448  
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson  
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.  
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.  
Nature 390, 364-370, 1997  
A:Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.  
Smith, H.O.; Woese, C.R.; Venter, J.C.  
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaea

A:Reference number: A69250; MUID:98049343; PMID:9389475

A:Accession: A69448

A&gt;Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-109 &lt;KLE&gt;

A:Cross-references: GB:AE000993; GB:AE000782; NID:G2689316; PIDN:AAB9665.1; PID:G264897;  
C:Superfamily: Archaeoglobus fulgidus conserved hypothetical protein AF1613

Query Match 92.9%; Score 26; DB 2; Length 109;  
Best Local Similarity 83.3%; Pred. No. 1.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
:|||||  
Db 25 IKEKAK 30

## RESULT 39

D70437

ATP synthase F0 subunit b - Aquifex aeolicus

C:Species: Aquifex aeolicus  
C>Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 05-Nov-1999  
C:Accession: D70437  
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O.V.  
V.  
Nature 392, 353-358, 1998  
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.  
A:Reference number: A70300; MUID:98196866; PMID:9537320  
A:Accession: D70437  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-185 <AQP>  
A:Cross-references: GB:AE000746; NID:G2983925; PIDN:AAC07478.1; PID:G2983929; GB:AE00065  
A:Experimental source: strain VF5  
C:Genetics:  
A:Gene: atpF2

Query Match 92.9%; Score 26; DB 2; Length 185;  
Best Local Similarity 83.3%; Pred. No. 2.1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
:|||||  
Db 123 IKEKAK 128

## RESULT 40

JQ1796

B2R protein - vaccinia virus (strain WR)

C:Species: vaccinia virus  
C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 20-Jun-2000  
C:Accession: JQ1796  
R:Smith, G.L.; Chan, Y.S.; Howard, S.T.  
J. Gen. Virol. 72, 1349-1376, 1991  
A:Title: Nucleotide sequence of 42kbp of vaccinia virus strain WR from near the right in  
A:Reference number: JQ1767; MUID:91259063; PMID:2045793  
A:Accession: JQ1796  
A:Molecule type: DNA  
A:Residues: 1-219 <SMI>  
A:Cross-references: DDBJ:D11079; NID:G222717; PIDN:BAA01832.1; PID:G222747

Query Match 92.9%; Score 26; DB 2; Length 219;  
Best Local Similarity 83.3%; Pred. No. 2.5e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
:|||||  
Db 141 IKEKAK 146

## RESULT 41

A42526

B2R protein - vaccinia virus (strain Copenhagen)

C;Species: vaccinia virus  
A;Date: host Homo sapiens (man)  
C;Date: 09-Nov-1990 #sequence\_revision 09-Nov-1990 #text\_change 08-Apr-1994  
C;Accession: A42526  
R;Johnson, G.P.  
submitted to GenBank, June 1990  
A;Reference number: A33172  
A;Accession: A42526  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-219 <JOH>

Query Match 92.9%; Score 26; DB 2; Length 219;  
Best Local Similarity 83.3%; Pred. No. 2.5e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
:|||||  
Db 141 IKEKAK 146

RESULT 42  
A40143  
placental lactogen precursor - sheep  
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 19-Jan-2001  
C;Accession: A40143  
R;Colosi, P.; Thordarson, G.; Hellmies, R.; Singh, K.; Forsyth, I.A.; Gluckman, P.; Wood  
Mol. Endocrinol. 3, 1462-1469, 1989  
A;Title: Cloning and expression of ovine placental lactogen.  
A;Reference number: A40143; MUID:90114213; PMID:2608069  
A;Accession: A40143  
A;Molecule type: mRNA  
A;Residues: 1-236 <COL>  
A;Cross-references: GB:M31660; NID:g166037; PIDN:AAA31577.1; PID:g166038  
A;Note: part of this sequence, including the amino end of the mature protein, was confir  
C;Superfamily: prolactin  
F;1-38/Domain: signal sequence #status predicted <SIG>  
F;39-236/Product: placental lactogen #status experimental <MAT>

Query Match 92.9%; Score 26; DB 2; Length 236;  
Best Local Similarity 83.3%; Pred. No. 2.7e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
:|||||  
Db 158 IKEKAK 163

RESULT 43  
G71869  
hypothetical protein jhp0939 - Helicobacter pylori (strain J99)  
C;Species: Helicobacter pylori  
A;Variety: strain J99  
C;Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 08-Oct-1999  
C;Accession: G71869  
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;  
Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;  
Nature 397, 176-180, 1999  
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path  
A;Reference number: A71800; MUID:99120557; PMID:9923682  
A;Accession: G71869  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-337 <ARN>  
A;Cross-references: GB:AE001523; GB:AE001439; NID:g4155513; PIDN:AAD06520.1; PID:g415552  
A;Experimental source: strain J99  
C;Genetics:  
A;Gene: jhp0939

Query Match 92.9%; Score 26; DB 2; Length 337;  
Best Local Similarity 83.3%; Pred. No. 3.8e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
:|||||  
Db 117 IKEKAK 122

## RESULT 44

E71101

probable geranylgeranyl pyrophosphate synthetase - Pyrococcus horikoshii  
C;Species: Pyrococcus horikoshii

C;Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 20-Jun-2000

C;Accession: E71101

R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki

M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kusuda, N.; Oguchi

DNA Res. 5, 55-76, 1998

A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic  
A;Reference number: A71000; MUID:98344137; PMID:9679194

A;Accession: E71101

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-342 <KAW>

A;Cross-references: GB:AP000004; NID:g3236131; PIDN:BAA30171.1; PID:g3257488

A;Experimental source: strain OT3

A;Note: this accession replaces an interim accession for a sequence replaced by GenBank

C;Genetics:

A;Gene: PH1072

C;Superfamily: prenyl transferase A

Query Match 92.9%; Score 26; DB 2; Length 342;

Best Local Similarity 83.3%; Pred. No. 3.8e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6

:|||||

Db 11 IKEKAK 16

## RESULT 45

A45402

transforming growth factor beta homolog Vgr-2 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 10-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 24-Nov-1999

C;Accession: A45402

R;Jones, C.M.; Simon-Chazottes, D.; Guenet, J.L.; Hogan, B.L.

Mol. Endocrinol. 6, 1961-1968, 1992

A;Title: Isolation of Vgr-2, a novel member of the transforming growth factor-beta-rela

A;Reference number: A45402; MUID:93125570; PMID:1480182

A;Accession: A45402

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-366 <JON>

A;Cross-references: GB:S52658; NID:g263309; PIDN:AAB24876.1; PID:g263310

A;Experimental source: embryo

A;Note: sequence extracted from NCBI backbone (NCBI:P122197)

C;Superfamily: inhibin

Query Match 92.9%; Score 26; DB 2; Length 366;

Best Local Similarity 83.3%; Pred. No. 4.1e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6

:|||||

Db 117 IKEKAK 122

## RESULT 46

A46607

growth/differentiation factor GDF-3 precursor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 24-Nov-1999

C;Accession: A46607

R;McPherron, A.C.; Lee, S.J.

J. Biol. Chem. 268, 3444-3449, 1993

A;Title: GDF-3 and GDF-9: two new members of the transforming growth factor-beta superfamily  
 A;Reference number: A46607; MUID:93155193; PMID:8429021  
 A;Accession: A46607  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-366 <MCP>  
 A;Cross-references: GB:L06443; NID:G293346; PIDN:AAAS3034.1; PID:G567205  
 C;Superfamily: inhibin

Query Match 92.9%; Score 26; DB 2; Length 366;  
 Best Local Similarity 83.3%; Pred. No. 4.1e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
 :|||||  
 Db 117 IREKAK 122

## RESULT 47

T52612  
 SRP receptor homolog FtsY precursor, chloroplast [validated] - Arabidopsis thaliana  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Date: 24-Oct-2000 #sequence\_revision 24-Oct-2000 #text\_change 01-Mar-2002  
 C;Accession: T52612  
 R;Kogata, N.; Nishio, K.; Hirohashi, T.; Kikuchi, S.; Nakai, M.  
 FEBS Lett. 447, 329-333, 1999  
 A;Title: Involvement of a chloroplast homologue of the signal recognition particle receptor in the import of SRP into the chloroplast  
 A;Reference number: Z26132  
 A;Accession: T52612  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-366 <KOG>  
 A;Cross-references: EMBL:AJ010820; PIDN:CA840382.1  
 A;Experimental source: cultivar Columbia  
 C;Genetics:  
 A;Genome: nuclear  
 A;Note: ftsY  
 C;Function:  
 A;Description: involved in the chloroplast SRP-dependent protein targeting to the thylakoid  
 C;Superfamily: docking protein  
 C;Keywords: chloroplast

Query Match 92.9%; Score 26; DB 2; Length 366;  
 Best Local Similarity 83.3%; Pred. No. 4.1e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
 :|||||  
 Db 56 IREKAK 61

## RESULT 48

T02470  
 hypothetical protein At2g45770 [imported] - Arabidopsis thaliana  
 N;Alternate names: cell division protein ftsY homolog F4118.25  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Date: 05-Mar-1999 #sequence\_revision 05-Mar-1999 #text\_change 16-Feb-2001  
 C;Accession: T02470; F84894  
 R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul  
 submitted to the EMBL Data Library, August 1998  
 A;Description: Arabidopsis thaliana chromosome II BAC F4118 genomic sequence.  
 A;Reference number: Z14674

A;Accession: T02470  
 A;Status: translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-373 <ROU>  
 A;Cross-references: EMBL:AC004665; NID:G3386593; PID:G3386617  
 A;Experimental source: cultivar Columbia  
 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.  
 eus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
 Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197  
 A;Accession: F84894  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-373 <STO>  
 A;Cross-references: GB:AE002093; NID:G3386617; PIDN:AAC28547.1; GSPDB:GN00139  
 C;Genetics:  
 A;Gene: F4118.25; At2g45770  
 A;Map position: 2  
 A;Introns: 102/3; 144/3; 169/2; 189/1; 201/3; 242/1; 265/1; 292/3; 315/3; 336/3

Query Match 92.9%; Score 26; DB 2; Length 373;  
 Best Local Similarity 83.3%; Pred. No. 4.2e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
 :|||||  
 Db 56 IREKAK 61

## RESULT 49

WBSDS  
 adenylsuccinate lyase (EC 4.3.2.2) - Bacillus subtilis  
 C;Species: Bacillus subtilis  
 C;Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 16-Jun-2000  
 C;Accession: C29326; A69684  
 R;Boole, D.J.; Zaikin, H.  
 J. Biol. Chem. 262, 8274-8287, 1987  
 A;Title: Cloning and characterization of a 12-gene cluster from Bacillus subtilis encoding adenylsuccinate lyase  
 A;Reference number: A29326; MUID:87250425; PMID:3036807  
 A;Accession: C29326  
 A;Molecule type: DNA  
 A;Residues: 1-431 <EBB>  
 A;Cross-references: EMBL:J02732; NID:G143363; PIDN:AAA22676.1; PID:G143366  
 R;Kunat, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertei  
 C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch  
 A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
 Nature 390, 249-256, 1997  
 A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall  
 iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.  
 Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois  
 A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue  
 Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetel  
 Bieger, M.; Rivolta, C.; Rocha E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon  
 A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero  
 akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpestra, P.; Tognoni, A.; Tosato, V.; Uchiyama  
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida  
 A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.  
 A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
 A;Reference number: A69580; MUID:98044033; PMID:9384377  
 A;Accession: A69684  
 A;Status: nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-431 <KUN>  
 A;Cross-references: GB:Z99107; GB:AL009126; NID:G2632866; PIDN:CAB12464.1; PID:G2632958  
 A;Experimental source: strain 168  
 C;Genetics:  
 A;Gene: purB  
 A;Map position: 18 min  
 C;Superfamily: fumarate hydratase  
 C;Keywords: amidine-lyase; carbon-nitrogen lyase; purine nucleotide biosynthesis

Query Match 92.9%; Score 26; DB 1; Length 431;  
 Best Local Similarity 83.3%; Pred. No. 4.8e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
 :|||||  
 Db 124 IREKAK 129

## RESULT 50

D90369

NADH oxidase SSO2025 [imported] - Sulfolobus solfataricus  
C:Species: Sulfolobus solfataricus  
C:Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 24-May-2001  
C:Accession: D90369  
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-  
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, R.  
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.  
submitted to GenBank, April 2001  
A:Description: Sulfolobus solfataricus complete genome.  
A:Reference number: A99139  
A:Accession: D90369  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-555 <KUR>  
A:Cross-references: GB:AE006641; NID:gi3815305; PIDN:AAK42211.1; GSPDB:GN00155  
C:Genetics:  
A:Gene: SSO2025

Query Match 92.9%; Score 26; DB 2; Length 555;  
Best Local Similarity 83.3%; Pred. No. 6.1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKEKAK 6  
:|||||  
Db 202 IREKAK 207

Search completed: April 19, 2004, 17:23:12  
Job time : 8 secs

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OM protein - protein search, using sw model

Run on: April 19, 2004, 17:13:16 ; Search time 17.1935 Seconds  
(without alignments)  
39.034 Million cell updates/sec

Title: US-10-726-692-20  
Perfect score: 73  
Sequence: 1 GHEGCRSAGEGS 13

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 50 summaries

Database : Issued Patents AA\*  
1: /cgn2\_6/ptodata/2/iaa/5A-COMB.pep:\*  
2: /cgn2\_6/ptodata/2/iaa/5B-COMB.pep:\*  
3: /cgn2\_6/ptodata/2/iaa/6A-COMB.pep:\*  
4: /cgn2\_6/ptodata/2/iaa/6B-COMB.pep:\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS-COMB.pep:\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	57.5	187	4	US-09-252-991A-26696
2	42	57.5	1073	4	US-09-252-991A-27341
3	41	56.2	178	4	US-09-252-991A-22153
4	41	56.2	642	4	US-09-252-991A-21889
5	41	56.2	711	4	US-09-252-991A-32397
6	41	56.2	846	1	US-08-356-354-2
7	41	56.2	846	2	US-08-778-656-2
8	41	56.2	908	1	US-08-356-354-6
9	41	56.2	908	2	US-08-778-656-6
10	41	56.2	1053	4	US-09-394-272-6
11	41	56.2	1054	1	US-08-356-354-4
12	41	56.2	1054	2	US-08-778-656-4
13	40	54.8	149	4	US-09-134-001C-3421
14	40	54.8	489	4	US-09-252-991A-16940
15	40	54.8	599	4	US-09-252-991A-20368
16	40	54.8	626	1	US-07-938-782A-2
17	40	54.8	626	1	US-08-630-524-2
18	40	54.8	626	4	US-09-578-441-5
19	40	54.8	626	5	PCT-US93-08131-2
20	39	53.4	137	4	US-09-252-991A-21910
21	39	53.4	443	4	US-09-252-991A-21563
22	39	53.4	469	4	US-09-347-650-16
23	38	52.1	142	4	US-09-252-991A-23673
24	38	52.1	184	4	US-09-252-991A-26628
25	38	52.1	259	4	US-09-252-991A-21547
26	38	52.1	458	4	US-09-252-991A-30327
27	38	52.1	461	4	US-09-345-473E-35

ALIGNMENTS

RESULT 1

US-09-252-991A-26696  
; Sequence 26696, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 26696  
; LENGTH: 187  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-26696

Query Match 57.5%; Score 42; DB 4; Length 187;  
Best Local Similarity 77.8%; Pred. No. 19;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GCRSAGEAG 12  
Db 1 GCRTGSAEG 9

RESULT 2

US-09-252-991A-27341  
; Sequence 27341, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 27341  
; LENGTH: 1073

; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: (803)  
; OTHER INFORMATION: Identity of amino acid at the above locations are unknown.  
US-09-252-991A-27341

Query Match 57.5%; Score 42; DB 4; Length 1073;

Best Local Similarity 50.0%; Pred. No. 1.1e+02; Indels 0; Gaps 0;  
Matches 6; Conservative 2; Mismatches 4;

QY 1 GHEGCRSGBAEG 12  
||:|||||:  
Db 890 GHQPCRGGSGQG 901

## RESULT 3

US-09-252-991A-22153  
; Sequence 22153, Application US/09252991A  
; Patent No. 6551795

; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A

; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 22153  
; LENGTH: 178

; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-22153

Query Match 56.2%; Score 41; DB 4; Length 178;

Best Local Similarity 53.8%; Pred. No. 27; Indels 0; Gaps 0;  
Matches 7; Conservative 1; Mismatches 5;

QY 1 GHEGCRSGBAEGS 13  
|:|||||:  
Db 96 GRGCRSGRGYGT 108

## RESULT 4

US-09-252-991A-21889  
; Sequence 21889, Application US/09252991A  
; Patent No. 6551795

; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A

; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 21889  
; LENGTH: 642

; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa

; FEATURE:

; NAME/KEY: UNSURE  
; LOCATION: (35)  
; OTHER INFORMATION: Identity of amino acid at the above locations are unknown.  
US-09-252-991A-21889

Query Match 56.2%; Score 41; DB 4; Length 642;  
Best Local Similarity 54.5%; Pred. No. 95;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GHEGCRSGEAE 11  
|:|||||:  
Db 565 GQGCRCRDGGE 575

## RESULT 5

US-09-252-991A-32397  
; Sequence 32397, Application US/09252991A  
; Patent No. 6551795

; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A

; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 32397  
; LENGTH: 711

; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-32397

Query Match 56.2%; Score 41; DB 4; Length 711;

Best Local Similarity 50.0%; Pred. No. 1.1e+02; Indels 0; Gaps 0;  
Matches 6; Conservative 2; Mismatches 4;

QY 2 HEGCRSGBAEGS 13  
|:|||||:  
Db 251 HPGCRHGDGRGT 262

## RESULT 6

US-08-356-354-2  
; Sequence 2, Application US/08356354  
; Patent No. 5767365

; GENERAL INFORMATION:  
; APPLICANT: SONNEWALD, Uwe

; TITLE OF INVENTION: DNA SEQUENCES AND PLASMIDS FOR THE  
; TITLE OF INVENTION: PREPARATION OF PLANTS WITH CHANGED SUCROSE CONCENTRATION

; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen  
; STREET: 1180 Avenue of the Americas

; CITY: New York  
; STATE: NY

; COUNTRY: US  
; ZIP: 10036-8403

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/356,354  
; FILING DATE: 20-DEC-1994

; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US PCT/EP93/01605  
; FILING DATE: 22-JUN-1993

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: DE P42 20 758.4  
;; FILING DATE: 24-JUN-1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Meilman, Edward A.  
;; REGISTRATION NUMBER: 24,735  
;; REFERENCE/DOCKET NUMBER: P/951-105  
;; TELEPHONE: (212) 382-0700  
;; TELEFAX: (212) 382-0888  
;; TELEX: 236925  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 846 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-356-354-2

Query Match 56.2%; Score 41; DB 1; Length 846;  
Best Local Similarity 66.7%; Pred. No. 1.3e+02;  
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 HEGCRSGEAGS 13  
||| |||  
Db 232 HEGDMDGETGS 243

RESULT 7  
US-08-778-656-2  
; Sequence 2, Application US/08778656  
; Patent No. 5976869  
; GENERAL INFORMATION:  
; APPLICANT: SONNEWALD, Uwe  
; TITLE OF INVENTION: 'DNA SEQUENCES AND PLASMIDS FOR THE  
; PREPARATION OF PLANTS WITH CHANGED SUCROSE CONCENTRATION  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen  
; STREET: 1180 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: US  
; ZIP: 10036-8403  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/778,656  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/356,354  
; FILING DATE: 20-DEC-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meilman, Edward A.  
; REGISTRATION NUMBER: 24,735  
; REFERENCE/DOCKET NUMBER: P/951-105  
; TELEPHONE: (212) 382-0700  
; TELEFAX: (212) 382-0888  
; TELEX: 236925  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 846 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-356-354-2

Query Match 56.2%; Score 41; DB 1; Length 846;  
Best Local Similarity 66.7%; Pred. No. 1.3e+02;  
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 HEGCRSGEAGS 13  
||| |||  
Db 232 HEGDMDGETGS 243

RESULT 7  
US-08-778-656-2  
; Sequence 2, Application US/08778656  
; Patent No. 5976869  
; GENERAL INFORMATION:  
; APPLICANT: SONNEWALD, Uwe  
; TITLE OF INVENTION: 'DNA SEQUENCES AND PLASMIDS FOR THE  
; PREPARATION OF PLANTS WITH CHANGED SUCROSE CONCENTRATION  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen  
; STREET: 1180 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: US  
; ZIP: 10036-8403  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/778,656  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/356,354  
; FILING DATE: 20-DEC-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meilman, Edward A.  
; REGISTRATION NUMBER: 24,735  
; REFERENCE/DOCKET NUMBER: P/951-105  
; TELEPHONE: (212) 382-0700  
; TELEFAX: (212) 382-0888  
; TELEX: 236925  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 846 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-356-354-2

;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-778-656-2

Query Match 56.2%; Score 41; DB 2; Length 846;  
Best Local Similarity 66.7%; Pred. No. 1.3e+02;  
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 HEGCRSGEAGS 13  
||| |||  
Db 232 HEGDMDGETGS 243

RESULT 8  
US-08-356-354-6  
; Sequence 6, Application US/08356354  
; Patent No. 5767365  
; GENERAL INFORMATION:  
; APPLICANT: SONNEWALD, Uwe  
; TITLE OF INVENTION: 'DNA SEQUENCES AND PLASMIDS FOR THE  
; PREPARATION OF PLANTS WITH CHANGED SUCROSE CONCENTRATION  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen  
; STREET: 1180 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: US  
; ZIP: 10036-8403  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/356,354  
; FILING DATE: 20-DEC-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US PCT/EP93/01605  
; FILING DATE: 22-JUN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE P42 20 758.4  
; FILING DATE: 24-JUN-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meilman, Edward A.  
; REGISTRATION NUMBER: 24,735  
; REFERENCE/DOCKET NUMBER: P/951-105  
; TELEPHONE: (212) 382-0700  
; TELEFAX: (212) 382-0888  
; TELEX: 236925  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 908 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-356-354-6

Query Match 56.2%; Score 41; DB 1; Length 908;  
Best Local Similarity 66.7%; Pred. No. 1.3e+02;  
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 HEGCRSGEAGS 13  
||| |||  
Db 294 HEGDMDGETGS 305

RESULT 9  
US-08-778-656-6  
; Sequence 6, Application US/08778656  
; Patent No. 5976869

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; GENERAL INFORMATION:
; APPLICANT: SONNEWALD, Uwe
; TITLE OF INVENTION: DNA SEQUENCES AND PLASMIDS FOR THE
; TITLE OF INVENTION: PREPARATION OF PLANTS WITH CHANGED SUCROSE CONCENTRATION
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen
; STREET: 1180 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10036-8403
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/778,656
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/356,354
; FILING DATE: 20-DEC-1994
; APPLICATION NUMBER: US PCT/EP93/01605
; FILING DATE: 22-JUN-1993
; PRIOR APPLICATION DATA: DE P42 20 758.4
; FILING DATE: 24-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Meilman, Edward A.
; REGISTRATION NUMBER: 24,735
; REFERENCE/DOCKET NUMBER: P/951-105
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 382-0700
; TELEFAX: (212) 382-0888
; TELEX: 236925
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 908 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-778-656-6

Query Match 56.2%; Score 41; DB 2; Length 908;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 HEGCRSGRAEGS 13
Db 294 HEGDMDGETEGS 305

RESULT 10
; Sequence 6, Application US/09394272
; Patent No. 6472588
; GENERAL INFORMATION:
; APPLICANT: Haigler, Candace H.
; APPLICANT: Holaday, A. Scott
; TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
; TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
; FILE REFERENCE: 201304/1000
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1053
; TYPE: PRT
; ORGANISM: Solanum tuberosum
; US-09-394-272-6

Query Match 56.2%; Score 41; DB 2; Length 908;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 HEGCRSGRAEGS 13
Db 294 HEGDMDGETEGS 305

US-09-394-272-6
; Sequence 6, Application US/09394272
; Patent No. 6472588
; GENERAL INFORMATION:
; APPLICANT: Haigler, Candace H.
; APPLICANT: Holaday, A. Scott
; TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
; TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
; FILE REFERENCE: 201304/1000
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1053
; TYPE: PRT
; ORGANISM: Solanum tuberosum
; US-09-394-272-6

Query Match 56.2%; Score 41; DB 4; Length 1053;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 HEGCRSGRAEGS 13
Db 439 HEGDMDGETEGS 450

RESULT 11
; US-08-356-354-4
; Sequence 4, Application US/08356354
; Patent No. 5767365
; GENERAL INFORMATION:
; APPLICANT: SONNEWALD, Uwe
; TITLE OF INVENTION: DNA SEQUENCES AND PLASMIDS FOR THE
; TITLE OF INVENTION: PREPARATION OF PLANTS WITH CHANGED SUCROSE CONCENTRATION
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen
; STREET: 1180 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10036-8403
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/356,354
; FILING DATE: 20-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/EP93/01605
; FILING DATE: 22-JUN-1993
; PRIOR APPLICATION DATA: DE P42 20 758.4
; FILING DATE: 24-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Meilman, Edward A.
; REGISTRATION NUMBER: 24,735
; REFERENCE/DOCKET NUMBER: P/951-105
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 382-0700
; TELEFAX: (212) 382-0888
; TELEX: 236925
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1054 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-356-354-4

Query Match 56.2%; Score 41; DB 1; Length 1054;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 HEGCRSGRAEGS 13
Db 440 HEGDMDGETEGS 451

RESULT 12
; US-08-778-656-4
; Sequence 4, Application US/08778656
; Patent No. 5976869
; GENERAL INFORMATION:
; APPLICANT: SONNEWALD, Uwe
; TITLE OF INVENTION: DNA SEQUENCES AND PLASMIDS FOR THE
```

TITLE OF INVENTION: PREPARATION OF PLANTS WITH CHANGED SUCROSE CONCENTRATION  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ostrolenk, Faber, Gorb & Soffen  
STREET: 1180 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: US  
ZIP: 10036-8403  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/778,656  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA: US 08/356,354  
FILING DATE: 20-DEC-1994  
APPLICATION NUMBER: US PCT/EP93/01605  
FILING DATE: 22-JUN-1993  
PRIOR APPLICATION DATA: DE P42 20 758.4  
FILING DATE: 24-JUN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Meilman, Edward A.  
REGISTRATION NUMBER: 24,735  
REFERENCE/DOCKET NUMBER: P/951-105  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 382-0700  
TELEFAX: (212) 382-0888  
TELEX: 236925  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1054 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-778-656-4

Query Match 56.2%; Score 41; DB 2; Length 1054;  
Best Local Similarity 66.7%; Pred. No. 1.6e+02;  
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 HEGCRSGEAGS 13  
||| ||| |||  
Db 440 HEGDMDGTEGS 451

RESULT 13  
US-09-134-001C-3421  
Sequence 3421, Application US/09134001C  
Patent No. 6380370  
GENERAL INFORMATION:  
APPLICANT: Lynn Doucette-Stamm et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: GTC-007  
CURRENT APPLICATION NUMBER: US/09/134,001C  
CURRENT FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US 60/064,964  
PRIOR FILING DATE: 1997-11-08  
PRIOR APPLICATION NUMBER: US 60/055,779  
PRIOR FILING DATE: 1997-08-14  
NUMBER OF SEQ ID NOS: 5674  
SEQ ID NO 3421  
LENGTH: 149  
TYPE: PRT  
ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-3421

Query Match 54.8%; Score 40; DB 4; Length 149;  
Best Local Similarity 75.0%; Pred. No. 32;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHEGCRSG 8  
||| ||| |||  
Db 135 GHGCGASG 142

RESULT 14  
US-09-252-991A-16940  
Sequence 16940, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 16940  
LENGTH: 489  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-16940

Query Match 54.8%; Score 40; DB 4; Length 489;  
Best Local Similarity 77.8%; Pred. No. 1e+02;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCRCGEAGG 12  
||| ||| |||  
Db 354 GCRAGEAGG 362

RESULT 15  
US-09-252-991A-20368  
Sequence 20368, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 20368  
LENGTH: 599  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-20368

Query Match 54.8%; Score 40; DB 4; Length 599;  
Best Local Similarity 53.8%; Pred. No. 1.3e+02;  
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 GHEGCRSGEAGS 13  
||| ||| |||  
Db 377 GHDRGRGQAECA 389

RESULT 16  
US-07-938-782A-2

; Sequence 2, Application US/07938782A  
; Patent No. 5525513  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Jane J.  
; APPLICANT: London, Irving M.  
; TITLE OF INVENTION: DNA Encoding the Heme-Regulated  
; TITLE OF INVENTION: Eukaryotic Initiation Factor 2 alpha kinase  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patrea L. Pabst  
; STREET: 2800 One Atlantic Center  
; STREET: 1201 West Peachtree Street  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: US  
; ZIP: 30309-3450  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/938,782A  
; FILING DATE: 31-AUG-1992  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pabst, Patrea L.  
; REGISTRATION NUMBER: 31,284  
; REFERENCE/DOCKET NUMBER: WU101CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (404)873-8794  
; TELEFAX: (404)873-8795  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 626 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: N-terminal  
; ORIGINAL SOURCE:  
; ORGANISM: Rabbit  
; CELL TYPE: Reticulocytes  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 166..170  
; OTHER INFORMATION: /label= P-56  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 454..459  
; OTHER INFORMATION: /label= P-52  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 506..510  
; OTHER INFORMATION: /label= P-74  
; US-07-938-782A-2

Query Match 54.8%; Score 40; DB 1; Length 626;  
Best Local Similarity 66.7%; Pred. No. 1.3e+02;  
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GHEGCRSGEAE 12  
| | | | |  
Db 4 GSAGTRGGEAE 15

RESULT 17  
US-08-630-524-2  
; Sequence 2, Application US/08630524  
; Patent No. 5690930  
; GENERAL INFORMATION:

; APPLICANT: Chen, Jane J.  
; APPLICANT: London, Irving M.  
; TITLE OF INVENTION: DNA Encoding the Heme-Regulated  
; TITLE OF INVENTION: Eukaryotic Initiation Factor 2 alpha kinase  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patrea L. Pabst  
; STREET: 2800 One Atlantic Center  
; STREET: 1201 West Peachtree Street  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: US  
; ZIP: 30309-3450  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/630,524  
; FILING DATE: 10-APR-1996  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/938,782  
; FILING DATE: 31-AUG-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pabst, Patrea L.  
; REGISTRATION NUMBER: 31,284  
; REFERENCE/DOCKET NUMBER: WU101CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (404)873-8794  
; TELEFAX: (404)873-8795  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 626 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: N-terminal  
; ORIGINAL SOURCE:  
; ORGANISM: Rabbit  
; CELL TYPE: Reticulocytes  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 166..170  
; OTHER INFORMATION: /label= P-56  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 454..459  
; OTHER INFORMATION: /label= P-52  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 506..510  
; OTHER INFORMATION: /label= P-74  
; US-08-630-524-2

Query Match 54.8%; Score 40; DB 1; Length 626;  
Best Local Similarity 66.7%; Pred. No. 1.3e+02;  
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GHEGCRSGEAE 12  
| | | | |  
Db 4 GSAGTRGGEAE 15

RESULT 18  
US-09-578-441-5  
; Sequence 5, Application US/09578441  
; Patent No. 6562571  
; GENERAL INFORMATION:

APPLICANT: Wu, J.H. David  
APPLICANT: Omata, Takeshi  
APPLICANT: Mantalaris, Athanassios  
APPLICANT: Chen, Yi-Guang  
APPLICANT: Tsai, Ying-Chueh  
TITLE OF INVENTION: HUMAN HEME-REGULATED INITIATION FACTOR 2.ALPHA KINASE  
FILE REFERENCE: 176/60571  
CURRENT APPLICATION NUMBER: US/09/578,441  
CURRENT FILING DATE: 2000-05-25  
PRIOR APPLICATION NUMBER: 60/135,713  
PRIOR FILING DATE: 1999-05-25  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 5  
LENGTH: 626  
TYPE: PRT  
ORGANISM: Oryctolagus cuniculus  
US-09-578-441-5

Query Match 54.8%; Score 40; DB 4; Length 626;  
Best Local Similarity 66.7%; Pred. No. 1.3e+02;  
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GHEGCRSGEAG 12  
| | | | |  
Db 4 GSAGTRGGEAG 15

RESULT 19  
PCT-US93-08131-2  
Sequence 2, Application PC/TUS9308131  
GENERAL INFORMATION:  
APPLICANT: Massachusetts Institute of Technology  
TITLE OF INVENTION: DNA Encoding the Heme-Regulated  
TITLE OF INVENTION: Eukaryotic Initiation Factor 2 alpha Kinase  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kilpatrick & Cody  
STREET: 1100 Peachtree Street  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: US  
ZIP: 30309

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/08131  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: MIT 5807  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404-815-6508  
TELEFAX: 404-815-6555  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 626 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Rabbit  
CELL TYPE: Reticulocytes  
FEATURE:

NAME/KEY: Peptide  
LOCATION: 166..170  
OTHER INFORMATION: /label= P-56  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 454..459  
OTHER INFORMATION: /label= P-52  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 506..510  
OTHER INFORMATION: /label= P-74  
PCT-US93-08131-2

Query Match 54.8%; Score 40; DB 5; Length 626;  
Best Local Similarity 66.7%; Pred. No. 1.3e+02;  
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GHEGCRSGEAG 12  
| | | | |  
Db 4 GSAGTRGGEAG 15

RESULT 20  
US-09-252-991A-21910  
Sequence 21910, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 21910  
LENGTH: 137  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-21910

Query Match 53.4%; Score 39; DB 4; Length 137;  
Best Local Similarity 70.0%; Pred. No. 42;  
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GHEGCRSGEA 10  
| | | | |  
Db 68 GHGCGSGAA 77

RESULT 21  
US-09-252-991A-21563  
Sequence 21563, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 21563  
LENGTH: 443  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-21563

Query Match 53.4%; Score 39; DB 4; Length 443;  
Best Local Similarity 58.3%; Pred. No. 1.4e+02;  
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GHEGCRSGAEG 12  
|||||:|:|  
Db 342 GHEGSAAGQALG 353

RESULT 22

US-09-347-650-16  
Sequence 16, Application US/09347650  
Patent No. 6576814  
GENERAL INFORMATION:

APPLICANT: Briggs, Steven  
TITLE OF INVENTION: Manipulation of Mlo Genes to Enhance Disease Resistance  
FILE REFERENCE: 5718-42035718/158714  
CURRENT APPLICATION NUMBER: US/09/347,650  
CURRENT FILING DATE: 1999-07-06  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 16  
LENGTH: 469  
TYPE: PRT  
ORGANISM: Zea mays  
FEATURE:  
OTHER INFORMATION: Mlo9

US-09-347-650-16

Query Match 53.4%; Score 39; DB 4; Length 469;  
Best Local Similarity 85.7%; Pred. No. 1.4e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 HEGCRSG 8  
|||||  
Db 14 HEGCREG 20

RESULT 23

US-09-252-991A-23673  
Sequence 23673, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 23673  
LENGTH: 142  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-23673

Query Match 52.1%; Score 38; DB 4; Length 142;  
Best Local Similarity 60.0%; Pred. No. 63;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCRSGAEGS 13  
|||||:|:  
Db 129 GCRSGSRGA 138

RESULT 24

US-09-252-991A-26628  
Sequence 26628, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 26628  
LENGTH: 184  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-26628

Query Match 52.1%; Score 38; DB 4; Length 184;  
Best Local Similarity 66.7%; Pred. No. 81;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCRSGAEG 12  
|||||:|:  
Db 1 GCRSGSAG 9

RESULT 25

US-09-252-991A-21547  
Sequence 21547, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 21547  
LENGTH: 259  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-21547

Query Match 52.1%; Score 38; DB 4; Length 259;  
Best Local Similarity 54.5%; Pred. No. 1.1e+02;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GHEGCRSGAEG 11  
|||||:|:  
Db 182 GHSGRGAAPRE 192

RESULT 26

US-09-252-991A-30327  
Sequence 30327, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788



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; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30327
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30327

Query Match      52.1%; Score 38; DB 4; Length 458;
Best Local Similarity 50.0%; Pred. No. 2e+02;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      3  EGCRSGAEG 12
      :||:|:|
Db      27  QGCGAGDGE 36

RESULT 27
US-09-345-473E-35
; Sequence 35, Application US/09345473E
; Patent No. 6558903
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin
; TITLE OF INVENTION: No. 6558903el Kinases and Uses Thereof
; FILE REFERENCE: 35800/183781
; CURRENT APPLICATION NUMBER: US/09/345,473E
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 461
; TYPE: PRT
; ORGANISM: C. elegans
US-09-345-473E-35

Query Match      52.1%; Score 38; DB 4; Length 461;
Best Local Similarity 50.0%; Pred. No. 2e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      1  GHEGCRSGAEG 12
      |:||:|:|
Db      65  GLSGCGQSGSEG 76

RESULT 28
US-09-489-039A-8129
; Sequence 8129, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 8129
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8129

Query Match      52.1%; Score 38; DB 4; Length 485;
Best Local Similarity 75.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  GHEGCRSG 8
      |||:|:|
Db      279  GHGCRIG 286

RESULT 29
US-09-252-991A-25203
; Sequence 25203, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25203
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25203

Query Match      52.1%; Score 38; DB 4; Length 518;
Best Local Similarity 46.2%; Pred. No. 2.3e+02;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      1  GHEGCRSGAEGS 13
      :||:|:|
Db      306  GDRCRCQGQARGA 318

RESULT 30
US-09-134-000C-4677
; Sequence 4677, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4677
; LENGTH: 910
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-4677

Query Match      52.1%; Score 38; DB 4; Length 910;
Best Local Similarity 75.0%; Pred. No. 4e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  GHEGCRSG 8
      |||:|:|
Db      688  GHRGCRLG 695

RESULT 31
US-09-314-268-162
; Sequence 162, Application US/09314268
; Patent No. 6346377
; GENERAL INFORMATION:
; APPLICANT: Doorbar, John
; TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO SCREENING FOR PAPILLOMA
; FILE REFERENCE: 3789/80902
; CURRENT APPLICATION NUMBER: US/09/314,268
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; CURRENT FILING DATE: 1999-03-19  
; EARLIER APPLICATION NUMBER: 09/314,268  
; EARLIER FILING DATE: 1999-05-18  
; NUMBER OF SEQ ID NOS: 179  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 162  
; TYPE: PRT  
; LENGTH: 34  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: cottontail rabbit  
; OTHER INFORMATION: papillomavirus  
US-09-314-268-162

Query Match 50.7%; Score 37; DB 4; Length 34;  
Best Local Similarity 62.5%; Pred. No. 22;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHEGCRSG 8  
||:||||  
Db 15 GHQGCNEG 22

RESULT 32  
US-09-166-350-16  
; Sequence 16, Application US/09166350A  
; Patent No. 6440663  
; GENERAL INFORMATION:  
; APPLICANT: Scanlan, Matthew  
; APPLICANT: Chen, Yao  
; APPLICANT: Stockert, Elisabeth  
; APPLICANT: Old, Lloyd  
; APPLICANT: Jager, Eike  
; APPLICANT: Knuth, Alex  
; TITLE OF INVENTION: Renal Cancer Associated Antigens and  
; TITLE OF INVENTION: Uses Therefor  
; FILE REFERENCE: L0461/7051  
; CURRENT APPLICATION NUMBER: US/09/166,350A  
; EARLIER FILING DATE: 1998-10-05  
; EARLIER APPLICATION NUMBER: US 09/166,350  
; EARLIER FILING DATE: 1998-10-05  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 16  
; LENGTH: 172  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-166-350-16

Query Match 50.7%; Score 37; DB 4; Length 172;  
Best Local Similarity 50.0%; Pred. No. 1.1e+02;  
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHEGCRSGEA 10  
||:||||:  
Db 14 GHQSCRLGDS 23

RESULT 33  
US-09-252-991A-27694  
; Sequence 27694, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 27694  
; LENGTH: 223  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-27694

Query Match 50.7%; Score 37; DB 4; Length 223;  
Best Local Similarity 66.7%; Pred. No. 1.4e+02;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 HEGCRSGEA 10  
|||||  
Db 66 HRCGRQGEPA 74

RESULT 34  
US-09-252-991A-31788  
; Sequence 31788, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 31788  
; LENGTH: 372  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-31788

Query Match 50.7%; Score 37; DB 4; Length 372;  
Best Local Similarity 66.7%; Pred. No. 2.4e+02;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GCRSGEAGEG 12  
|||||  
Db 50 GCHGGEAGEG 58

RESULT 35  
US-09-252-991A-29057  
; Sequence 29057, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 29057  
; LENGTH: 467  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-29057

Query Match 50.7%; Score 37; DB 4; Length 467;  
Best Local Similarity 63.6%; Pred. No. 3e+02;  
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GHEGCRSGEAB 11  
|: |||||  
Db 73 GYRGARSGAEG 83

RESULT 36  
US-09-252-991A-20429  
; Sequence 20429, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 20429  
; LENGTH: 478  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-20429

Query Match 50.7%; Score 37; DB 4; Length 478;  
Best Local Similarity 60.0%; Pred. No. 3e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 3; Gaps 0;

QY 1 GHEGCRSGEAB 10  
|| |||||  
Db 246 GHRRCRAGRA 255

RESULT 37  
US-09-252-991A-27765  
; Sequence 27765, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 27765  
; LENGTH: 586  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-27765

Query Match 50.7%; Score 37; DB 4; Length 586;  
Best Local Similarity 58.3%; Pred. No. 3.7e+02;  
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GHEGCRSGEAB 12  
|| |||||  
Db 401 GNGSRSGRADG 412

RESULT 38  
US-09-252-991A-30673  
; Sequence 30673, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 30673  
; LENGTH: 593  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-30673

Query Match 50.7%; Score 37; DB 4; Length 593;  
Best Local Similarity 66.7%; Pred. No. 3.8e+02;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GCRSGEAB 12  
|| |||||  
Db 490 GCHGGEAG 498

RESULT 39  
US-09-252-991A-31187  
; Sequence 31187, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 31187  
; LENGTH: 649  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-31187

Query Match 50.7%; Score 37; DB 4; Length 649;  
Best Local Similarity 46.2%; Pred. No. 4.1e+02;  
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHEGCRSGEAB 13  
|: |||||  
Db 384 GNLGAGEAGQT 396

RESULT 40  
US-09-252-991A-30056  
; Sequence 30056, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 30056

; LENGTH: 875  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-30056

Query Match 50.7%; Score 37; DB 4; Length 875;  
Best Local Similarity 71.4%; Pred. No. 5.5e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 HEGCRSG 8  
|:|:|:|  
DB 158 HQCRAG 164

RESULT 41  
US-08-727-034-3  
; Sequence 3, Application US/08727034  
; Patent No. 5665872  
; GENERAL INFORMATION:  
; APPLICANT: SAITO, YASHUSHI  
; APPLICANT: IWASAKI, AKIO  
; APPLICANT: ARAI, KOICHI  
; APPLICANT: YAMAZAKI, HIROYUKI  
; TITLE OF INVENTION: NOVEL LDL RECEPTOR ANALOG PROTEIN AND  
; TITLE OF INVENTION: THE GENE CODING THEREFOR  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
; ADDRESSEE: P.C.  
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22202

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/727,034  
; FILING DATE: 08-OCT-1996  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 261440/1995  
; FILING DATE: 09-OCT-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 102451/1996  
; FILING DATE: 24-APR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OBLON, NORMAN F.  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 80-079-0  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-413-3000  
; TELEFAX: 703-413-2220  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2213 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-727-034-3

Query Match 50.7%; Score 37; DB 1; Length 2213;  
Best Local Similarity 38.5%; Pred. No. 1.4e+03;  
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 HEGCRSGEAGS 13  
|:|:|:|:|  
DB 1492 GHQDCQDQDEAN 1504

RESULT 42  
US-09-489-039A-13756  
; Sequence 13756, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709-2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 13756  
; LENGTH: 398  
; TYPE: PRT  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-13756

0;

Query Match 50.0%; Score 36.5; DB 4; Length 398;  
Best Local Similarity 69.2%; Pred. No. 3e+02;  
Matches 9; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 1 GHEGCRSGE-AEG 12  
|:|:|:|:|:|  
DB 300 GHKGRVGEAEG 312

RESULT 43  
US-08-874-569B-14  
; Sequence 14, Application US/08874569B  
; Patent No. 6306650  
; GENERAL INFORMATION:  
; APPLICANT: Townes, Tim M.  
; APPLICANT: Donze, David  
; TITLE OF INVENTION: DELTA-ERYTHROID KRUPPEL-LIKE FACTORS AND  
; TITLE OF INVENTION: METHODS OF USE  
; FILE REFERENCE: 05118.0008U2  
; CURRENT APPLICATION NUMBER: US/08/874,569B  
; CURRENT FILING DATE: 1997-06-13  
; PRIOR APPLICATION NUMBER: 60/019,769  
; PRIOR FILING DATE: 1996-06-14  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 23  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:\ No. 6306650e =  
US-08-874-569B-14

Query Match 49.3%; Score 36; DB 4; Length 23;  
Best Local Similarity 46.2%; Pred. No. 21;  
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 GHEGCRSGEAGS 13  
|:|:|:|:|:|  
DB 2 GHEGCGKSYSKS 14

RESULT 44  
US-09-955-518-14  
; Sequence 14, Application US/09955518  
; Patent No. 6475740  
; GENERAL INFORMATION:  
; APPLICANT: Townes, Tim M.  
; APPLICANT: Donze, David  
; TITLE OF INVENTION: DELTA-ERYTHROID KRUPPEL-LIKE FACTORS AND  
; TITLE OF INVENTION: METHODS OF USE  
; FILE REFERENCE: 05118.0008U2

;; CURRENT APPLICATION NUMBER: US/09/955,518  
;; CURRENT FILING DATE: 2001-09-18  
;; PRIOR APPLICATION NUMBER: 60/019,769  
;; PRIOR FILING DATE: 1996-06-14  
;; NUMBER OF SEQ ID NOS: 21  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 14  
;; LENGTH: 23  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: \ No. 6475740e =  
;; OTHER INFORMATION: synthetic construct  
US-09-955-518-14

Query Match 49.3%; Score 36; DB 4; Length 23;  
Best Local Similarity 46.2%; Pred. No. 21;  
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 GHEGCRSGEAGS 13  
||| |  
Db 2 GHEGCGKSYKSS 14  
||| |

RESULT 45  
US-08-570-227A-9  
;; Sequence 9, Application US/08570227A  
;; Patent No. 5981217  
;; GENERAL INFORMATION:  
;; APPLICANT: Subramaniam, M.  
;; APPLICANT: Spelsberg, T. C.  
;; TITLE OF INVENTION: DNA ENCODING TGF-BETA INDUCIBLE  
;; TITLE OF INVENTION: EARLY FACTOR-1 (TIEF-1), A GENE EXPRESSED  
;; TITLE OF INVENTION: BY OSTEOBLASTS  
;; NUMBER OF SEQUENCES: 11  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A.  
;; STREET: P.O. Box 2938  
;; CITY: Minneapolis  
;; STATE: MN  
;; COUNTRY: USA  
;; ZIP: 55402

;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: DOS  
;; SOFTWARE: FastSeq Version 2.0  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/570,227A  
;; FILING DATE: 11-DEC-1995  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER:  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Woessner, Warren D  
;; REGISTRATION NUMBER: 30,440  
;; REFERENCE/DOCKET NUMBER: 150.157US1  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 612-359-3260  
;; TELEFAX: 612-359-3263  
;; TELEX:  
;; INFORMATION FOR SEQ ID NO: 9:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 77 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-570-227A-9

Query Match 49.3%; Score 36; DB 2; Length 77;  
Best Local Similarity 46.2%; Pred. No. 71;

Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
QY 1 GHEGCRSGEAGS 13  
||| |  
Db 2 GHEGCGKSYKSS 14  
||| |

RESULT 46  
US-09-077-991-11  
;; Sequence 11, Application US/09077991  
;; Patent No. 6207375  
;; GENERAL INFORMATION:  
;; APPLICANT: Subramaniam, M.  
;; APPLICANT: Spelsberg, T.C.  
;; APPLICANT: Roche, P.C.  
;; TITLE OF INVENTION: TGF-Beta inducible early factor-1  
;; TITLE OF INVENTION: (TIEF-1) and a method to detect breast cancer  
;; FILE REFERENCE: 150.157US2  
;; CURRENT APPLICATION NUMBER: US/09/077,991  
;; CURRENT FILING DATE: 1998-07-07  
;; EARLIER APPLICATION NUMBER: PCT/US96/19555  
;; EARLIER FILING DATE: 1996-12-11  
;; EARLIER APPLICATION NUMBER: US 08/570,227  
;; EARLIER FILING DATE: 1995-12-11  
;; NUMBER OF SEQ ID NOS: 13  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO 11  
;; LENGTH: 77  
;; TYPE: PRT  
;; ORGANISM: Mus musculus  
US-09-077-991-11

Query Match 49.3%; Score 36; DB 3; Length 77;  
Best Local Similarity 46.2%; Pred. No. 71;  
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 GHEGCRSGEAGS 13  
||| |  
Db 2 GHEGCGKSYKSS 14  
||| |

RESULT 47  
US-09-071-035-434  
;; Sequence 434, Application US/09071035  
;; Patent No. 6448043  
;; GENERAL INFORMATION:  
;; APPLICANT: Gil H. Choi  
;; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides  
;; NUMBER OF SEQUENCES: 496  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Human Genome Sciences, Inc.  
;; STREET: 9410 Key West Avenue  
;; CITY: Rockville  
;; STATE: Maryland  
;; COUNTRY: USA  
;; ZIP: 20850  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
;; COMPUTER: HP Vectra 486/33  
;; OPERATING SYSTEM: MSDOS version 6.2  
;; SOFTWARE: ASCII Text  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/071,035  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER:  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: A. Anders Brookes  
;; REGISTRATION NUMBER: 36,373  
;; REFERENCE/DOCKET NUMBER: PB369P2  
;; TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512  
INFORMATION FOR SEQ ID NO: 434:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 128 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-071-035-434

Query Match 49.3%; Score 36; DB 4; Length 128;  
Best Local Similarity 75.0%; Pred. No. 1.2e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCRSGEAE 11  
||:|||||  
DB 16 GCKSGEKE 23

RESULT 48  
US-09-134-000C-6310  
Sequence 6310, Application US/09134000C  
Patent No. 6617156  
GENERAL INFORMATION:  
APPLICANT: Lynn Doucette-Stamm et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

FILE REFERENCE: 032796-032  
CURRENT APPLICATION NUMBER: US/09/134,000C  
PRIOR FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US 60/055,778  
PRIOR FILING DATE: 1997-08-15  
NUMBER OF SEQ ID NOS: 6812  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 6310  
LENGTH: 135  
TYPE: PRT  
ORGANISM: Enterococcus faecalis  
US-09-134-000C-6310

Query Match 49.3%; Score 36; DB 4; Length 135;  
Best Local Similarity 75.0%; Pred. No. 1.2e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCRSGEAE 11  
||:|||||  
DB 23 GCKSGEKE 30

RESULT 49  
US-09-252-991A-25250  
Sequence 25250, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
PRIOR FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 25250  
LENGTH: 151  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-25250

Query Match 49.3%; Score 36; DB 4; Length 151;

Best Local Similarity 66.7%; Pred. No. 1.4e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCRSGEAE 12  
||||:|  
DB 26 GCRSGQHNG 34

RESULT 50  
US-09-252-991A-19744  
Sequence 19744, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
PRIOR FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 19744  
LENGTH: 162  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-19744

Query Match 49.3%; Score 36; DB 4; Length 162;  
Best Local Similarity 75.0%; Pred. No. 1.5e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHEGCRSG 8  
|:|||||  
DB 33 GRSGCRSG 40

Search completed: April 19, 2004, 17:24:47  
Job time : 18.1935 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 19, 2004, 17:11:35 ; Search time 38.5806 Seconds  
(without alignments)  
106.316 Million cell updates/sec

Title: US-10-726-692-20

Perfect score: 73

Sequence: 1 GHEGCRSGEAGS 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 50 summaries

Database :

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	60.3	261	10 Q94LD2	Q94ld2 oryza sativ
2	44	60.3	802	4 Q9Y2J5	Q9y2j5 homo sapien
3	44	60.3	802	4 Q8X52	Q8x52 homo sapien
4	43	58.9	118	10 Q7XP56	Q7xp56 oryza sativ
5	43	58.9	1537	4 Q8WY29	Q8wy29 homo sapien
6	43	58.9	4599	4 Q8NZR2	Q8nzz2 homo sapien
7	42	57.5	124	10 Q8H2G9	Q8h2g9 oryza sativ
8	42	57.5	186	5 Q9TFX2	Q9tfx2 lumbricus t
9	42	57.5	261	10 Q43150	Q43150 sambucus ni
10	42	57.5	266	10 Q9FP09	Q9fp09 oryza sativ
11	42	57.5	466	16 Q88Q52	Q88q52 pseudomonas
12	42	57.5	997	3 Q74242	Q74242 cryptococcu
13	42	57.5	1429	5 Q21213	Q21213 caenorhabdi
14	41	56.2	263	16 Q82Q46	Q82q46 streptomyce
15	41	56.2	605	16 Q89VW1	Q89vw1 bradyrhizob
16	41	56.2	703	2 Q9PBF9	Q9pbf9 uncultured

17	41	56.2	716	5 Q9BL30	Q9bl30 caenorhabdi
18	41	56.2	4599	11 Q9J118	Q9j118 mus musculoc
19	40	54.8	144	16 Q8CT00	Q8ct00 staphylococ
20	40	54.8	152	12 Q70885	Q70885 equine arte
21	40	54.8	152	12 Q9PX34	Q9px34 equine arte
22	40	54.8	152	12 Q9WEX9	Q9wex9 equine arte
23	40	54.8	152	12 Q9PX35	Q9px35 equine arte
24	40	54.8	152	12 Q70882	Q70882 equine arte
25	40	54.8	152	12 Q70880	Q70880 equine arte
26	40	54.8	152	12 Q70881	Q70881 equine arte
27	40	54.8	152	12 Q88674	Q88674 equine arte
28	40	54.8	152	12 Q70879	Q70879 equine arte
29	40	54.8	152	12 Q70886	Q70886 equine arte
30	40	54.8	152	12 Q9QKH1	Q9qkh1 equine arte
31	40	54.8	152	12 Q70883	Q70883 equine arte
32	40	54.8	152	12 Q9QKF2	Q9qkf2 equine arte
33	40	54.8	209	16 Q7URS4	Q7urs4 rhodopirell
34	40	54.8	224	10 Q8SOH3	Q8soh3 oryza sativ
35	40	54.8	292	2 Q8GFC1	Q8gfc1 photorhabdu
36	40	54.8	310	5 Q8IHK4	Q8ihk4 babesia div
37	40	54.8	331	5 Q8IHK2	Q8ihk2 babesia div
38	40	54.8	340	16 Q92P75	Q92p75 rhizobium m
39	40	54.8	341	5 Q8T117	Q8t117 babesia div
40	40	54.8	341	5 Q8IHK5	Q8ihk5 babesia div
41	40	54.8	353	7 Q9BCW3	Q9bcw3 gallus gall
42	40	54.8	379	2 Q9EYU5	Q9eyu5 rhizobium l
43	40	54.8	379	16 Q98AW1	Q98aw1 rhizobium l
44	40	54.8	384	16 Q9AMS5	Q9ams5 bradyrhizob
45	40	54.8	491	5 Q9U135	Q9u135 leishmania
46	40	54.8	629	10 Q8S1A6	Q8s1a6 oryza sativ
47	40	54.8	703	2 Q9EXP9	Q9exp9 bacteroides
48	40	54.8	1005	13 Q7T2V3	Q7t2v3 xenopus lae
49	40	54.8	1017	5 Q8SQJ6	Q8sqj6 encephalito
50	39	53.4	131	13 Q98UD3	Q98ud3 xenopus lae

ALIGNMENTS

RESULT 1

Q94LD2 PRELIMINARY; PRT; 261 AA.

AC Q94LD2;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Oryza sativa (Rice).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzaceae; Oryza.  
OX NCBI\_TaxID=4530;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Nipponbare;  
RA Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Ganeberg K.,  
RA Brenner M., Burgess S., Hance M., Shvartsbeyn M., Tsitrin T.,  
RA Riggs F., Hsiao J., Ziemann V., Blunt S., Pai G., Vanaken S.E.,  
RA Utterback T.R., Feldblyum T.V., Quackenbush J., Salzberg S.L.,  
RA White O., Fraser C.M.;  
RT "Oryza sativa chromosome 3 BAC OSJNBA0026A15 genomic sequence."  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AC084404; AAK50593.1; -  
DR Gramene; Q94LD2; -  
KW Hypothetical protein.  
SQ SEQUENCE 261 AA; 27090 MW; 4FCFB97E2910A498 CRC64;

Query Match 60.3%; Score 44; DB 10; Length 261;

Best Local Similarity 68.8%; Pred. No. 13;

Matches 11; Conservative 1; Mismatches 0; Indels 4; Gaps 2;

QY 1 GHE--GCR--SGEARG 12

||: ||| |||||

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Db 52 CHDGRSGCRNSGEAEG 67

RESULT 2
Q9Y2J5 PRELIMINARY; PRT; 802 AA.
ID Q9Y2J5
AC Q9Y2J5;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein KIAA0990 (Chondroitin synthase).
DE KIAA0990 OR CHSY.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=99246063; PubMed=10231032;
RA Nagase T., Ishikawa K., Suyama H., Kikuno R., Hirose M.,
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XIII.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 6:63-70(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21486534; PubMed=11514575;
RA Kitagawa H., Uyama T., Sugahara K.;
RT "Molecular Cloning and Expression of a Human Chondroitin Synthase.";
RL J. Biol. Chem. 276:38721-38726(2001).
DR EMBL; AB023207; BAA76834.1; -.
DR EMBL; AB071402; BAB64936.1; -.
DR InterPro; IPR008428; CHGN.
DR Pfam; PF05679; CHGN; 1.
KW Hypothetical protein.
SQ SEQUENCE 802 AA; 91729 MW; 9115C204FAP298D7 CRC64;

Query Match 60.3%; Score 44; DB 4; Length 802;
Best Local Similarity 72.7%; Pred. No. 39;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGCRSGEAEGS 13
Db 46 EGCRSQQAAS 56

RESULT 3
Q86X52 PRELIMINARY; PRT; 802 AA.
ID Q86X52
AC Q86X52;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Carbohydrate (Chondroitin) synthase 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC046247; AAH46247.1; -.
SQ SEQUENCE 802 AA; 91784 MW; 5B4C02670332FA0E CRC64;

Query Match 60.3%; Score 44; DB 4; Length 802;
Best Local Similarity 72.7%; Pred. No. 39;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGCRSGEAEGS 13

Db 52 CHDGRSGCRNSGEAEG 67

RESULT 4
Q7XP56 PRELIMINARY; PRT; 118 AA.
ID Q7XP56
AC Q7XP56;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE OSUNBA0013K16.11 protein.
DE OSUNBA0013K16.11.
GN OSUNBA0013K16.11.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Han B., Feng Q., Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X.,
RA Liu Y.L., Mu J., Yu Z., Chen L., Fan D.L., Meng Q.J., Zhang L.,
RA Lu Y.Q., Yu S.L., Liu X.H., Lu T.T., Zhang Y.J., Lu Y., Li C., Li T.,
RA Zhang Y., Hu H., Jia P.X., Qian Y.M., Ying K., Zhou B., Chen Z.H.,
RA Hao P., Zhang L., Wu M., Zhang R.Q., Guan J.P., Fu G., Wang S.Y.,
RA Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.P., Tu Y.F., Jia J., Yin H.F.,
RA Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y., Shao C.Y., Sun Y.,
RA Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W., Sheng H.H.,
RA Gu J.L., Chen S.T., Ni L., Zhu F.H., Hong G.F.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL662957; CAE03762.1; -.
SQ SEQUENCE 118 AA; 12527 MW; A6A9F45B83270D33 CRC64;

Query Match 58.9%; Score 43; DB 10; Length 118;
Best Local Similarity 72.7%; Pred. No. 8.9;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 HEGCRSGEAEG 12
Db 97 HGGCRSEEEG 107

RESULT 5
Q8WY29 PRELIMINARY; PRT; 1537 AA.
ID Q8WY29
AC Q8WY29;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Candidate tumor suppressor protein (Fragment).
DE LRP1B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20487554; PubMed=11031110;
RA Liu C.-X., Musco S., Lisitsyna N.M., Yaklichkin S.Y., Lisitsyn N.A.;
RT "Genomic organization of a new candidate tumor suppressor gene,
RT LRP1B.";
RL Genomics 69:271-274(2000).
DR EMBL; AF283408; AAL38109.1; -.
DR EMBL; AF283376; AAL38109.1; JOINED.
DR EMBL; AF283377; AAL38109.1; JOINED.
DR EMBL; AF283378; AAL38109.1; JOINED.
DR EMBL; AF283379; AAL38109.1; JOINED.
DR EMBL; AF283380; AAL38109.1; JOINED.
DR EMBL; AF283381; AAL38109.1; JOINED.
DR EMBL; AF283382; AAL38109.1; JOINED.
DR EMBL; AF283383; AAL38109.1; JOINED.
DR EMBL; AF283384; AAL38109.1; JOINED.
DR EMBL; AF283385; AAL38109.1; JOINED.
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DR EMBL; AF283386; AAL38109.1; JOINED.
DR EMBL; AF283387; AAL38109.1; JOINED.
DR EMBL; AF283388; AAL38109.1; JOINED.
DR EMBL; AF283389; AAL38109.1; JOINED.
DR EMBL; AF283390; AAL38109.1; JOINED.
DR EMBL; AF283391; AAL38109.1; JOINED.
DR EMBL; AF283392; AAL38109.1; JOINED.
DR EMBL; AF283393; AAL38109.1; JOINED.
DR EMBL; AF283394; AAL38109.1; JOINED.
DR EMBL; AF283395; AAL38109.1; JOINED.
DR EMBL; AF283396; AAL38109.1; JOINED.
DR EMBL; AF283397; AAL38109.1; JOINED.
DR EMBL; AF283398; AAL38109.1; JOINED.
DR EMBL; AF283399; AAL38109.1; JOINED.
DR EMBL; AF283400; AAL38109.1; JOINED.
DR EMBL; AF283401; AAL38109.1; JOINED.
DR EMBL; AF283402; AAL38109.1; JOINED.
DR EMBL; AF283403; AAL38109.1; JOINED.
DR EMBL; AF283404; AAL38109.1; JOINED.
DR EMBL; AF283405; AAL38109.1; JOINED.
DR EMBL; AF283406; AAL38109.1; JOINED.
DR EMBL; AF283407; AAL38109.1; JOINED.
DR GO; GO:0016020; C-membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR001881; EGF CA.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR002172; LDL_receptor_A.
DR InterPro; IPR000033; LDL_receptor_rep.
DR InterPro; IPR001005; MYD_DNA_binding.
DR InterPro; IPR00169; SHprot_acsite.
DR Pfam; PF00057; ldl_recept_a; 32.
DR Pfam; PF00058; ldl_recept_b; 34.
DR PRINTS; PRO0261; LDLRECEPTOR.
DR SMART; SM00179; EGF CA; 4.
DR SMART; SM00192; LDLA; 32.
DR SMART; SM00135; LY; 33.
DR PROSITE; PS00010; ASX_HYDROXYL; 4.
DR PROSITE; PS00022; EGF_1; 5.
DR PROSITE; PS01186; EGF_2; 9.
DR PROSITE; PS01187; EGF CA; 3.
DR PROSITE; PS01209; LDLRA_1; 27.
DR PROSITE; PS00068; LDLRA_2; 32.
DR PROSITE; PS00037; MYB_1; 1.
DR PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.
DR EGF-like domain; Lipoprotein; Receptor.
KW EGF-like domain; Lipoprotein; Receptor.
SQ SEQUENCE 4599 AA; 515498 MW; 9A97A555F1FAAE66 CRC64;

Query Match 58.9%; Score 43; DB 4; Length 4599;
Best Local Similarity 61.5%; Pred. No. 3.3e+02;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GHEGCRSGEAGS 13
|||:|||||
Db 3574 GHEDCKYGEDEKS 3586

RESULT 7
Q8H2G9 PRELIMINARY; PRT; 124 AA.
AC Q8H2G9;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE P0676F10.31 protein.
GN P0676F10.31.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, PAC
clone:P0676F10."
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF005813; BAC20632.1; -- DB88B75467DB01AF CRC64;
SQ SEQUENCE 124 AA; 12790 MW;

Query Match 57.5%; Score 42; DB 10; Length 124;
Best Local Similarity 61.5%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GHEGCRSGEAGS 13
|||:|||||

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DR	GO: 0006943; F:phosphatase activity; IEA.	OS	<i>Pseudomonas putida</i> (strain K12470).
DR	GO: 0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.	OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
DR	GO: 0005975; P:carbohydrate metabolism; IEA.	OC	Pseudomonadaceae; Pseudomonas.

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OX NCBI_TaxID=160488;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22423060; PubMed=12534463;
RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
RA Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
RA Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzes A.,
RA Uterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,
RA Lauber J., Stjepandic D., Hohelsel J., Straetz M., Heim S.,
RA Kiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuemmli B.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative analysis of the
RT metabolically versatile Pseudomonas putida KT2440."
RL Environ. Microbiol. 4:799-808 (2002).
DR EMBL; AB016776; AAN66271.1; -
DR TIGR; PF06646; -
RW Hypothetical protein; Complete proteome.
SQ SEQUENCE 466 AA; 48738 MW; FF7C1BAA4B2B706B CRC64;

Query Match 57.5%; Score 42; DB 16; Length 466;
Best Local Similarity 70.0%; Pred. No. 51;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGRSGEAG 12
DB 375 EACRAGETEG 384
| | | | |
| | | | |

RESULT 12
O74242 PRELIMINARY; PRT; 997 AA.
AC O74242;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Plasma membrane H(+)-ATPase 1 (EC 3.6.1.35).
GN PMAI.
OS Cryptococcus neoformans (Filobasidiella neoformans).
OC Eukaryota; Fungi; Basidiomycota; Hymenycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX NCBI_TaxID=5207;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B-3501;
RX MEDLINE=20568793; PubMed=11118522;
RA Gorgojo B., Portillo F., Martinez-Suarez J.V.;
RT "Sequencing and heterologous expression in Saccharomyces cerevisiae of
RT a Cryptococcus neoformans cDNA encoding a plasma membrane H(+)-
RT ATPase."
RL Biochim. Biophys. Acta 1509:103-110 (2000).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2
CC ATPASES).
DR EMBL; AF077766; AAC27788.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0015662; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:0016887; F:ATPase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR GO; GO:0015992; P:proton transport; IEA.
DR InterPro; IPR006534; ATPase-IIIA_H.
DR InterPro; IPR001757; ATPase_EI-E2.
DR InterPro; IPR004014; Cation_ATPase_N.
DR InterPro; IPR008250; E1-E2_ATPase_Reg.
DR InterPro; IPR005834; Hydrolase.
DR InterPro; IPR006595; H_ATPase.
DR Pfam; PF00690; Cation_ATPase_N; 1.
DR Pfam; PF00122; E1-E2_ATPase; 1.
DR Pfam; PF00702; Hydrolase; 1.
DR PRINTS; PR00119; CATATPASE.

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DR PRINTS; PR00120; HATPASE.
DR TIGR; TIGR01647; ATPase-IIIA_H; 1.
DR TIGR; TIGR01494; ATPase_P-type; 4.
DR PROSITE; PS00154; ATPase_EI-E2; 1.
KW ATP-binding; Hydrolase; Phosphorylation; Transmembrane.
SQ SEQUENCE 997 AA; 108693 MW; ECAEB09A66F7A744 CRC64;

Query Match 57.5%; Score 42; DB 3; Length 997;
Best Local Similarity 47.4%; Pred. No. 1.1e+02;
Matches 9; Conservative 1; Mismatches 1; Indels 8; Gaps 1;

QY 2 HEG-----CRSGEAG 12
DB 257 HEGDECFGSGTCKQGEAG 275
| | | | |
| | | | |

RESULT 13
Q21213 PRELIMINARY; PRT; 1429 AA.
ID Q21213
AC Q21213
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE C24F3.5 protein.
GN C24F3.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Wild A.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL022716; CAA18775.1; -.
DR EMBL; AL021570; CAA18775.1; JOINED.
DR EMBL; Z69664; CAA18775.1; JOINED.
DR EMBL; Z69664; CAA93518.1; -.
DR EMBL; AL022716; CAA93518.1; JOINED.
DR EMBL; AL021570; CAA93518.1; JOINED.
DR EMBL; AL021570; CAA16510.1; -.
DR EMBL; AL022716; CAA16510.1; JOINED.
DR EMBL; Z69664; CAA16510.1; JOINED.
DR FIR; T19422; T19422.
DR WormPep; C24F3.5; CEI9700.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. . .; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003439; ABC transporter.
DR Pfam; PF00005; ABC tran; 1.
DR PROSITE; PS50893; ABC TRANSPORTER 2; 1.
SQ SEQUENCE 1429 AA; 162819 MW; 836741887E3EC1F3 CRC64;

Query Match 57.5%; Score 42; DB 5; Length 1429;
Best Local Similarity 77.8%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHEGCRSGE 9
DB 406 GHHGCGSGE 414
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RESULT 14
Q82Q46 PRELIMINARY; PRT; 263 AA.
ID Q82Q46
AC Q82Q46;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative TetR-family transcriptional regulator.
GN SAV675.
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

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OC Streptomycineae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxID=33903;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=21477403; PubMed=11572948;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT "Genome sequence of an industrial microorganism Streptomycetes
RT avermitilis: deducing the ability of producing secondary
RT metabolites.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=22608306; PubMed=12692362;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomycetes avermitilis.";
RL Nat. Biotechnol. 21:526-531(2003).
DR EMBL; AF005023; BAC68385.1; -.
DR GO; GO:0003700; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001647; HTH_Tetr.
DR Pfam; PF00440; tetr; 1.
DR PRINTS; PR00455; HTHETR.
KW Complete proteome.
SQ SEQUENCE 263 AA; 27729 MW; 0CEDC998E434D184 CRC64;

Query Match 56.2%; Score 41; DB 16; Length 263;
Best Local Similarity 66.7%; Pred. No. 44;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GHEGCRSGEAG 12
Db 105 GHAGVRSGLVEG 116
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RESULT 15
Q89WV1 PRELIMINARY; PRT; 605 AA.
AC Q89WV1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE B1r0944 protein.
GN B1R0944.
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA 110;
RX MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimpō S., Tsuruoka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT Bradyrhizobium japonicum USDA110.";
RL DNA Res. 9:189-197(2002).
DR EMBL; AF005938; BAC46209.1; -.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001309; ICE_P20.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PROSITE; PS0208; CASPASE_P20; 1.
KW Complete proteome.
SQ SEQUENCE 605 AA; 63393 MW; 2EA39F13BB478766 CRC64;

Query Match 56.2%; Score 41; DB 2; Length 703;
Best Local Similarity 58.3%; Pred. No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GHEGCRSGEAG 12
Db 318 GHEGSRRTGGQ 329
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RESULT 17
Q9BL30 PRELIMINARY; PRT; 716 AA.
AC Q9BL30;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN Y71H2AM.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Leonard S.;
RT "The sequence of C. elegans cosmid Y71H2AM.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBSJ databases.
RN [3]

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RP SEQUENCE FROM N.A.
RC STRAIN-Bristol N2;
RT "Direct Submission.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC024859; AAK29976.1; -.
DR HSSP; O60911; 1FHO.
DR WormPep; Y71H2AM.3; CE26272.
DR GO; GO:0004182; F:carboxypeptidase A activity; IEA.
DR GO; GO:0008234; F:cysteine-type peptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000668; Peptidase C1.
DR InterPro; IPR000834; Peptidase_M14.
DR Pfam; PF00112; Peptidase_C1; 1.
DR ProDom; PD000158; Peptidase_C1; 1.
DR SMART; SM00645; Pept C1; 1.
DR PROSITE; PS00133; CARBOXYPEPT_ZN_2; 1.
SQ SEQUENCE 716 AA; 80007 MW; A7595D3F01F82740 CRC64;

Query Match 56.2%; Score 41; DB 5; Length 716;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ECSRGEAEGS 13
DB 628 EGLRSEAEAGS 638

RESULT 18
ID Q9J118 PRELIMINARY; PRT; 4599 AA.
AC Q9J118;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Low density lipoprotein receptor related protein LRP1B/LRP-DIT.
GN LRP1B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Yaklichkin S., Lisitsyn N.;
RT "The structure of the mouse homologue of the human candidate tumor
suppressor gene LRP1B/LRP-DIT.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF270884; AAF81758.1; -.
DR HSSP; Q07954; 1CR8.
DR MGD; MGI:2151136; Lrp1b.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000152; ASX hydroxyl_S.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002172; LDL_receptor_A.
DR InterPro; IPR000033; Ldl_receptor_rep.
DR InterPro; IPR000169; SHprot_acsite.
DR Pfam; PF00008; EGF; 15.
DR Pfam; PF00057; ldl_recept_a; 32.
DR Pfam; PF00058; ldl_recept_b; 33.
DR PRINTS; PR00261; LDLRECEPTOR.
DR SMART; SM00179; EGF_CA; 4.
DR SMART; SM00192; LDLA; 32.
DR SMART; SM00135; LV; 33.
DR PROSITE; PS00010; ASX_HYDROXYL; 4.
DR PROSITE; PS00022; EGF_1; 5.
DR PROSITE; PS01186; EGF_2; 9.
DR PROSITE; PS01187; EGF_CA; 3.

DR PROSITE; PS01209; LDLRA_1; 27.
DR PROSITE; PS00068; LDLRA_2; 32.
DR PROSITE; PS00139; THIOLEPROTEASE_CYS; 1.
KW EGF-like domain; Lipoprotein; Receptor.
SQ SEQUENCE 4599 AA; 513623 MW; 11462A3354FFB200 CRC64;

Query Match 56.2%; Score 41; DB 11; Length 4599;
Best Local Similarity 63.6%; Pred. No. 7.4e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GHEGCRGEAE 11
DB 3574 GHEDCKYGEDE 3584

RESULT 19
ID Q8CT00 PRELIMINARY; PRT; 144 AA.
AC Q8CT00;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Conserved hypothetical protein.
GN SE0818.
OS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1282;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 12228;
RA Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,
Chen Z., Wen Y.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE016746; AAO04415.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 144 AA; 16595 MW; 7003BEEB876D5AB CRC64;

Query Match 54.8%; Score 40; DB 16; Length 144;
Best Local Similarity 75.0%; Pred. No. 36;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHEGCRSG 8
DB 130 GHGCGASG 137

RESULT 20
ID O70885 PRELIMINARY; PRT; 152 AA.
AC O70885;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Strain 86AB-A1 ORF4.
OS Equine arteritis virus (EAV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Arteriviridae; Arterivirus.
OX NCBI_TaxID=11047;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=86AB-A1;
RA Archambault D., Laganier G., Carman S., St-Laurent G.;
RX Archambault D., Laganier G., Carman S., St-Laurent G.;
RT "Comparison of nucleic acid sequences and phylogenetic
analysis of open reading frames 3 and 4 of various equine arteritis
virus isolates.";
RL Vet. Res. 28:505-516(1997).
DR EMBL; AF001093; AAC14212.1; -.
DR InterPro; IPR004257; GP4.
DR Pfam; PF03010; GP4; 1.
DR ProDom; PD006770; GP4; 1.
SQ SEQUENCE 152 AA; 17172 MW; 99F7455093DB087A CRC64;
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Query Match          54.8%; Score 40; DB 12; Length 152;
Best Local Similarity 85.7%; Pred. No. 38;
Matches 6; Conservative 1; Mismatches 0; Gaps 0;

QY 1 GHEGCRS 7
Db 46 GHEGCRN 52

RESULT 21
Q9PX34
ID Q9PX34 PRELIMINARY; PRT; 152 AA.
AC Q9PX34;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE ORF4.
OS Equine arteritis virus (EAV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Arteriviridae; Arterivirus.
OX NCBI_TaxID=11047;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=P2, A2, A3, and A4;
RX MEDLINE=99394666; PubMed=10466790;
RA Balasuriya U.B.R., Hedges J.F., Nadler S.A., McCollum W.H.,
RA Timoney P.J., MacLachlan N.J.;
RT "Genetic Stability of Equine Arteritis Virus during Horizontal and
RT Vertical Transmission in an Outbreak of Equine Viral Arteritis.";
RL J. Gen. Virol. 80:1949-1958(1999).
DR EMBL; AF118776; AAD54725.1; -.
DR EMBL; AF118770; AAD54689.1; -.
DR EMBL; AF118771; AAD54695.1; -.
DR EMBL; AF118772; AAD54701.1; -.
DR InterPro; IPR004257; GP4.
DR Pfam; PF03010; GP4; 1.
DR ProDom; PD006770; GP4; 1.
DR ProDom; PD006770; GP4; 1.
SQ SEQUENCE 152 AA; 17124 MW; 5F8FF3D15420985F CRC64;

Query Match          54.8%; Score 40; DB 12; Length 152;
Best Local Similarity 85.7%; Pred. No. 38;
Matches 6; Conservative 1; Mismatches 0; Gaps 0;

QY 1 GHEGCRS 7
Db 46 GHEGCRN 52

RESULT 22
Q9WEX9
ID Q9WEX9 PRELIMINARY; PRT; 152 AA.
AC Q9WEX9;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE GP4 protein.
OS Equine arteritis virus (EAV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Arteriviridae; Arterivirus.
OX NCBI_TaxID=11047;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E88;
RX MEDLINE=99214302; PubMed=10196259;
RA Hedges J.F., Balasuriya U.B., Timoney P.J., McCollum W.H.,
RA MacLachlan N.J.;
RT "Genetic divergence with emergence of novel phenotypic variants of
RT equine arteritis virus during persistent infection of stallions.";
RL J. Virol. 73:3672-3681(1999).
DR EMBL; AF107277; AAD31156.1; -.
DR InterPro; IPR004257; GP4.
DR Pfam; PF03010; GP4; 1.
DR ProDom; PD006770; GP4; 1.

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SQ SEQUENCE 152 AA; 17167 MW; 72ECAF5B1ACDF9F9 CRC64;

Query Match          54.8%; Score 40; DB 12; Length 152;
Best Local Similarity 85.7%; Pred. No. 38;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHEGCRS 7
Db 46 GHEGCRN 52

RESULT 23
Q9PX35
ID Q9PX35 PRELIMINARY; PRT; 152 AA.
AC Q9PX35;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE ORF4.
OS Equine arteritis virus (EAV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Arteriviridae; Arterivirus.
OX NCBI_TaxID=11047;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BT-PA96, R1, and P1;
RX MEDLINE=99394666; PubMed=10466790;
RA Balasuriya U.B.R., Hedges J.F., Nadler S.A., McCollum W.H.,
RA Timoney P.J., MacLachlan N.J.;
RT "Genetic Stability of Equine Arteritis Virus during Horizontal and
RT Vertical Transmission in an Outbreak of Equine Viral Arteritis.";
RL J. Gen. Virol. 80:1949-1958(1999).
DR EMBL; AF118781; AAD54755.1; -.
DR EMBL; AF118773; AAD54707.1; -.
DR EMBL; AF118775; AAD54719.1; -.
DR InterPro; IPR004257; GP4.
DR Pfam; PF03010; GP4; 1.
DR ProDom; PD006770; GP4; 1.
DR ProDom; PD006770; GP4; 1.
SQ SEQUENCE 152 AA; 17150 MW; 5E47F3CD85E193B4 CRC64;

Query Match          54.8%; Score 40; DB 12; Length 152;
Best Local Similarity 85.7%; Pred. No. 38;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHEGCRS 7
Db 46 GHEGCRN 52

RESULT 24
Q070882
ID Q070882 PRELIMINARY; PRT; 152 AA.
AC Q070882;
DT 01-AUG-1998 (TReMBLrel. 07, Created)
DT 01-AUG-1998 (TReMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Strain 19933 ORF4.
OS Equine arteritis virus (EAV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Arteriviridae; Arterivirus.
OX NCBI_TaxID=11047;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=19933;
RX MEDLINE=98089613; PubMed=9428144;
RA Archambault D., Laganier G., Carman S., St-Laurent G.;
RT "Comparison of nucleic and amino acid sequences and phylogenetic
RT analysis of open reading frames 3 and 4 of various equine arteritis
RT virus isolates.";
RL Vet. Res. 28:505-516(1997).
DR EMBL; AF001090; AAC14209.1; -.
DR InterPro; IPR004257; GP4.
DR Pfam; PF03010; GP4; 1.

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DR ProDom; PD006770; GP4; 1.
SQ SEQUENCE 152 AA; 17110 MW; 5E74AESB4422EBAA CRC64;

Query Match      54.8%; Score 40; DB 12; Length 152;
Best Local Similarity 85.7%; Pred. No. 38;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHEGCRS 7
DB 46 GHEGCRN 52

RESULT 25
O70880 PRELIMINARY; PRT; 152 AA.
AC O70880;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Strain 11958 ORF4.
OS Equine arteritis virus (EAV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Arteriviridae; Arterivirus.
OX NCBI_TaxID=11047;
RN [1]_TaxID=11047;
RP SEQUENCE FROM N.A.
RC STRAIN=11958;
RX MEDLINE=98089613; PubMed=9428144;
RA Archambault D., Laganier G., Carman S., St-Laurent G.;
RT "Comparison of nucleic and amino acid sequences and phylogenetic
RT analysis of open reading frames 3 and 4 of various equine arteritis
RT virus isolates.";
RL Vet. Res. 28:505-516(1997).
DR EMBL; AF001088; AAC14207.1; -.
DR InterPro; IPR004257; GP4.
DR Pfam; PF03010; GP4; 1.
DR ProDom; PD006770; GP4; 1.
SQ SEQUENCE 152 AA; 17194 MW; 0428F3862962FEE1 CRC64;

Query Match      54.8%; Score 40; DB 12; Length 152;
Best Local Similarity 85.7%; Pred. No. 38;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHEGCRS 7
DB 46 GHEGCRN 52

RESULT 26
O70881 PRELIMINARY; PRT; 152 AA.
AC O70881;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Strain 15492 ORF4.
OS Equine arteritis virus (EAV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Arteriviridae; Arterivirus.
OX NCBI_TaxID=11047;
RN [1]_TaxID=11047;
RP SEQUENCE FROM N.A.
RC STRAIN=15492;
RX MEDLINE=98089613; PubMed=9428144;
RA Archambault D., Laganier G., Carman S., St-Laurent G.;
RT "Comparison of nucleic and amino acid sequences and phylogenetic
RT analysis of open reading frames 3 and 4 of various equine arteritis
RT virus isolates.";
RL Vet. Res. 28:505-516(1997).
DR EMBL; AF001089; AAC14208.1; -.
DR InterPro; IPR004257; GP4.
DR Pfam; PF03010; GP4; 1.
DR ProDom; PD006770; GP4; 1.
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SQ SEQUENCE 152 AA; 17113 MW; 1D5680450B43CDA8 CRC64;

Query Match      54.8%; Score 40; DB 12; Length 152;
Best Local Similarity 85.7%; Pred. No. 38;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHEGCRS 7
DB 46 GHEGCRN 52

RESULT 27
Q88674 PRELIMINARY; PRT; 152 AA.
ID Q88674;
AC Q88674;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Viral protein.
OS Equine arteritis virus (EAV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Arteriviridae; Arterivirus.
OX NCBI_TaxID=11047;
RN [1]_TaxID=11047;
RP SEQUENCE FROM N.A.
RC STRAIN=modified Bucyrus;
RA Yamaguchi S.;
RT "Infectious CDNA clones of equine arteritis virus.";
RL Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; D28527; BA005881.1; -.
DR InterPro; IPR004257; GP4.
DR Pfam; PF03010; GP4; 1.
DR ProDom; PD006770; GP4; 1.
SQ SEQUENCE 152 AA; 17102 MW; F5A4AB4A9F289D3D CRC64;

Query Match      54.8%; Score 40; DB 12; Length 152;
Best Local Similarity 85.7%; Pred. No. 38;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHEGCRS 7
DB 46 GHEGCRN 52

RESULT 28
O70879 PRELIMINARY; PRT; 152 AA.
ID O70879;
AC O70879;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Strain T1329 ORF4.
OS Equine arteritis virus (EAV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Arteriviridae; Arterivirus.
OX NCBI_TaxID=11047;
RN [1]_TaxID=11047;
RP SEQUENCE FROM N.A.
RC STRAIN=T1329;
RX MEDLINE=98089613; PubMed=9428144;
RA Archambault D., Laganier G., Carman S., St-Laurent G.;
RT "Comparison of nucleic and amino acid sequences and phylogenetic
RT analysis of open reading frames 3 and 4 of various equine arteritis
RT virus isolates.";
RL Vet. Res. 28:505-516(1997).
DR EMBL; AF001087; AAC14206.1; -.
DR InterPro; IPR004257; GP4.
DR Pfam; PF03010; GP4; 1.
DR ProDom; PD006770; GP4; 1.
SQ SEQUENCE 152 AA; 17181 MW; 9F5E1A7EF24B53BC CRC64;

Query Match      54.8%; Score 40; DB 12; Length 152;
Best Local Similarity 85.7%; Pred. No. 38;
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Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHEGCRS 7  
|||||:  
Db 46 GHEGCRN 52

## RESULT 29

OT0886 PRELIMINARY; PRT; 152 AA.  
AC O70886;  
DT 01-AUG-1998 (TREMBlrel. 07, Created)  
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE Strain Arvac ORF4.  
OS Equine arteritis virus (EAV).  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
OC Arteriviridae; Arterivirus.  
OX NCBI\_TaxID=11047;  
RN [1]\_SEQUENCE FROM N.A.  
RP STRAIN=Arvac;  
RX MEDLINE=98089613; PubMed=9428144;  
RA Archambault D., Laganier G., Carman S., St-Laurent G.;  
RT "Comparison of nucleic and amino acid sequences and phylogenetic  
RT analysis of open reading frames 3 and 4 of various equine arteritis  
RT virus isolates.";  
RL Vet. Res. 28:505-516(1997).  
DR EMBL; AF001094; AAC14213.1; -.  
DR InterPro; IPR004257; GP4.  
DR Pfam; PF03010; GP4; 1.  
DR ProDom; PD006770; GP4; 1.  
SQ SEQUENCE 152 AA; 17074 MW; 9864D4F75A0A63FE CRC64;

Query Match 54.8%; Score 40; DB 12; Length 152;  
Best Local Similarity 85.7%; Pred. No. 38;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHEGCRS 7  
|||||:  
Db 46 GHEGCRN 52

## RESULT 30

Q9QKH1 PRELIMINARY; PRT; 152 AA.  
AC Q9QKH1;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE ORF4.  
OS Equine arteritis virus (EAV).  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
OC Arteriviridae; Arterivirus.  
OX NCBI\_TaxID=11047;  
RN [1]\_SEQUENCE FROM N.A.  
RP STRAIN=A1;  
RX MEDLINE=99394666; PubMed=10466790;  
RA Balasuriya U.B., Hedges J.F., Nadler S.A., McCollum W.H.,  
RA Timoney P.J., MacLachlan N.J.;  
RT "Genetic stability of equine arteritis virus during horizontal and  
RT vertical transmission in an outbreak of equine viral arteritis.";  
RL J. Gen. Virol. 80:1949-1958(1999).  
DR EMBL; AF118769; AAD54683.1; -.  
DR InterPro; IPR004257; GP4.  
DR Pfam; PF03010; GP4; 1.  
DR ProDom; PD006770; GP4; 1.  
SQ SEQUENCE 152 AA; 16995 MW; 5F8FE7815B70835F CRC64;

Query Match 54.8%; Score 40; DB 12; Length 152;  
Best Local Similarity 85.7%; Pred. No. 38;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHEGCRS 7  
|||||:  
Db 46 GHEGCRN 52

## RESULT 31

OT0883 PRELIMINARY; PRT; 152 AA.  
AC O70883;  
DT 01-AUG-1998 (TREMBlrel. 07, Created)  
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE Strain Vienna ORF4.  
OS Equine arteritis virus (EAV).  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
OC Arteriviridae; Arterivirus.  
OX NCBI\_TaxID=11047;  
RN [1]\_SEQUENCE FROM N.A.  
RP STRAIN=Vienna;  
RX MEDLINE=98089613; PubMed=9428144;  
RA Archambault D., Laganier G., Carman S., St-Laurent G.;  
RT "Comparison of nucleic and amino acid sequences and phylogenetic  
RT analysis of open reading frames 3 and 4 of various equine arteritis  
RT virus isolates.";  
RL Vet. Res. 28:505-516(1997).  
DR EMBL; AF001091; AAC14210.1; -.  
DR InterPro; IPR004257; GP4.  
DR Pfam; PF03010; GP4; 1.  
DR ProDom; PD006770; GP4; 1.  
SQ SEQUENCE 152 AA; 17050 MW; 7FDB93A38A2164BB CRC64;

Query Match 54.8%; Score 40; DB 12; Length 152;  
Best Local Similarity 85.7%; Pred. No. 38;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHEGCRS 7  
|||||:  
Db 46 GHEGCRN 52

## RESULT 32

Q9QKF2 PRELIMINARY; PRT; 152 AA.  
AC Q9QKF2;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE ORF4.  
OS Equine arteritis virus (EAV).  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
OC Arteriviridae; Arterivirus.  
OX NCBI\_TaxID=11047;  
RN [1]\_SEQUENCE FROM N.A.  
RP STRAIN=RQ;  
RX MEDLINE=99394666; PubMed=10466790;  
RA Balasuriya U.B., Hedges J.F., Nadler S.A., McCollum W.H.,  
RA Timoney P.J., MacLachlan N.J.;  
RT "Genetic stability of equine arteritis virus during horizontal and  
RT vertical transmission in an outbreak of equine viral arteritis.";  
RL J. Gen. Virol. 80:1949-1958(1999).  
DR EMBL; AF118782; AAD54761.1; -.  
DR InterPro; IPR004257; GP4.  
DR Pfam; PF03010; GP4; 1.  
DR ProDom; PD006770; GP4; 1.  
SQ SEQUENCE 152 AA; 17138 MW; 0E5AF3C4178C256F CRC64;

Query Match 54.8%; Score 40; DB 12; Length 152;  
Best Local Similarity 85.7%; Pred. No. 38;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;



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QY 1 GHEGCRS 7
DB 46 GHEGCRN 52

RESULT 33
Q7URS4 PRELIMINARY; PRT; 209 AA.
AC Q7URS4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE Probable two component system response regulator.
GN RB5477.
OS Rhodopirellula baltica.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxID=117;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416;
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
RA Schlesner H., Amann R., Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete Pirellula sp.
RL strain 1."
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
DR EMBL; BX294142; CAD74264.1; -.
KW Complete proteome.
SQ SEQUENCE 209 AA; 23562 MW; BDB2D3290341A50 CRC64;

Query Match 54.8%; Score 40; DB 16; Length 209;
Best Local Similarity 60.0%; Pred. No. 52;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 HEGCRSGEAE 11
DB 196 HQGCSAETE 205

RESULT 34
Q8S0H3 PRELIMINARY; PRT; 224 AA.
AC Q8S0H3;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE B142C05.27 protein.
GN B142C05.27.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, BAC
clone: B1142C05."
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP003410; BAB89127.1; -.
DR Gramene; Q8S0H3; -.
SQ SEQUENCE 224 AA; 23355 MW; 86985008FE9D9024 CRC64;

Query Match 54.8%; Score 40; DB 10; Length 224;
Best Local Similarity 77.8%; Pred. No. 56;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCRSGEAE 12
DB 120 GCRSGRAG 128

RESULT 35
Q8GFC1 PRELIMINARY; PRT; 292 AA.
AC Q8GFC1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hpad.
GN HPAD.
OS Photorhabdus luminescens (Xenorhabdus luminescens).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=29488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=W14;
RX MEDLINE=21185117; PubMed=11286884;
RA Waterfield N.R., Bowen D.J., Fetherston J.D., Perry R.D.,
RA ffrrench-Constant R.H.;
RT "The tc genes of Photorhabdus: a growing family.";
RL Trends Microbiol. 9:185-191(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=W14;
RA Waterfield N.R., ffrrench-Constant R.H.;
RT "Pathogenicity islands in Photorhabdus luminescens strain W14.";
RL Trends Microbiol. 0:0-0(2002).
DR EMBL; AF346500; AA017180.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0001584; P:rhodopsin-like receptor activity; IEA.
DR GO; GO:0005725; P:aromatic compound metabolism; IEA.
DR GO; GO:0005118; P:electron transport; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR004183; LiGB.
DR Pfam; PF02900; LiGB; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
SQ SEQUENCE 292 AA; 33043 MW; A6D7474EB4BCC084 CRC64;

Query Match 54.8%; Score 40; DB 2; Length 292;
Best Local Similarity 54.5%; Pred. No. 72;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 HEGCRSGEAE 12
DB 25 HHGCRQGAIDG 35

RESULT 36
Q8IHK4 PRELIMINARY; PRT; 310 AA.
AC Q8IHK4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Glycosylphosphatidylinositol-anchored merozoite surface protein
(fragment).
GN 37.
OS Babesia divergens.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX NCBI_TaxID=32595;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17/05/A;
RA Delbecq S., Vallet A., Precigout E., Carcy B., Gorenflot A.;
RT "Bd37 is a Babesia divergens polymorphic protein.";
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ509156; CAD48925.1; -.
KW Merozoite.
FT NON_TER 310 310
```

SQ SEQUENCE 310 AA; 33463 MW; D2958FF9653C3DB2 CRC64;  
Query Match 54.8%; Score 40; DB 5; Length 310;  
Best Local Similarity 46.2%; Pred. No. 77;  
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
QY 1 GHEGCRSGEAGS 13  
DB 293 GHDDCAAGSGQS 305  
RESULT 37  
Q8IHK2  
ID Q8IHK2 PRELIMINARY; PRT; 331 AA.  
AC Q8IHK2;  
DT 01-MAR-2003 (TREMBlrel. 23, Created)  
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Glycosylphosphatidylinositol-anchored merozoite surface protein.  
GN 37.  
OS Babesia divergens.  
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.  
OX NCBI\_TaxID=32595;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=71/07/B;  
RA Delbecq S., Vallet A., Precigout E., Carcy B., Gorenflot A.;  
RT "Bd37 is a Babesia divergens polymorphic protein.";  
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ509158; CAD48927.1; --  
KW Merozoite.  
SQ SEQUENCE 331 AA; 35604 MW; 40F37301334E19CC CRC64;  
Query Match 54.8%; Score 40; DB 5; Length 331;  
Best Local Similarity 46.2%; Pred. No. 82;  
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
QY 1 GHEGCRSGEAGS 13  
DB 293 GHDDCAAGSGQS 305  
RESULT 38  
Q92P75  
ID Q92P75 PRELIMINARY; PRT; 340 AA.  
AC Q92P75;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Probable high-affinity zinc uptake system ABC transporter protein.  
GN ZNUA OR R01915 OR SMC04245.  
OS Rhizobium meliloti (Sinorhizobium meliloti).  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.  
OX NCBI\_TaxID=382;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=1021;  
RX MEDLINE=21396507; PubMed=11481430;  
RA Capela D., Barloy-Hubler P., Gouzy J., Bothe G., Ampe F., Batut J.,  
RA Boistard P., Becker A., Routry M., Cadieu E., Dreano S., Gloux S.,  
RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,  
RA Pohl T., Portetelle D., Puehler B., Fumelle B., Ramsperger U.,  
RA Renard C., Thebaud P., Vandenbol M., Weidner S., Galibert F.;  
RT "Analysis of the chromosome sequence of the legume symbiont Sinorhizobium meliloti strain 1021.";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).  
DR EMBL; AL591788; CAC46494.1; --  
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.  
DR GO; GO:0005488; F:binding; IEA.  
DR InterPro; IPR006127; SBP\_bac\_9.  
DR Pfam; PF01297; SBP\_bac\_9; 1.

KW Complete proteome.  
SQ SEQUENCE 340 AA; 35947 MW; A6F134A651EF5C17 CRC64;  
Query Match 54.8%; Score 40; DB 16; Length 340;  
Best Local Similarity 47.4%; Pred. No. 84;  
Matches 9; Conservative 2; Mismatches 2; Indels 6; Gaps 1;  
QY 1 GHEGCRSGEAGS 13  
DB 135 GHEGHEDHGDHAGEAGA 153  
RESULT 39  
Q8T117  
ID Q8T117 PRELIMINARY; PRT; 341 AA.  
AC Q8T117;  
DT 01-JUN-2002 (TREMBlrel. 21, Created)  
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)  
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
DE Glycosylphosphatidylinositol-anchored merozoite surface protein precursor.  
GN 39.  
OS Babesia divergens.  
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.  
OX NCBI\_TaxID=32595;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Rouen 1987;  
RA Delbecq S., Precigout E., Vallet A., Schettters T., Gorenflot A.;  
RT "Babesia divergens: cloning and characterization of Bd37, a potential vaccine against babesiosis.";  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ422214; CAD19563.1; --  
KW Signal; Merozoite.  
FT SIGNAL 1 19 POTENTIAL.  
SQ SEQUENCE 341 AA; 36282 MW; D41552A2PFC2B66E CRC64;  
Query Match 54.8%; Score 40; DB 5; Length 341;  
Best Local Similarity 46.2%; Pred. No. 84;  
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
QY 1 GHEGCRSGEAGS 13  
DB 303 GHDDCAAGSGQS 315  
RESULT 40  
Q8IHK5  
ID Q8IHK5 PRELIMINARY; PRT; 341 AA.  
AC Q8IHK5;  
DT 01-MAR-2003 (TREMBlrel. 23, Created)  
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Glycosylphosphatidylinositol-anchored merozoite surface protein.  
GN 37.  
OS Babesia divergens.  
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.  
OX NCBI\_TaxID=32595;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Weybridge;  
RA Delbecq S., Vallet A., Precigout E., Carcy B., Gorenflot A.;  
RT "Bd37 is a Babesia divergens polymorphic protein.";  
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ509155; CAD48924.1; --  
KW Merozoite.  
SQ SEQUENCE 341 AA; 36266 MW; D9505B2328B67A6 CRC64;  
Query Match 54.8%; Score 40; DB 5; Length 341;  
Best Local Similarity 46.2%; Pred. No. 84;  
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
QY 1 GHEGCRSGEAGS 13  
DB 303 GHDDCAAGSGQS 315

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Db 303 GHHDCAAGSGQGS 315
RESULT 41
Q9BCW3 PRELIMINARY; PRT; 353 AA.
AC Q9BCW3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MHC Rfp-Y class I alpha chain.
GN YFV.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]_TaxID=9031;
RP SEQUENCE FROM N.A.
RX MEDLINE=89030642; PubMed=3141149;
RA Guillemot F., Billault A., Pourquie O., Behar G., Chausse A.M.,
RA Zoorob R., Kreibich G., Auffray C.;
RT "A molecular map of the chicken major histocompatibility complex: the
RT class II beta genes are closely linked to the class I genes and the
RT nucleolar organizer.";
RL EMBO J. 7:2775-2785(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX PubMed=11207289;
RA Afanasieff M., Goto R.M., Ha J., Sherman M.A., Zhong L., Auffray C.,
RA Coudert F., Zoorob R., Miller M.M.;
RT "At least One Class I Gene in Restriction Fragment Pattern-Y (Rfp-Y),
RT the Second MHC Gene Cluster in the Chicken, Is Transcribed,
RT Polymorphic, and Shows Divergent Specialization in Antigen Binding
RT Region.";
RL J. Immunol. 166:3324-3333(2001).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN) (BY SIMILARITY).
DR EMBL; AF218783; AAK15583.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00447; ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC_I; 1.
DR SMART; SM00407; IGc1; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
DR Glycoprotein; Transmembrane.
SQ SEQUENCE 353 AA; 39058 MW; A6A10A3BCFC22323D CRC64;

Query Match 54.8%; Score 40; DB 7; Length 353;
Best Local Similarity 61.5%; Pred. No. 87;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GHEGCRSGEAGS 13
Db 337 GHDESSGSGATGS 349

RESULT 42
Q9EYU5 PRELIMINARY; PRT; 379 AA.
AC Q9EYU5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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DE BioF (7-keto-8-amino-pelargonic acid synthetase protein).
GN BioF.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]_TaxID=381;
RP SEQUENCE FROM N.A.
RX STRAIN=R7A;
RC MEDLINE=21220762; PubMed=11320134;
RA Sullivan J.T., Brown S.D., Vocum R.R., Ronson C.W.;
RT "The bio operon on the acquired symbiosis island of Mesorhizobium sp.
RT strain R7A includes a novel gene involved in pimeloyl-CoA synthesis.";
RL Microbiology 147:1315-1322(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=R7A;
RC MEDLINE=2199272; PubMed=12003951;
RA Sullivan J.T., Trzebiatowski J.R., Cruickshank R.W., Gouzy J.,
RA Brown S.D., Elliot R.M., Fleetwood D.J., McCallum N.G., Rossbach U.,
RA Stuart G.S., Weaver J.E., Webby R.J., de Bruijn F.J., Ronson C.W.;
RT "Comparative sequence analysis of the symbiosis island of
RT Mesorhizobium loti strain R7A.";
RL J. Bacteriol. 184:3086-3095(2002).
DR EMBL; AF311738; AAG47792.1; -.
DR HSSP; AL672114; CAD31400.1; -.
DR GO; GO:0008483; P:transaminase activity; IEA.
DR GO; GO:0009058; P:biosynthesis; IEA.
DR InterPro; IPR004839; Aminotrans_I/II.
DR Pfam; PF00155; aminotran_1_2; 1.
SQ SEQUENCE 379 AA; 40399 MW; 3B02D5848CF700F9 CRC64;

Query Match 54.8%; Score 40; DB 2; Length 379;
Best Local Similarity 70.0%; Pred. No. 93;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 HEGCRSGEAE 11
Db 127 HEGARAGRAE 136

RESULT 43
Q98AW1 PRELIMINARY; PRT; 379 AA.
AC Q98AW1;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 8-amino-7-oxononanoate synthase, KAPA synthase.
GN MLL5830.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]_TaxID=381;
RP SEQUENCE FROM N.A.
RX STRAIN=MAFP303099;
RC MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR EMBL; AP003007; BAB52211.1; -.
DR GO; GO:0008483; P:transaminase activity; IEA.
DR GO; GO:0009058; P:biosynthesis; IEA.
DR InterPro; IPR004839; Aminotrans_I/II.
DR Pfam; PF00155; aminotran_1_2; 1.
KW Complete proteome.
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SQ SEQUENCE 379 AA; 40271 MW; 67859C2B5D9541E1 CRC64;
Query Match 54.8%; Score 40; DB 16; Length 379;
Best Local Similarity 70.0%; Pred. No. 93;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 HEGCRSGEAE 11
Db 127 HEGARAGRAE 136

RESULT 44
Q9AMS5
ID Q9AMS5 PRELIMINARY; PRT; 384 AA.
AC Q9AMS5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ID901 (8-amino-7-oxononanoate synthase).
GN ID901 OR BIOF OR BLR2097.
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1108PC4;
RX MEDLINE=21101824; PubMed=11157954;
RA Gottfert M., Rothlisberger S., Kundig C., Beck C., Marty R.,
RA Hennecke H.;
RT "Potential symbiosis-specific genes uncovered by sequencing a 410-kb
RT DNA region of the Bradyrhizobium japonicum chromosome.";
RL J. Bacteriol. 183:1405-1412(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA 110;
RX MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimp S., Tsuruoka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT Bradyrhizobium japonicum USDA110.";
RL DNA Res. 9:189-197(2002).
DR EMBL; AF322013; AAG61072.1; -.
DR EMBL; AF005942; BAC47362.1; -.
DR HSSP; P12998; 1BS0.
DR GO; GO:0008483; F:transaminase activity; IEA.
DR GO; GO:0009058; P:biosynthesis; IEA.
DR InterPro; IPR004839; Aminotrans_I/II.
DR Pfam; PF00155; aminotran_1_2; 1.
KW Complete proteome.
SQ SEQUENCE 384 AA; 41376 MW; DC40495CCCC4A7698 CRC64;
Query Match 54.8%; Score 40; DB 16; Length 384;
Best Local Similarity 70.0%; Pred. No. 95;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 HEGCRSGEAE 11
Db 130 HEGARAGRAE 139

RESULT 45
Q9U135
ID Q9U135 PRELIMINARY; PRT; 491 AA.
AC Q9U135;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN L4520.08.
OS Leishmania major.

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OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Friedlin;
RA Hilbert H., Wedler H., Wedler E., Duesterhoeft A., Ivens A.C.,
RA Lawson D., Quail M., Rajandream M.A., Barrell B.G.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Friedlin;
RX MEDLINE=98146435; PubMed=9477341;
RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
RA Smith D.F.;
RT "A physical map of the Leishmania major Friedlin genome.";
RL Genome Res. 8:135-145(1998).
DR EMBL; AL117268; CAB5511.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR004776; Auxin eff.
DR Pfam; PF03547; Auxin eff. 1.
KW Hypothetical protein.
SQ SEQUENCE 491 AA; 53473 MW; C4CB0C840E08582C CRC64;
Query Match 54.8%; Score 40; DB 5; Length 491;
Best Local Similarity 70.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGCGRSGEAE 12
Db 190 DGCVDGEAEG 199

RESULT 46
Q8S1A6
ID Q8S1A6 PRELIMINARY; PRT; 629 AA.
AC Q8S1A6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE B114B07.16 protein.
GN B114B07.16.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC
RT clone:B114B07.16";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF003334; BAB90006.1; -.
DR Gramene; Q8S1A6; -.
SQ SEQUENCE 629 AA; 68639 MW; 724C08A73DCB785D CRC64;
Query Match 54.8%; Score 40; DB 10; Length 629;
Best Local Similarity 58.3%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GHEGCRSGEAE 12
Db 183 GHLGCRSGGG 194

RESULT 47
Q9EXP9
ID Q9EXP9 PRELIMINARY; PRT; 703 AA.
AC Q9EXP9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

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DE Mobilisation protein A.
GN MOBA.
OS Bacteroides nodosus (Dichelobacter nodosus).
OG Plasmid DNA.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Cardiobacteriales;
CX Cardiobacteriaceae; Dichelobacter.
RN NCBI_TaxID=870;
[1]
RP SEQUENCE FROM N.A.
RA Whittle G., Katz M.E., Clayton E.H., Cheatham B.F.;
RT "Identification and characterization of a native D. nodosus plasmid,
RT pDN1."
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y19120; CAC20100.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR GO; GO:0009291; P:unidirectional conjugation; IEA.
DR InterPro; IPR005053; MObA_MobL.
DR Pfam; PF03389; MObA_MobL_1.
KW Plasmid.
SQ SEQUENCE 703 AA; 78872 MW; B057B18C5F299B8 CRC64;

Query Match 54.8%; Score 40; DB 2; Length 703;
Best Local Similarity 58.3%; Pred. No. 1.7e+02;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GHEGCRSGEAG 12
DB 318 GHEGSRRTG 329
|||||:|

RESULT 48
Q7T2V3 PRELIMINARY; PRT; 1005 AA.
AC Q7T2V3;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mixed lineage kinase 2.
GN MLK2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22637861; PubMed=12753919;
RA Poiras L., Jean S., Islam N., Moss T.;
RT "PAK interacts with NCK and MLK2 to regulate the activation of jun N-
RT terminal kinase."
RL FEBS Lett. 543:129-135(2003).
DR EMBL; AF510499; AAP46399.1; -.
KW Kinase.
SQ SEQUENCE 1005 AA; 111874 MW; B406102A77244309 CRC64;

Query Match 54.8%; Score 40; DB 13; Length 1005;
Best Local Similarity 53.8%; Pred. No. 2.4e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 GHEGCRSGEAGS 13
DB 928 GGDACSGSAGEA 940
|:|:|:|:|:|:|

RESULT 49
Q8SQJ6 PRELIMINARY; PRT; 1017 AA.
AC Q8SQJ6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Chromosome segregation protein of the SMC family.
GN ECU09_1910.

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OS Encephalitozoon cuniculi.
OC Eukaryota; Fungi; Microsporidia; Unikaryonidae; Encephalitozoon.
OX NCBI_TaxID=6035;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=GB-M1;
RC STRAIN=GB-M1;
RA Genoscope;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21576510; PubMed=11719806;
RA Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarar P.,
RA Prenier G., Barbe V., Peyretailade E., Brottier P., Wincker P.,
RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
RA Weissenbach J., Vivares C.P.;
RT "Genome sequence and gene compaction of the eukaryote parasite
RT Encephalitozoon cuniculi."
RL Nature 414:450-453(2001).
DR EMBL; AL590451; CAD27164.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti...; IEA.
DR GO; GO:0007053; P:chromosome segregation; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003439; ABC transporter.
DR InterPro; IPR003405; SMC_C.
DR InterPro; IPR003395; SMC_N.
DR Pfam; PF02483; SMC_C; 1.
DR Pfam; PF02463; SMC_N; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
SQ SEQUENCE 1017 AA; 117312 MW; 12194088B5CC3C7 CRC64;

Query Match 54.8%; Score 40; DB 5; Length 1017;
Best Local Similarity 66.7%; Pred. No. 2.5e+02;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 HEGCRSGEAGS 13
DB 63 HEGSRAMEEGS 74
|||||:|:|:|:|:|:|

RESULT 50
Q98UD3 PRELIMINARY; PRT; 131 AA.
AC Q98UD3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CAR-binding factor A (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Arano T., Yoshizato K.;
RT "Isolation of genes involved in intestinal remodeling during anuran
RT metamorphosis."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF170342; AAK11515.1; -.
DR HSP; P09651; 1HA1.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR00504; RNA_rec_mot.
DR Pfam; PF00076; rrm; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS0102; RRM; 1.
DR PROSITE; PS00030; RRM_RNP_1; 1.
FT NON_TER 131 131
SQ SEQUENCE 131 AA; 14156 MW; 72C57D5E6EAA7D7 CRC64;

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Query Match 53.4%; Score 39; DB 13; Length 131;  
Best Local Similarity 58.3%; Pred. No. 49;  
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GHEGCRSGEAG 12  
||| : |||  
Db 16 GHEACDAEAG 27

Search completed: April 19, 2004, 17:22:04  
Job time : 41.5806 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 19, 2004, 17:08:15 ; Search time 7.33871 Seconds  
(without alignments)  
92.239 Million cell updates/sec

Title: US-10-726-692-20

Perfect score: 73

Sequence: 1 GHEGCRSGEAGS 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	56.2	1053	1 SPS_SOLTU	Q43845 solanum tub
2	40	54.8	152	1 YOR4_EAV	P28994 equine arte
3	40	54.8	164	1 YOR2_AZOVI	O69219 azotobacter
4	40	54.8	626	1 E2K1_RABIT	P33279 o eukaryoti
5	39	53.4	292	1 PUR3_ARATH	P52422 arabidopsis
6	38	52.1	450	1 YEGD_ECOLI	P36928 escherichia
7	38	52.1	880	1 PODK_RICPR	Q92455 rickettsia
8	38	52.1	882	1 PPDK_RICCN	Q92418 rickettsia
9	38	52.1	1819	1 GCP6_HUMAN	Q96717 homo sapien
10	37	50.7	212	1 VE4_CREPK	P03124 cottontail
11	37	50.7	278	1 AS13_HUMAN	Q8WKK3 homo sapien
12	37	50.7	333	1 CATJ_MOUSE	Q9R014 mus musculu
13	37	50.7	416	1 FILA_HUMAN	P20930 homo sapien
14	37	50.7	610	1 CC20_YEAST	P26309 saccharomyc
15	37	50.7	797	1 STR3_MOUSE	Q9ERG2 mus musculu
16	37	50.7	797	1 STR3_MOUSE	Q13033 homo sapien
17	37	50.7	1621	1 ALK_MOUSE	P97793 mus musculu
18	37	50.7	2213	1 SORL_RABIT	Q95209 o sortilin
19	37	50.7	2215	1 SORL_MOUSE	O88307 m sortilin
20	36	49.3	72	1 MT13_MYTED	P80248 mytilus edu
21	36	49.3	72	1 MT14_MYTED	P80249 mytilus edu
22	36	49.3	72	1 MT1A_MYTED	O62546 mytilus edu
23	36	49.3	72	1 MT1B_MYTED	O62554 mytilus edu
24	36	49.3	73	1 MT_PERVI	Q9U568 perna virid
25	36	49.3	207	1 YQJ1_ECOLI	Q46872 escherichia
26	36	49.3	231	1 ISTE_PSEFL	Q51762 pseudomonas
27	36	49.3	263	1 DAPS_LISIN	Q92aa1 listeria in
28	36	49.3	277	1 IMD_STRCN	O33611 streptomyce
29	36	49.3	309	1 POB8_BRAJA	O95fg4 bradyrhizob
30	36	49.3	339	1 SYFA_CLOAB	O975k9 clostridium
31	36	49.3	351	1 ADH_MYCPN	F75214 mycoplasma
32	36	49.3	358	1 KLFI_MOUSE	P46099 mus musculu
33	36	49.3	413	1 YPIA_CAEEL	Q95qu0 caenorhabdi

34	36	49.3	435	1 TMS4_MOUSE	Q8vca5 mus musculu
35	36	49.3	451	1 NFS1_MOUSE	Q92lj3 mus musculu
36	36	49.3	451	1 NFS1_RAT	Q99p39 rattus norv
37	36	49.3	457	1 NFS1_HUMAN	Q9Y977 homo sapien
38	36	49.3	594	1 Y410_ARATH	P16128 arabidopsis
39	36	49.3	629	1 GIDA_BACRA	O811b3 bacillus an
40	36	49.3	629	1 GIDA_BACCR	O814f7 bacillus ce
41	36	49.3	630	1 GIDA_CLOPE	Q8xh31 clostridium
42	36	49.3	640	1 PPCM_CHICK	P21642 gallus gall
43	36	49.3	704	1 CLIF6_HUMAN	Q96ny7 homo sapien
44	36	49.3	704	1 FBL1_CHICK	O73775 gallus gall
45	36	49.3	727	1 VP4_EDVA	P22474 rice dwarf
46	36	49.3	796	1 MEN_DROME	P52302 drosophila
47	36	49.3	1181	1 MKX1_RAT	Q9qzm6 rattus norv
48	35	47.9	56	1 NT1_SYNVU	P30565 synechococc
49	35	47.9	89	1 TUBE_MYCTU	P02944 mycobacteri
50	35	47.9	179	1 CBFA_MAIZE	P25309 zea mays (m

## ALIGNMENTS

RESULT 1

ID	SPS_SOLTU	STANDARD;	PRT;	1053 AA.
AC	Q43845;			
DT	15-DEC-1998 (Rel. 37, Created)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DT	15-DEC-1998 (Rel. 37, Last annotation update)			
DE	Sucrose-phosphate synthase (EC 2.4.1.14) (UDP-glucose-fructose-phosphate glucosyltransferase).			
GN	SPS.			
OS	Solanum tuberosum (Potato).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;			
OC	lamids; Solanales; Solanaceae; Solanum.			
OX	NCBI_TaxId=4113;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Desiree; TISSUE=Leaf;			
RX	MEDLINE=95201832; PubMed=7894514;			
RA	Zrenner R., Salanoubat M., Willmitzer L., Sonnewald U.;			
RT	"Evidence of the crucial role of sucrose synthase for sink strength using transgenic potato plants (Solanum tuberosum L.).";			
RL	Plant J. 7:97-107(1995).			
CC	FUNCTION: Involved in the regulation of carbon partitioning in the leaves of plants. May regulate the synthesis of sucrose and therefore play a major role as a limiting factor in the export of photoassimilates out of the leaf.			
CC	CATALYTIC ACTIVITY: UDP-glucose + D-fructose 6-phosphate = UDP + sucrose 6-phosphate.			
CC	ENZYMATIC REGULATION: Activity regulated by phosphorylation and moderated by concentration of metabolites and light.			
CC	PATHWAY: Sucrose synthesis.			
CC	SUBUNIT: Homodimer or homotetramer (By similarity).			
CC	PTM: Phosphorylated. However, phosphorylation is not essential for enzyme function (By similarity).			
CC	SIMILARITY: Belongs to the glycosyltransferase family 1.			
CC	SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC	EMBL; X73477; CAA51872.1; -			
CC	PIR; S34172; S34172.			
CC	InterPro: IPR001296; Glyco trans 1.			
CC	Pfam; PF00534; Glycosyltransf_1; 1.			
CC	Transferrase; Glycosyltransferase; Phosphorylation.			
CC	SEQUENCE 1053 AA; 118292 MW; D6C933798567B20A CRC64;			

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Query Match          56.2%; Score 41; DB 1; Length 1053;
Best Local Similarity 66.7%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 HEGCRSGEAEGS 13
Db 439 HEGDMDGETEGS 450

RESULT 2
YOR4 EAV          STANDARD; PRT; 152 AA.
AC P28994;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE Hypothetical 17.2 kDa protein (ORF4).
OS Equine arteritis virus (EAV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Arteriviridae; Arterivirus.
NCBI_TaxID=11047;
RX STRAIN=Bucyrus;
RC MEDLINE=91237805; PubMed=1851863;
RA den Boon J.A., Snijder E.J., Chirnside E.D., de Vries A.A.F.,
RA Horzinek M.C., Spaan W.J.M.;
RT "Equine arteritis virus is not a togavirus but belongs to the
RT coronaviruslike superfamily.";
RL J. Virol. 65:2910-2920(1991).
CC 1- FUNCTION: Possible envelope protein.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF010139; AAC24480.1; -.
DR PIR; T44280; T44280.
DR InterPro; IPR000944; UPF0074.
DR Pfam; PF02082; Rrf2; 1.
DR ProDom; PD003632; UPF0074; 1.
DR TIGRFAMs; TIGR00738; rrf2_super; 1.
DR PROSITE; PS01332; UPF0074; 1.
KW Hypothetical protein.
SQ SEQUENCE 164 AA; 17831 MW; B03C777BF30654CE CRC64;

Query Match          54.8%; Score 40; DB 1; Length 164;
Best Local Similarity 77.8%; Pred. No. 6;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHEGCRSGE 9
Db 94 GDRGCRSGE 102

RESULT 4
EZKL_RABIT          STANDARD; PRT; 626 AA.
ID E2KJ_RABIT
AC P33279;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Eukaryotic translation initiation factor 2 alpha kinase 1
DE (EC 2.7.1.37) (Heme-regulated eukaryotic initiation factor eIF-2-alpha
DE kinase) (Heme-regulated inhibitor) (Heme-controlled repressor) (HCR)
DE (Hemin-sensitive initiation factor-2 alpha kinase).
GN EIF2AK1 OR HRI.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
RX SEQUENCE FROM N.A.
RC TISSUE=Reticulocytes;
RX MEDLINE=91352063; PubMed=1679235;
RA Chen J.-J., Throop M.S., Gehrke L., Kuo I., Pal J.K., Brodsky M.,
RA London I.M.;
RT "Cloning of the cDNA of the heme-regulated eukaryotic initiation
RT factor 2 alpha (eIF-2 alpha) kinase of rabbit reticulocytes: homology
RT to yeast GCN2 protein kinase and human double-stranded-RNA-dependent
RT eIF-2 alpha kinase.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:7729-7733(1991).
RN [2]
RN SEQUENCE OF 166-178; 454-467 AND 506-525.
RP TISSUE=Reticulocytes;
RX MEDLINE=91110520; PubMed=1671169;
RA Chen J.-J., Pal J.K., Petryshyn R., Kuo I., Yang J.M., Throop M.S.,
RA Gehrke L., London I.M.;
RT "Amino acid microsequencing of internal tryptic peptides of heme-
RT regulated eukaryotic initiation factor 2 alpha subunit kinase:
RT homology to protein kinases.";

```



Proc. Natl. Acad. Sci. U.S.A. 88:315-319(1991).  
 [3] PHOSPHORYLATION OF EIF2S1 AT SER-48.  
 CC TISSUE-Reticulocytes;  
 RN MEDLINE=86304412; PubMed=3745199;  
 RA Wittenhall R.E.H., Kudlicki W., Kramer G., Hardesty B.;  
 RT "The NH2-terminal sequence of the alpha and gamma subunits of  
 RT eukaryotic initiation factor 2 and the phosphorylation site for the  
 RT heme-regulated eif-2 alpha kinase.";  
 RL J. Biol. Chem. 261:12444-12447(1986).  
 RN [4]  
 RN REVIEW.  
 RN MEDLINE=95201039; PubMed=7893826;  
 RX Chen J.-J., Crosby J.S., London I.M.;  
 RA "Regulation of heme-regulated eif-2 alpha kinase and its expression  
 RT in erythroid cells.";  
 RL Biochimie 76:761-769(1994).  
 RN [5]  
 RN MUTAGENESIS OF LYS-199, AUTOPHOSPHORYLATION, AND HEME-BINDING.  
 RX MEDLINE=20138267; PubMed=10671563;  
 RA Rafie-Kolpin M., Chefalo P.J., Hussain Z., Hahn J., Uma S.,  
 RA Matts R.L., Chen J.-J.;  
 RT "Two heme-binding domains of heme-regulated eukaryotic initiation  
 RT factor-2alpha kinase. N terminus and kinase insertion.";  
 RL J. Biol. Chem. 275:5171-5178(2000).  
 RN [6]  
 RN INTERACTION WITH A MULTIPROTEIN COMPLEX CONTAINING HSP90; PPP5C AND  
 RX CDC37.  
 RX MEDLINE=22017694; PubMed=12022881;  
 RA Shao J., Hartson S.D., Matts R.L.;  
 RT "Evidence that protein phosphatase 5 functions to negatively modulate  
 RT the maturation of the Hsp90-dependent heme-regulated eif2alpha  
 RT kinase.";  
 RL Biochemistry 41:6770-6779(2002).  
 RN [7]  
 RN REGULATION BY NITRIC OXIDE AND CARBON MONOXIDE.  
 RX MEDLINE=22319058; PubMed=12431098;  
 RA Ishikawa H., Yun B.-G., Takahashi S., Horii H., Matts R.L.,  
 RA Ishimori K., Morishima I.;  
 RT "NO-induced activation mechanism of the heme-regulated eif2alpha  
 RT kinase.";  
 RL J. Am. Chem. Soc. 124:13696-13697(2002).  
 CC -!- FUNCTION: Mediates down-regulation of protein synthesis in heme-  
 CC deficient reticulocytes and in response to various stress  
 CC conditions by the phosphorylation of Eif2S1 at Ser-48 and Ser-51.  
 CC Protein synthesis is inhibited at the level of initiation.  
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
 CC -!- ENZYME REGULATION: Hemin inactivates Eif2AK1 by promoting the  
 CC formation of a disulfide-linked homodimer. Binding of nitric oxide  
 CC (NO) to the heme iron in the N-terminal heme-binding domain  
 CC activates the kinase activity, while binding of carbon monoxide  
 CC (CO) suppresses kinase activity.  
 CC -!- SUBUNIT: Synthesized in an inactive form that binds to the N-  
 CC terminal domain of CDC37. Has to be associated with a multiprotein  
 CC complex containing Hsp90, CDC37 and PPP5C for maturation and  
 CC activation by autophosphorylation. The phosphatase PPP5C modulates  
 CC this activation. Homodimer; non-covalently bound in the absence of  
 CC hemin. Converted to an inactive disulfide linked homodimer in the  
 CC presence of hemin.  
 CC -!- TISSUE SPECIFICITY: Reticulocytes.  
 CC -!- PTM: Activated by autophosphorylation (at least 5 moles of  
 CC phosphate per mole of enzyme). Phosphorylated predominantly on  
 CC serine and threonine residues, but also on tyrosine residues (By  
 CC similarity).  
 CC -!- MISCELLANEOUS: Can bind 2 molecules of heme per polypeptide chain.  
 CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. GCN2  
 CC subfamily.  
 CC -!- SIMILARITY: Contains 2 heme regulatory motif (HRM) repeats.  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; M69035; AAA31241.1; -;  
 CC PIR; A41284; A41284;  
 DR GO; GO:0005737; Cytoplasm; ISS.  
 DR GO; GO:0005524; P:ATP binding; NAS.  
 DR GO; GO:0004694; F:eukaryotic translation initiation factor 2a. . . ; IDA.  
 DR GO; GO:0020037; F:heme binding; ISS.  
 DR GO; GO:0042803; P:protein homodimerization activity; ISS.  
 DR GO; GO:0046777; P:autophosphorylation; ISS.  
 DR GO; GO:0008285; P:negative regulation of cell proliferation; ISS.  
 DR GO; GO:0046986; P:negative regulation of hemoglobin biosynthesis; ISS.  
 DR GO; GO:0045993; P:negative regulation of translational initia. . . ; ISS.  
 DR GO; GO:0018105; P:peptidyl-serine phosphorylation; IDA.  
 DR GO; GO:0006417; P:regulation of protein biosynthesis; NAS.  
 DR GO; GO:0009605; P:response to external stimulus; ISS.  
 DR GO; GO:0006950; P:response to stress; ISS.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR008271; Ser\_Thr\_pkin\_AS.  
 DR Pfam; PF00069; pkinase; 1.  
 DR ProDom; PD000001; Prot\_kinase; 2.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
 KW Transferase; Kinase; Serine/threonine-protein kinase;  
 KW Protein synthesis inhibitor; ATP-binding; Repeat; Phosphorylation.  
 FT DOMAIN 170 578  
 FT NP\_BIND 176 184  
 FT BINDING 199 199  
 FT ACT\_SITE 437 437  
 FT REPEAT 405 410  
 FT REPEAT 547 552  
 FT MOD\_RES 483 483  
 FT MUTAGEN 199 199  
 FT SEQUENCE 626 AA; 70274 MW; 4E47CC0173289B57 CRC64;  
 SQ  
 Query Match 54.8%; Score 40; DB 1; Length 626;  
 Best Local Similarity 66.7%; Pred. No. 26;  
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 GHEGCRSGEAG 12  
 DB 4 GSAGTRGGEAG 15  
 RESULT 5  
 PUR3\_ARATH  
 ID PUR3\_ARATH STANDARD; PRT; 292 AA.  
 AC P52422;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Phosphoribosylglycinamide formyltransferase, chloroplast precursor  
 DE (EC 2.1.2.2) (GART) (GAR transferase) (5'-phosphoribosylglycinamide  
 DE transformylase).  
 GN PUR3 OR AT1G31220 OR F28K20.18.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=95004650; PubMed=7920700;  
 RA Schnorr K.M., Nygaard P., Laloue M.;  
 RT "Molecular characterization of Arabidopsis thaliana cDNAs encoding  
 RL three purine biosynthetic enzymes.";  
 RN Plant J. 6:113-121(1994).  
 RP REVISIONS.

```

RA Schnorr K.M.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=cv. Columbia;
RC MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Egu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.B., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marzalli A.,
RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Uterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT thaliana.";
RL Nature 408:816-820(2000).
CC -!- CATALYTIC ACTIVITY: 10-formyltetrahydrofolate + N(1)-(5-phospho-D-
CC ribosyl)glycinamide = tetrahydrofolate + N(2)-formyl-N(1)-(5-
CC phospho-D-ribosyl)glycinamide.
CC -!- PATHWAY: De novo purine biosynthesis; third step.
CC -!- SUBCELLULAR LOCATION: Chloroplast.
CC -!- SIMILARITY: TO OTHER GART FROM BACTERIA AND EUKARYOTES.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC
CC EMBL; X74767; CAAS2779.2; -.
CC EMBL; AC004793; AAD21688.1; -.
CC PIR; D86438; D86438.
CC HSP; P08179; IGRC.
CC InterPro; IPR002376; formyl_transf.
CC InterPro; IPR001555; GART_AS.
CC Pfam; PF00551; formyl_transf; 1.
CC DR PROSITE; PS00373; GART; 1.
CC Purine biosynthesis; Transferase; Chloroplast; Transient peptide.
FT TRANSIT 1 ? CHLOROPLAST (POTENTIAL).
FT CHAIN ? 292 PHOSPHORIBOSYLGLYCNAMIDE
FT FORMYLTRANSFERASE.
FT ACT_SITE 227 227 BY SIMILARITY.
FT SEQUENCE 292 AA; 32170 MW; 880DBE443C7B493C CRC64;
SQ
Query Match 53.4%; Score 39; DB 1; Length 292;
Best Local Similarity 54.5%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2 HEGCGRGEAEG 12
Db 95 HEGCSDGSVNG 105
RESULT 6
ID YEGD_ECOLI STANDARD; PRT; 450 AA.
AC P36928; P76392;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical chaperone protein yegD.
GN YEGD OR B2069.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=K12 / MG1655;
RC MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=K12;
RC MEDLINE=97251358; PubMed=9097040;
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,
RA Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,
RA Saito N., Sampei G., Seki Y., Sivasubramanian S., Tagami H.,
RA Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 40.1-50.0 min region on the linkage map.";
RL DNA Res. 3:379-392(1996).
RN [3]
RP SEQUENCE OF 1-147 FROM N.A.
RX MEDLINE=85054800; PubMed=6094528;
RA Nakabepu Y., Miyata T., Kondo H., Iwanaga S., Sekiguchi M.;
RT "Structure and expression of the alka gene of Escherichia coli
RT involved in adaptive response to alkylating agents.";
RL J. Biol. Chem. 259:13730-13736(1984).
RN [4]
RP IDENTIFICATION.
RX MEDLINE=95026987; PubMed=7940673;
RA Borodovsky M., Koonin E.V., Rudd K.E.;
RT "New genes in old sequence: a strategy for finding genes in the
RT bacterial genome.";
RL Trends Biochem. Sci. 19:309-313(1994).
RN [5]
RP IDENTIFICATION.
RX MEDLINE=95075659; PubMed=7984428;
RA Borodovsky M., Rudd K.E., Koonin E.V.;
RT "Intrinsic and extrinsic approaches for detecting genes in a
RT bacterial genome.";
RL Nucleic Acids Res. 22:4756-4767(1994).
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AE000297; AAC75130.1; ALT_INIT.
CC EMBL; D90845; BAA15927.1; -.
CC EMBL; K02498; -; NOT_ANNOTATED_CDS.
CC EcoGene; EG12200; yegD.
CC InterPro; IPR001023; Hsp70.
CC Pfam; PF00012; HSP70; 2.
CC ProDom; PD000089; Hsp70; 2.
CC PROSITE; PS00297; HSP70_1; FALSE_NEG.
CC PROSITE; PS00329; HSP70_2; 1.
CC PROSITE; PS01036; HSP70_3; FALSE_NEG.
CC Hypothetical protein; Chaperone; ATP-binding; Complete proteome.
CC CONFLICT 145 147 LPE -> GIL (IN REF. 3).
CC SEQUENCE 450 AA; 49371 MW; C25A8AE1D6F44C2D CRC64;
SQ
Query Match 52.1%; Score 38; DB 1; Length 450;

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Best Local Similarity 75.0%; Pred. No. 40; Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHEGCRSG 8  
 DB 244 GHGCKRIG 251

RESULT 7  
 PDK RICPR STANDARD; PRT; 880 AA.  
 AC Q92D5; 349 405  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Pyruvate,phosphate dikinase (EC 2.7.9.1) (Pyruvate,orthophosphate dikinase)  
 GN PDK OR RP492.  
 OS Rickettsia prowazekii.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;  
 OC Rickettsiaceae; Rickettsiae; Rickettsia.  
 OX NCBI\_TaxID=782;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Madrid E;  
 RX MEDLINE=99039499; PubMed=9823893;  
 RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,  
 RA Sikeritz-Ponten T., Almark U.C.M., Podowski A.K.,  
 RA Eriksson A.-S., Winkler H.H., Kurland C.G.;  
 RT "The genome sequence of Rickettsia prowazekii and the origin of mitochondria";  
 RT Nature 396:133-140(1998).  
 RL Nature 396:133-140(1998).  
 CC -!- FUNCTION: Catalyzes the reversible phosphorylation of pyruvate and phosphate (By similarity).  
 CC -!- CATALYTIC ACTIVITY: ATP + pyruvate + phosphate = AMP + phosphoenolpyruvate + diphosphate.  
 CC -!- COFACTOR: Magnesium ion (By similarity).  
 CC -!- SUBUNIT: Homodimer (By similarity).  
 CC -!- DOMAIN: The N-terminal domain contains the ATP/Pi active site, the central domain the pyrophosphate/phosphate carrier His-460, and the C-terminal domain the pyruvate active site.  
 CC -!- MISCELLANEOUS: The reaction takes place in three steps, each mediated by a carrier histidine residue located on the surface of the central domain. The two first partial reactions are catalyzed at an active site located on the N-terminal domain, and the third partial reaction is catalyzed at an active site located on the C-terminal domain. For catalytic turnover, the central domain swivels from the concave surface of the N-terminal domain to that of the C-terminal domain.  
 CC -!- SIMILARITY: Belongs to the PEP-utilizing enzyme family.  
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 CC EMBL; AJ235272; CNA14944.1; .  
 CC PIR; F71652; F71652.  
 CC HSSP; P22983; 2DIK.  
 CC InterPro; IPR008279; PEP mobile.  
 CC InterPro; IPR001021; PEP-utilizers.  
 CC InterPro; IPR002192; PDK\_N term.  
 CC Pfam; PF00391; PEP-utilizers; 1.  
 CC Pfam; PF02896; PEP-utilizers C; 1.  
 CC Pfam; PF01326; PDK\_N term; 1.  
 CC ProDom; PD000940; PEP-utilizers; 1.  
 CC ProSITE; PS00370; PEP-ENZYMES PHOS\_SITE; 1.  
 CC ProSITE; PS00742; PEP-ENZYMES; 1.  
 KW Transfrase; Kinase; ATP-binding; Magnesium; Phosphorylation; Complete proteome.

FT DOMAIN 1 348 N-TERMINAL.  
 FT DOMAIN 349 405 LINKER 1.  
 FT DOMAIN 406 503 CENTRAL.  
 FT DOMAIN 504 538 LINKER 2.  
 FT DOMAIN 539 880 C-TERMINAL.  
 FT ACT\_SITE 460 TELE-PHOSPHOHISTIDINE INTERMEDIATE (BY SIMILARITY).  
 FT NP\_BIND 97 ATP (POTENTIAL).  
 FT NP\_BIND 246 ATP (POTENTIAL).  
 FT METAL 329 MAGNESIUM 1 (PROBABLE).  
 FT METAL 331 MAGNESIUM 1 (PROBABLE).  
 FT METAL 343 MAGNESIUM 1 (PROBABLE).  
 FT METAL 750 MAGNESIUM 2 (PROBABLE).  
 FT METAL 774 MAGNESIUM 2 (PROBABLE).  
 FT MOD\_RES 458 PHOSPHORYLATION (BY SIMILARITY).  
 SQ SEQUENCE 880 AA; 98302 MW; C8CB877B7EAF3AFC64;

Query Match 52.1%; Score 38; DB 1; Length 880;  
 Best Local Similarity 75.0%; Pred. No. 82; Mismatches 0; Gaps 0;  
 Matches 6; Conservative 0; Indels 2; Indels 0; Gaps 0;

QY 1 GHEGCRSG 8  
 DB 668 GHGCKRIG 675

RESULT 8  
 PDK RICCN STANDARD; PRT; 882 AA.  
 AC Q92H18;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Pyruvate,phosphate dikinase (EC 2.7.9.1) (Pyruvate,orthophosphate dikinase)  
 GN PDK OR RC0783.  
 OS Rickettsia conorii.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;  
 OC Rickettsiaceae; Rickettsiae; Rickettsia.  
 OX NCBI\_TaxID=781;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Malish 7;  
 RX MEDLINE=21442074; PubMed=11557893;  
 RA Ogata H., Audic S., Renseto-Audiffren P., Fournier P.-E., Barbe V.,  
 RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,  
 RA Raoult D.;  
 RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii";  
 RT Science 293:2093-2098(2001).  
 CC -!- FUNCTION: Catalyzes the reversible phosphorylation of pyruvate and phosphate (By similarity).  
 CC -!- CATALYTIC ACTIVITY: ATP + pyruvate + phosphate = AMP + phosphoenolpyruvate + diphosphate.  
 CC -!- COFACTOR: Magnesium ion (By similarity).  
 CC -!- SUBUNIT: Homodimer (By similarity).  
 CC -!- DOMAIN: The N-terminal domain contains the ATP/Pi active site, the central domain the pyrophosphate/phosphate carrier His-463, and the C-terminal domain the pyruvate active site.  
 CC -!- MISCELLANEOUS: The reaction takes place in three steps, each mediated by a carrier histidine residue located on the surface of the central domain. The two first partial reactions are catalyzed at an active site located on the N-terminal domain, and the third partial reaction is catalyzed at an active site located on the C-terminal domain. For catalytic turnover, the central domain swivels from the concave surface of the N-terminal domain to that of the C-terminal domain.  
 CC -!- SIMILARITY: Belongs to the PEP-utilizing enzyme family.  
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CC -----  
CC EMBL; AB008634; AL03321.1; --  
CC PIR; G97797; G97797.  
CC InterPro; IPR008279; PEP mobile.  
DR InterPro; IPR00121; PEP utilizers.  
DR InterPro; IPR002192; PEP N term.  
DR Pfam; PF00391; PEP-utilizers; 1.  
DR Pfam; PF02896; PEP-utilizers; C; 1.  
DR Pfam; PF01326; PEP N term; 1.  
DR ProDom; PD000940; PEP utilizers; 1.  
DR PROSITE; PS00742; PEP ENZYMES 2; 1.  
DR PROSITE; PS00370; PEP ENZYMES PHOS SITE; 1.  
KW Transferase; kinase; ATP-binding; Magnesium; Phosphorylation;  
Complete proteome.  
FT DOMAIN 1 351 N-TERMINAL.  
FT DOMAIN 352 408 LINKER 1.  
FT DOMAIN 409 506 CENTRAL.  
FT DOMAIN 507 541 LINKER 2.  
FT DOMAIN 542 882 C-TERMINAL.  
FT ACT\_SITE 463 463 TELE-PHOSPHOHISTIDINE INTERMEDIATE  
(BY SIMILARITY).  
FT NP\_BIND 100 100 ATP (POTENTIAL).  
FT NP\_BIND 249 249 ATP (POTENTIAL).  
FT METAL 332 332 MAGNESIUM 1 (PROBABLE).  
FT METAL 334 334 MAGNESIUM 1 (PROBABLE).  
FT METAL 346 346 MAGNESIUM 1 (PROBABLE).  
FT METAL 753 753 MAGNESIUM 2 (PROBABLE).  
FT METAL 777 777 MAGNESIUM 2 (PROBABLE).  
FT MOD\_RES 461 461 PHOSPHORYLATION (BY SIMILARITY).  
SQ SEQUENCE 882 AA; 98278 MW; 8B4AEB53F6F63D3 CRC64;  
Query Match 52.1%; Score 38; DB 1; Length 882;  
Best Local Similarity 75.0%; Pred. No. 82;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 CHEGCSG 8  
Db 671 GHRGCRLG 678  
RESULT 9  
GCP6\_HUMAN STANDARD; PRT; 1819 AA.  
AC Q96RT7; Q9BY91; Q9UGX3; Q9UGX4;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Gamma-tubulin complex component 6 (GCP-6).  
GN TUBGCP6 OR GCP6 OR KIAA1659.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
[1]  
RP SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.  
RX MEDLINE=2151508; PubMed=11694571;  
RA Murphy S.M., Preble A.M., Patel U.K., O'Connell K.L., Dias D.P.,  
RA Moritz M., Agard D., Stults J.T., Stearns T.;  
RT "GCP5 and GCP6: two new members of the human gamma-tubulin complex.";  
RL Mol. Biol. Cell 12:3340-3352(2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20057165; PubMed=10591208;  
RA Dunham I., Hunt A.R., Collins J.E., Bruskewich R., Beare D.M.,  
RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,  
RA Baggeley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,  
RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,  
RA Burrill W.D., Burton J., Carter C., Carter N.P., Chen Y., Clark G.,  
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,  
RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,  
RA Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,

RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,  
RA Gilbert J.G.R., Goward M.E., Grafton D.V., Griffiths M.N.D., Hall C.,  
RA Hall R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S.,  
RA Hunt S.E., Jones M.C., Kerhaw J., Kimberley A.M., King A.,  
RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,  
RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,  
RA Mcclay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,  
RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,  
RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,  
RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,  
RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,  
RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.B.,  
RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,  
RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,  
RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,  
RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Matsuyama S.,  
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,  
RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,  
RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,  
RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,  
RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,  
RA Zhan M., Zhang G., Chisoe S., Murray J., Miller N., Minx P.,  
RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,  
RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,  
RA Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,  
RA Scheet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J.,  
RA Korf I., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,  
RA Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S.,  
RA Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,  
RA Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P.,  
RA Peyraud M., Kedra D., Seroussi E., Fransson I., Tapia I., Bruder C.E.,  
RA O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,  
RA Khan A.S., Lane L., Tilahun Y., Wright H.;  
RT "The DNA sequence of human chromosome 22.";  
RL Nature 402:489-495(1999).  
RN [3]  
RP SEQUENCE OF 33-1819 FROM N.A. (ISOFORM 2).  
RC TISSUE=Brain;  
RX MEDLINE=21156230; PubMed=11258795;  
RA Hiroseawa M., Nagase T., Murahashi Y., Kikuno R., Ohara O.;  
RT "Identification of novel transcribed sequences on human chromosome 22  
by expressed sequence tag mapping.";  
RL DNA Res. 8:1-9(2001).  
CC -!- FUNCTION: Gamma-tubulin complex is necessary for microtubule  
nucleation at the centrosome.  
CC -!- SUBUNIT: Gamma-tubulin complex is composed of gamma-tubulin, GCP2,  
GCP3, GCP4, GCP5 and GCP6.  
CC -!- SUBCELLULAR LOCATION: Centrosome.  
CC -!- ALTERNATIVE PRODUCTS:  
Event=Alternative splicing; Named isoforms=2;  
Name=1;  
IsoId=Q96RT7-1; Sequences=Displayed;  
Name=2;  
IsoId=Q96RT7-2; Sequences=VSP 001624;  
CC Note=No experimental confirmation available;  
CC -!- SIMILARITY: Belongs to the GCP family.  
CC -!- CAUTION: Ref.3 sequence differs from that shown due to frameshifts  
in positions 1371 and 1758.  
-----  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
CC EMBL; AF272887; AAK82968.1; --  
DR EMBL; AL022328; CAB63046.1; ALT SEQ.  
DR EMBL; AL022328; CAB63047.1; ALT\_SEQ.  
DR EMBL; AB051456; BAB33339.1; ALT\_FRAME.  
DR Genew; HGNC:18127; TUBGCP6.  
DR GO; GO:0008274; C:gamma-tubulin ring complex; IDA.

DR GO: GO:0008017; F-microtubule binding; IDA.  
DR GO: GO:0007020; P-microtubule nucleation; IDA.  
DR InterPro: IPR007259; SPC97\_Spc98.  
DR Pfam: PF04130; SPC97\_Spc98; 1.

KW Microtubule; Repeat; Alternative splicing.  
FT DOMAIN 1027 1269 9 X 27 AA TANDEM REPEATS.  
FT REPEAT 1027 1053 1.  
FT REPEAT 1054 1080 2.  
FT REPEAT 1081 1107 3.  
FT REPEAT 1108 1134 4.  
FT REPEAT 1135 1161 5.  
FT REPEAT 1162 1188 6.  
FT REPEAT 1189 1215 7.  
FT REPEAT 1216 1242 8.  
FT REPEAT 1243 1269 9.  
FT VARSPLIC 1724 1757 Missing (in isoform 2).  
FT FTIG=VSP 001624.  
FT S -> L (IN REF. 3).  
FT CONFLICT 1377 1377 A -> T (IN REF. 2 AND 3).  
FT CONFLICT 1621 1621 L -> V (IN REF. 2).  
FT CONFLICT 1621 1621 L -> V (IN REF. 2).  
SQ SEQUENCE 1819 AA; 200455 MW; 923576544D34594A CRC64;

-Query Match 52.1%; Score 38; DB 1; Length 1819;  
Best Local Similarity 63.6%; Pred. No. 1.8e+02;  
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GHGCRSGBAE 11  
Db 839 GGQGCDSGAE 849

RESULT 10  
VE4 CRPVK STANDARD; PRT; 212 AA.  
AC P03124;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DE 01-OCT-1996 (Rel. 34, Last annotation update)  
DE Probable E4 protein.  
GN E4.

OS Cottontail rabbit (shope) papillomavirus (strain Kansas) (CRPV).  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Papillomavirus.  
OX NCBI\_TaxId=31553;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85166175; PubMed=2984661;  
RA Giri I., Danos O., Yaniv M.;  
RT "Genomic structure of the cottontail rabbit (Shope) papillomavirus."  
RL Proc. Natl. Acad. Sci. U.S.A. 82:1580-1584(1985).  
CC -----  
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CC -----  
CC EMBL; K02708; -; NOT\_ANNOTATED\_CDS.  
DR PIR; A03674; W4WLRB.  
KW Early protein.  
SQ SEQUENCE 212 AA; 24104 MW; 9FB8DA3FB14ADB5B CRC64;

Query Match 50.7%; Score 37; DB 1; Length 212;  
Best Local Similarity 62.5%; Pred. No. 26;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GHGCRSG 8  
Db 156 GHQGCNEG 163

RESULT 11  
AS13 HUMAN STANDARD; PRT; 278 AA.  
ID AS13 HUMAN STANDARD; PRT; 278 AA.  
AC Q8WKK3; Q8WEP7; Q9H821;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ankyrin repeat and SOCS box containing protein 13 (ASB-13).  
GN ASB13.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxId=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RA Kile B.T., Nicola N.A.;  
RT "SOCS box proteins."  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RA Isozaki T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,  
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,  
RA Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,  
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,  
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,  
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,  
RA Ninomiya K., Iwayanagi T.;  
RT "NEO human cDNA sequencing project."  
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM 2).  
RC TISSUE=Uterus;  
RX MEDLINE=23388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=1;  
CC IsoId=Q8WKK3-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=Q8WKK3-2; Sequence=VSP 000272, VSP 000273;  
CC Note=No experimental confirmation available;  
CC -!- SIMILARITY: Contains 6 ANK repeats.  
CC -!- SIMILARITY: Contains 1 SOCS box domain.  
CC -!- CAUTION: Ref.1 sequence differs from that shown due to a  
CC frameshift in position 14.  
CC -----  
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CC -----  
CC

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DR EMBL; AF403031; AAL57350.1; ALT_FRAME.
DR EMBL; AK023196; BAB14456.1; -.
DR EMBL; BC012056; AAH12056.1; -.
DR Genew; HGNC:19765; ASB13.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR001496; SOCS_C.
DR Pfam; PF00023; ank; 6.
DR PRINTS; PR01415; ANKYRIN.
DR SMART; SM00248; ANK; 6.
DR PROSITE; PS50088; ANK REPEAT; 6.
DR PROSITE; PS50297; ANK REP REGION; 1.
DR PROSITE; PS50225; SOCS; 1.
KW ANK repeat; Repeat; Alternative splicing.
FT REPEAT 18 47 ANK 1.
FT REPEAT 51 80 ANK 2.
FT REPEAT 84 113 ANK 3.
FT REPEAT 116 145 ANK 4.
FT REPEAT 149 178 ANK 5.
FT REPEAT 181 210 ANK 6.
FT DOMAIN 229 278 SOCS BOX.
FT VARSPPLIC 173 173 G -> A (in isoform 2).
FT VARSPPLIC 174 278 /FTID=VSP 000272.
FT VARSPPLIC 174 278 Missing (in isoform 2).
FT CONFLICT 104 104 L -> S (IN REF. 2).
FT CONFLICT 129 129 S -> D (IN REF. 1).
SQ SEQUENCE 278 AA; 30007 MW; 6E54725A70AB32EF CRC64;

Query Match 50.7%; Score 37; DB 1; Length 278;
Best Local Similarity 60.0%; Pred. No. 35;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 HEGCRSGEAE 11
||| ||| |||
DB 122 HEACMSGSSSE 131

RESULT 12
CATU_MOUSE
ID CATU_MOUSE STANDARD; PRT; 333 AA.
AC Q9R014; Q9WV51;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cathepsin J precursor (EC 3.4.22.-) (Cathepsin P) (Catlrp-p).
GN CTSJ OR CTSP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=99456833; PubMed=10526153;
RA Tislar K., Deussing J., Peters C.;
RT "Cathepsin J, a novel murine cysteine protease of the papain family
with a placenta-restricted expression.";
RL FEBS Lett. 459:299-304(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Placenta;
RA Sol-Church K., French J., Troeber D., Mason R.W.;
RT "Cloning of a mouse cysteine protease.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Lysosomal (Potential).
CC -!- TISSUE SPECIFICITY: Expressed in placenta.
CC -!- SIMILARITY: Belongs to peptidase family C1.
-----
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CC EMBL; AF136272; AAF13142.1; -.
CC EMBL; AF158182; AAD41898.1; -.
DR HSSP; P07711; 1CJL.
DR MEROPS; C01.038; -.
DR MGD; MGI:1349426; Ctsj.
DR InterPro; IPR000668; Peptidase_C1.
DR InterPro; IPR00169; SHprot_acsite.
DR Pfam; PF00112; Peptidase_C1; 1.
DR PRINTS; PR00705; PAPAIN.
DR ProDom; PD000158; Peptidase_C1; 1.
DR SMART; SM00645; Pept_C1; 1.
DR PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.
DR PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.
DR PROSITE; PS00640; THIOL_PROTEASE_ASN; 1.
KW Hydrolase; Thiol protease; Glycoprotein; Lysosome; Zymogen; Signal.
FT SIGNAL 1 17 POTENTIAL.
FT PROPEP 18 112 ACTIVATION PEPTIDE.
FT CHAIN 113 333 CATHEPSIN J.
FT ACT_SITE 137 137 BY SIMILARITY.
FT ACT_SITE 275 275 BY SIMILARITY.
FT ACT_SITE 299 299 BY SIMILARITY.
FT DISULFID 134 177 BY SIMILARITY.
FT DISULFID 168 210 BY SIMILARITY.
FT DISULFID 268 321 BY SIMILARITY.
FT CARBOHYD 71 71 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 216 216 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 220 220 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 267 267 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 42 42 P -> PK (IN REF. 2).
SQ SEQUENCE 333 AA; 37147 MW; F9A8FF1D5A13B721 CRC64;

Query Match 50.7%; Score 37; DB 1; Length 333;
Best Local Similarity 60.0%; Pred. No. 43;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHEGCRSGEA 10
|::|||::|
DB 173 GNKGCSGTA 182

RESULT 13
FILA_HUMAN
ID FILA_HUMAN STANDARD; PRT; 416 AA.
AC P20930;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Filaggrin precursor (Fragment).
GN FLG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89296901; PubMed=2740331;
RA McKinley-Grant L.J., Idler W.W., Bernstein I.A., Parry D.A.D.,
RA Canizarro L., Croce C.M., Huebner K., Lessin S.R., Steinert P.M.;
RT "Characterization of a cDNA clone encoding human filaggrin and
localization of the gene to chromosome region 1q21.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:4848-4852(1989).
RN [2]
RP CITRULLINATION.
RX MEDLINE=96374388; PubMed=8780679;
RA Seneshu T., Kan S., Ogawa H., Manabe M., Asaga H.;
RT "Preferential demination of keratin K1 and filaggrin during the
terminal differentiation of human epidermis.";
RL Biochem. Biophys. Res. Commun. 225:712-719(1996).
CC -!- FUNCTION: Aggregates keratin intermediate filaments and promotes
disulfide-bond formation among the intermediate filaments during
```



CC terminal differentiation of mammalian epidermis.  
 CC -!- PTM: Filaggrin is initially synthesized as a large, insoluble,  
 CC highly phosphorylated precursor containing many tandem copies of  
 CC 324 AA, which are not separated by "large linker". The precursor  
 CC is deposited as keratohyalin granules. During terminal  
 CC differentiation it is dephosphorylated and proteolytically  
 CC cleaved.  
 CC -!- PTM: Undergoes deamination of some arginine residues  
 CC (citrullination).  
 CC -----  
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 CC -----  
 CC EMBL; M24355; AA52454.1; -.  
 CC PIR; A32947; A32947.  
 CC Genew; HGNC:3748; FLG.  
 CC MIM; 135940; -.  
 CC GO; GO:0005882; C:intermediate filament; NAS.  
 CC GO; GO:0005198; F:structural molecule activity; NAS.  
 CC GO; GO:0007275; P:development; NAS.  
 CC InterPro; IPR003303; Filaggrin.  
 CC Pfam; PF03516; Filaggrin; 2.  
 CC PRINTS; PR00487; FILAGGRIN.  
 CC Phosphorylation; Citrullination; Developmental protein.  
 CC NON\_TER 1  
 CC SEQUENCE 416 AA; 44105 MW; DEEA3218BA043F32 CRC64;  
 CC  
 CC Query Match 50.7%; Score 37; DB 1; Length 416;  
 CC Best Local Similarity 53.8%; Pred. No. 54;  
 CC Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
 CC  
 CC QY 1 GHEGCRSGEABGS 13  
 CC || || || || ||  
 CC Db 76 GHRGSSSGRQGS 88  
 CC  
 CC RESULT 14  
 CC CC20\_YEAST STANDARD; PRT; 610 AA.  
 CC AC P26309;  
 CC DT 01-MAY-1992 (Rel. 22, Created)  
 CC DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 CC DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 CC DE Cell division control protein 20.  
 CC GN CDC20 OR YGL116W.  
 CC OS Saccharomyces cerevisiae (Baker's yeast).  
 CC OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 CC OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 CC OX NCBI\_TaxId=4932;  
 CC (1)  
 CC SEQUENCE FROM N.A.  
 CC STRAIN=A364A;  
 CC MEDLINE=92017840; PubMed=1922065;  
 CC RA Sethi N., Monteaudo M.C., Koshland D., Hogan E., Burke D.J.;  
 CC RT "The CDC20 gene product of Saccharomyces cerevisiae, a beta-transducin  
 CC RT homolog, is required for a subset of microtubule-dependent cellular  
 CC RT processes.";  
 CC RL Mol. Cell. Biol. 11:5592-5602(1991).  
 CC (2)  
 CC RP SEQUENCE FROM N.A.  
 CC RA Lauquin G.;  
 CC RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
 CC (3)  
 CC RP SEQUENCE OF 50-610 FROM N.A.  
 CC RA Doi A., Doi K.;  
 CC RL Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.  
 CC (4)  
 CC RP INTERACTION WITH PDS1.

RX MEDLINE=21437412; PubMed=11553328;  
 RA Hilioti Z., Chung Y.-S., Mochizuki Y., Hardy C.F.J., Cohen-Fix O.;  
 RT "The anaphase inhibitor pds1 binds to the APC/C-associated protein  
 RT Cdc20 in a destruction box-dependent manner.";  
 RL Curr. Biol. 11:1347-1352(2001).  
 RN (5)  
 RP REVIEW.  
 RX MEDLINE=22347229; PubMed=12459453;  
 RA Irniger S.;  
 RT "Cyclin destruction in mitosis: a crucial task of Cdc20.";  
 RL FEBS Lett. 532:7-11(2002).  
 CC -!- FUNCTION: Activator protein, which is required for proteolytic  
 CC destruction of cyclins during mitosis. Acts via its interaction  
 CC with the ubiquitin ligase APC/C complex. Plays an essential role  
 CC in mitosis' exit by directing degradation of CLB2 cyclin. Also  
 CC required for two microtubule-dependent processes, nuclear  
 CC movements prior to anaphase and chromosome separation. CDC20 may  
 CC modulate microtubule structure either by promoting microtubule  
 CC disassembly or by altering the surface of the microtubules.  
 CC -!- SIMILARITY: Contains 7 WD repeats.  
 CC -!- CAUTION: Ref.1 sequence differs from that shown due to a  
 CC frameshift in position 502.  
 CC -----  
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 CC -----  
 CC EMBL; X59428; CAA42058.1; ALT\_FRAME.  
 CC EMBL; 272638; CAA96824.1; -.  
 CC EMBL; D16506; BAA03957.1; -.  
 CC PIR; S64126; S64126.  
 CC GerMOnline; 141164; -.  
 CC SGD; S0003084; CDC20.  
 CC InterPro; IPR000002; Fizzy.  
 CC InterPro; IPR001680; WD40.  
 CC Pfam; PF00400; WD40; 5.  
 CC ProDom; PD004563; Fizzy; 1.  
 CC SMART; SM00320; WD40; 5.  
 CC PROSITE; PS00678; WD\_REPEATS\_1; 4.  
 CC PROSITE; PS00682; WD\_REPEATS\_2; 2.  
 CC PROSITE; PS0294; WD\_REPEATS\_REGION; 1.  
 CC Cell division; Mitosis; Activator; Microtubule; Repeat; WD repeat.  
 KW REPEAT 257 296 WD 1.  
 FT REPEAT 299 338 WD 2.  
 FT REPEAT 342 379 WD 3.  
 FT REPEAT 383 422 WD 4.  
 FT REPEAT 425 467 WD 5.  
 FT REPEAT 469 519 WD 6.  
 FT REPEAT 523 562 WD 7.  
 FT CONFLICT 318 319 IG -> MA (IN REF. 3).  
 FT CONFLICT 502 519 PENALISVNYETKFKVAE -> QRMQSLFIMKQSKLOK  
 FT (IN REF. 1).  
 FT CONFLICT 520 610 MISSING (IN REF. 1).  
 SQ SEQUENCE 610 AA; 67359 MW; CCE7CD149C1F5ACF CRC64;  
 CC  
 CC Query Match 50.7%; Score 37; DB 1; Length 610;  
 CC Best Local Similarity 54.5%; Pred. No. 82;  
 CC Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 CC  
 CC QY 1 GHEGCRSGEAB 11  
 CC || || || || ||  
 CC Db 577 GKEGCRINDXE 587  
 CC  
 CC RESULT=15  
 CC STR3\_MOUSE  
 CC ID STR3\_MOUSE STANDARD; PRT; 796 AA.  
 CC AC Q9ERG2;  
 CC DT 28-FEB-2003 (Rel. 41, Created)

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DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Striatin 3 (Cell-cycle autoantigen SG2NA) (S/G2 antigen).
GN STRN3 OR SG2NA OR GS2NA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RA Castets F., Rakitina T.; PubMed=10748158;
RT "Expression analysis of SG2NA isoform.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RN TISSUE SPECIFICITY.
RP MEDLINE=20347911; PubMed=10748158;
RX Castets F., Rakitina T., Gaillard S., Moqrigh A., Mattei M.-G.,
RA Monneron A.;
RT "Zinedin, SG2NA, and striatin are calmodulin-binding, WD repeat
RT proteins principally expressed in the brain.";
RL J. Biol. Chem. 275:19970-19977(2000).
CC -!- FUNCTION: Binds calmodulin in a calcium dependent manner. May
CC function as scaffolding or signaling protein (By similarity).
CC -!- SUBUNIT: INTERACTS WITH PROTEIN PHOSPHATASE 2A (PP2A) (POTENTIAL).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic and membrane-bound.
CC -!- TISSUE SPECIFICITY: MAINLY EXPRESSED IN THE BRAIN AND MUSCLES BUT
CC IS ALSO DETECTED AT LOW LEVELS IN VARIOUS TISSUES SUCH AS KIDNEY,
CC SPLEEN AND LUNG.
CC -!- SIMILARITY: Belongs to the WD-repeat striatin family.
CC -!- SIMILARITY: Contains 6 WD repeats.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF307777; AAC24454.1; -.
CC MGI; MGI:2151064; Strn3.
CC InterPro; IPR001680; WD40.
CC Pfam; PF00400; WD40; 6.
CC PRINTS; PR00320; GPROTEINRPT.
CC ProDom; PD0000018; WD40; 2.
CC SMART; SM00320; WD40; 7.
CC PROSITE; PS00678; WD_REPEATS_1; 2.
CC PROSITE; PS50082; WD_REPEATS_2; 4.
CC PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Calmodulin-binding; Repeat; WD repeat; Coiled coil; Antigen.
FT DOMAIN 77 136 COILED COIL (POTENTIAL).
FT REPEAT 477 516 WD 1.
FT REPEAT 530 569 WD 2.
FT REPEAT 583 622 WD 3.
FT REPEAT 678 717 WD 4.
FT REPEAT 720 759 WD 5.
FT REPEAT 766 795 WD 6.
FT DOMAIN 6 13 POLY-GLY.
FT SITE 71 79 CAVEOLIN-BINDING (POTENTIAL).
SQ SEQUENCE 796 AA; 87150 MW; 161FAF5DDEBE23DD CRC64;

Query Match      50.7%; Score 37; DB 1; Length 796;
Best Local Similarity 70.0%; Pred. No. 1.le+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 HEGCRSGEAE 11
      ||| | | |
Db      405 HEGARAEAE 414

RESULT 16
STR3_HUMAN

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ID STR3_HUMAN STANDARD; PRT; 797 AA.
AC Q13033; OGNRA5;
DT 15-JUL-1998 (Rel. 36, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Striatin 3 (Cell-cycle autoantigen SG2NA) (S/G2 antigen).
DE Striatin 3 (Cell-cycle autoantigen SG2NA) (S/G2 antigen).
GN STRN3 OR SG2NA OR GS2NA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A. (ISOFORM ALPHA).
RP TISSUE=Liver;
RX MEDLINE=95169142; PubMed=7864889;
RA Muro Y., Chan E.K., Landberg G., Tan E.M.;
RT "A cell-cycle nuclear autoantigen containing WD-40 motifs expressed
RT mainly in S and G2 phase cells.";
RL Biochem. Biophys. Res. Commun. 207:1029-1037(1995).
RN [2]
RP SEQUENCE OF 120-797 FROM N.A. (ISOFORM BETA).
RX MEDLINE=20347911; PubMed=10748158;
RA Castets F., Rakitina T., Gaillard S., Moqrigh A., Mattei M.-G.,
RA Monneron A.;
RT "Zinedin, SG2NA, and striatin are calmodulin-binding, WD repeat
RT proteins principally expressed in the brain.";
RL J. Biol. Chem. 275:19970-19977(2000).
CC -!- FUNCTION: Binds calmodulin in a calcium dependent manner. May
CC function as scaffolding or signaling protein.
CC -!- SUBUNIT: INTERACTS WITH PROTEIN PHOSPHATASE 2A (PP2A) (POTENTIAL).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic and membrane-bound (By
CC similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Additional isoforms seem to exist;
CC Name=Beta;
CC IsoId=Q13033-1; Sequence=Displayed;
CC Name=Alpha;
CC IsoId=Q13033-2; Sequence=VSP_006786;
CC -!- SIMILARITY: Belongs to the WD-repeat striatin family.
CC -!- SIMILARITY: Contains 6 WD repeats.
CC -!- CAUTION: Was originally (Ref.1) thought to be nuclear.
CC -----
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CC -----
CC EMBL; U17989; AAB81551.1; -.
CC EMBL; AF243424; AAF81201.1; -.
CC PIR; JC2522; JC2522.
CC Genew; HGNC:15720; STRN3.
CC GO; GO:0005829; C:cytosol; NAS.
CC GO; GO:0005624; C:membrane fraction; NAS.
CC GO; GO:0005634; C:nucleus; IDA.
CC GO; GO:0005516; F:calmodulin binding; NAS.
CC GO; GO:0007049; P:cell cycle; IDA.
CC InterPro; IPR001680; WD40.
CC Pfam; PF00400; WD40; 6.
CC PRINTS; PR00320; GPROTEINRPT.
CC ProDom; PD0000018; WD40; 2.
CC SMART; SM00320; WD40; 7.
CC PROSITE; PS00678; WD_REPEATS_1; 2.
CC PROSITE; PS50082; WD_REPEATS_2; 4.
CC PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Calmodulin-binding; Repeat; WD repeat; Coiled coil; Antigen;
KW Alternative splicing.
FT DOMAIN 77 136 COILED COIL (POTENTIAL).
FT REPEAT 166 183 CALMODULIN-BINDING (POTENTIAL).
FT REPEAT 478 517 WD 1.

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FT REPEAT 531 570 WD 2.
FT REPEAT 584 623 WD 3.
FT REPEAT 679 718 WD 4.
FT REPEAT 721 760 WD 5.
FT REPEAT 767 796 WD 6.
FT DOMAIN 6 13 POLY-GLY.
FT SITE 71 79 CAVEOLIN-BINDING (POTENTIAL).
FT VARSPLIC 330 413 Missing (in isoform Alpha).
FT SEQUENCE 797 AA; 87133 MW; AD83F259C52185D CRC64;

Query Match 50.7%; Score 37; DB 1; Length 797;
Best Local Similarity 70.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 HEGCRSGEAE 11
DB 406 HEGARAEEAE 415

RESULT 17
ALK MOUSE STANDARD; PRT; 1621 AA.
ID ALK MOUSE STANDARD; PRT; 1621 AA.
AC P97793;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE ALK tyrosine kinase receptor precursor (EC 2.7.1.112) (Anaplastic
DE lymphoma kinase).
GN ALK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SOURCE FROM N.A.
RC TISSUE=Brain, and Testis;
RX MEDLINE=9717863; PubMed=9053841;
RA Iwahara T., Fujimoto J., Wen D., Cupples R., Bucay N., Arakawa T.,
RA Mori S., Ratzkin B., Yamamoto T.;
RT "Molecular characterization of ALK, a receptor tyrosine kinase
RT expressed specifically in the nervous system.";
RL Oncogene 14:439-449(1997).
CC -!- FUNCTION: Orphan receptor with a tyrosine-protein kinase activity.
CC Appears to play an important role in the normal development and
CC function of the nervous system.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC -!- SIMILARITY: Belongs to the Tyr family of protein kinases. Insulin
CC receptor subfamily.
CC -!- SIMILARITY: Contains 1 LDL-receptor class A domain.
CC -!- SIMILARITY: Contains 2 MAM domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D83002; BAA11673.1; -
CC F01; T30200; T30200.
CC HSP; P08631; IAD5.
CC MGD; MG1:103305; Alk.
CC InterPro; IPR002172; LDL receptor_A.
CC InterPro; IPR000998; MAM domain.
CC InterPro; IPR000719; Prot kinase.
CC InterPro; IPR002011; RecepttyrkinII.
CC InterPro; IPR001245; Tyr_pkinase_AS.
CC InterPro; IPR008266; Tyr_pkinase_1.
CC Pfam; PF00629; MAM; 1.

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DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PD00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00192; LDLA; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00740; MAM_1; FALSE_NEG.
DR PROSITE; PS00060; MAM_2; 2.
DR PROSITE; PS01209; LDLA_1; FALSE_NEG.
DR PROSITE; PS00668; LDLA_2; FALSE_NEG.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
DR Phosphatase; Tyrosine-protein kinase; Transmembrane; ATP-binding;
KW Phosphorylation; Receptor; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 1621 ALK TYROSINE KINASE RECEPTOR.
FT DOMAIN 19 1042 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1043 1063 POTENTIAL.
FT DOMAIN 1064 1621 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 268 431 MAM 1.
FT DOMAIN 441 477 LDL-RECEPTOR CLASS A.
FT DOMAIN 482 640 MAM 2.
FT DOMAIN 1120 1396 PROTEIN KINASE.
FT DOMAIN 820 944 GLY-RICH.
FT NP_BIND 1126 1134 ATP (BY SIMILARITY).
FT BINDING 1154 1154 ATP (BY SIMILARITY).
FT ACT_SITE 1253 1253 BY SIMILARITY.
FT MOD_RES 1286 1286 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CARBOHYD 174 174 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 248 248 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 328 328 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 415 415 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 428 428 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 449 449 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 567 567 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 575 575 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 631 631 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 673 673 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 713 713 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 812 812 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 868 868 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 890 890 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 990 990 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 1621 AA; 174919 MW; 16E252BF21AADE22 CRC64;

Query Match 50.7%; Score 37; DB 1; Length 1621;
Best Local Similarity 54.5%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 HEGCRSGEAE 12
DB 462 HQDCAQGEDEG 472

RESULT 18
SORL RABIT STANDARD; PRT; 2213 AA.
ID SORL RABIT STANDARD; PRT; 2213 AA.
AC Q95209;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Sortilin-related receptor precursor (Sorting protein-related receptor
DE containing LDLR class A repeats) (SorLA) (SorLA-1) (Low-density
DE lipoprotein receptor relative with 11 ligand-binding repeats) (LDLR
DE relative with 11 ligand-binding repeats) (LR11).
GN SORL1.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]

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FT CARBOHYD 2053 2053 N-LINKED (GLNAC. . .) (POTENTIAL).  
 FT CARBOHYD 2068 2068 N-LINKED (GLNAC. . .) (POTENTIAL).  
 FT CARBOHYD 2075 2075 N-LINKED (GLNAC. . .) (POTENTIAL).  
 FT CARBOHYD 2091 2091 N-LINKED (GLNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 2213 AA; 247764 MW; A54232645A5A0DDA CRC64;  
 Query Match 50.7%; Score 37; DB 1; Length 2213;  
 Best Local Similarity 38.5%; Pred. No. 3.3e+02;  
 Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 GHEGCRSGEARGES 13  
 ||:|:|:|:  
 Db 1492 GHQDCQDGGDEAN 1504  
 RESULT 19  
 SORL MOUSE  
 ID SORL MOUSE STANDARD; PRT; 2215 AA.  
 AC Q88307; O54711; O70581;  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Sortilin-related receptor precursor (Sortin-1) (Low-density  
 containing LDLR class A repeats) (msSortin-1)  
 DE lipoprotein receptor relative with 11 ligand-binding repeats (LDLR  
 relative with 11 ligand-binding repeats) (LR11) (Gp250).  
 GN SORL1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=98392848; PubMed=9726247;  
 RA Kanaki T., Bujo H., Hirayama S., Tanaka K., Yamazaki H., Seimiya K.,  
 RA Morisaki N., Schneider W.J., Saito Y.;  
 RT "Developmental regulation of Ldlr expression in murine brain.";  
 RL DNA Cell Biol. 17:647-657(1998).  
 RN [2]  
 RP SEQUENCE OF 183-2215 FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=98168844; PubMed=9510025;  
 RA Hermans-Borgmeyer I., Hampe W., Schinke B., Methner A., Nykjaer A.,  
 RA Suenens U., Fenger U., Herbarth B., Schaller H.C.;  
 RT "Unique expression pattern of a novel mosaic receptor in the  
 developing cerebral cortex.";  
 RL Mech. Dev. 70:65-76(1998).  
 RN [3]  
 RP SEQUENCE OF 1119-1713 FROM N.A.  
 RC STRAIN=Swiss Webster;  
 RA Boehmelt G., Antonio L., Iscove N.N.;  
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Likely to be a multifunctional endocytic receptor, that  
 may be implicated in the uptake of lipoproteins and of proteases.  
 CC Binds LDL, the major cholesterol-carrying lipoprotein of plasma,  
 CC and transports it into cells by endocytosis. Binds the receptor-  
 CC associated protein (RAP). Could play a role in cell-cell  
 CC interaction. May play a role in neural organization, as well as  
 CC the establishment of embryonic organ systems.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
 CC -!- TISSUE SPECIFICITY: Abundant in brain, where it is mainly  
 CC expressed in adult cerebellum, hippocampal ca regions, dentate  
 CC gyrus, and to a much lesser extent in the cerebral cortex.  
 CC Detectable in kidney, skeletal muscle, lung and spleen, but not in  
 CC the liver.  
 CC -!- DEVELOPMENTAL STAGE: Expressed as early as embryonic day 6.5  
 CC (E6.5) and peaks at E11, the main location is in the CNS during  
 CC development. At early stages, it is abundant in a subpopulation of  
 CC neurons in the cerebral cortex, in the hippocampus, and granular  
 CC and Purkinje cell layers in the cerebellum, whereas in the adult,  
 CC expression in cerebellar granular cells and in the cerebral cortex  
 CC is low. Expression occurs also in a variety of glands and organs

CC during organogenesis.  
 CC -!- PTM: THE PROPEPTIDE REMOVED IN THE N-TERMINUS MAY BE CLEAVED BY  
 CC FURIN OR HOMOLOGOUS PROTEASES (BY SIMILARITY).  
 CC -!- SIMILARITY: Contains 5 BNR repeats.  
 CC -!- SIMILARITY: Contains 1 EGF-like domain.  
 CC -!- SIMILARITY: Contains 11 LDL-receptor class A domains.  
 CC -!- SIMILARITY: Contains 6 fibronectin type III domains.  
 CC  
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 CC  
 CC EMBL; AB015790; BAA31219.1; -;  
 CC EMBL; AF031816; AAC16739.1; -;  
 CC EMBL; Y12004; CAA72732.1; -;  
 CC FIR; T00348; T00348.  
 CC HSP; P01130; IAUJ.  
 CC MGD; MGI:1202296; Sor11.  
 CC InterPro; IPR006209; EGF like.  
 CC InterPro; IPR008957; FN III-like.  
 CC InterPro; IPR003961; FN III.  
 CC InterPro; IPR002860; GH BNR.  
 CC InterPro; IPR006210; IEGF.  
 CC InterPro; IPR002172; LDL receptor A.  
 CC InterPro; IPR000033; Ldl\_receptor\_rep.  
 CC InterPro; IPR006581; VPS10.  
 CC Pfam; PF02012; BNR; 5.  
 CC Pfam; PF00041; FN3; 4.  
 CC Pfam; PF00057; Ldl\_recept\_a; 11.  
 CC Pfam; PF00058; Ldl\_recept\_b; 5.  
 CC PRINTS; SM00261; LDLRECEPTOR.  
 CC SMART; SM00181; EGF; 1.  
 CC SMART; SM00060; FN3; 4.  
 CC SMART; SM00192; LDLA; 11.  
 CC SMART; SM00135; LY; 5.  
 CC SMART; SM00602; VPS10; 1.  
 CC PROSITE; PS01186; EGF 2; 1.  
 CC PROSITE; PS01209; LDLRA\_1; 10.  
 CC PROSITE; PS50068; LDLRA\_2; 11.  
 CC Endocytosis; Receptor; Transmembrane; EGF-like domain; Repeat;  
 CC Glycoprotein; LDL; Lipid transport; Cholesterol metabolism; Signal;  
 CC Developmental protein.  
 FT SIGNAL 1 28  
 FT PROPEP 29 81  
 FT  
 FT CHAIN 82 2215  
 FT DOMAIN 82 2138  
 FT TRANSMEM 2139 2159  
 FT DOMAIN 2160 2215  
 FT REPEAT 136 147  
 FT REPEAT 232 243  
 FT REPEAT 441 452  
 FT REPEAT 521 532  
 FT REPEAT 562 573  
 FT DOMAIN 803 977  
 FT REPEAT 803 806  
 FT REPEAT 847 850  
 FT REPEAT 891 894  
 FT REPEAT 934 937  
 FT REPEAT 974 977  
 FT DOMAIN 1026 1072  
 FT DOMAIN 1076 1114  
 FT DOMAIN 1115 1155  
 FT DOMAIN 1156 1194  
 FT DOMAIN 1197 1237  
 FT DOMAIN 1237 1273  
 FT DOMAIN 1273 1317  
 FT DOMAIN 1323 1361  
 FT DOMAIN 1366 1405



```

DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Metallothionein 10-IV (MT-10-IV).
OS Mytilus edulis (Blue mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
OC Mytiloidea; Mytilidae; Mytilus.
OX NCBI_TaxID=6550;
RN [1]
RP SEQUENCE.
RX MEDLINE=94062828; PubMed=8243463;
RA Mackay E.A., Overnell J., Dunbar B., Davidson I., Hunziker P.E.,
RA Kaegi J.H.R., Fothergill J.E.;
RT "Complete amino acid sequences of five dimeric and four monomeric
RT forms of metallothionein from the edible mussel Mytilus edulis.";
RL Eur. J. Biochem. 218:183-194(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Digestive gland;
RX MEDLINE=99206055; PubMed=10190057;
RA Barsyte D., White K.N., Lovejoy D.A.;
RT "Cloning and characterization of metallothionein cDNAs in the mussel
RT Mytilus edulis L. digestive gland.";
RL Comp. Biochem. Physiol. 122C:287-296(1999).
CC -!- FUNCTION: The metallothioneins are involved in the cellular
CC sequestration of toxic metal ions.
CC -!- SUBUNIT: Monomer.
CC -!- INDUCTION: By cadmium.
CC -!- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 2.
CC
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CC
DR EMBL; AJ007506; CAA07546.1; --
DR EMBL; AJ005455; CAA0552.1; --
DR PIR; S39419; S39419.
DR InterPro; IPR003019; Metallthion_
DR Pfam; PF00131; metalthio; 1.
DR PRINTS; PR00875; MTWOLLUSC.
KW Metal-binding; Metal-thiolate cluster; Cadmium.
FT INIT MET 0
SQ SEQUENCE 72 AA; 6979 MW; 7FA028637D837269 CRC64;

Query Match 49.3%; Score 36; DB 1; Length 72;
Best Local Similarity 75.0%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 EGCRCGEA 10
Db 21 EGCRCGDA 28

RESULT 22
MT1A MYTED STANDARD; PRT; 72 AA.
AC P80246;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)

QY 3 EGCRCGEA 10
Db 21 EGCRCGDA 28

RESULT 22
MT1A MYTED STANDARD; PRT; 72 AA.
AC P80246;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)

```

```

DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Metallothionein 10-1a (MT-10-1a).
OS Mytilus edulis (Blue mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
OC Mytiloidea; Mytilidae; Mytilus.
OX NCBI_TaxID=6550;
RN [1]
RP SEQUENCE.
RX MEDLINE=94062828; PubMed=8243463;
RA Mackay E.A., Overnell J., Dunbar B., Davidson I., Hunziker P.E.,
RA Kaegi J.H.R., Fothergill J.E.;
RT "Complete amino acid sequences of five dimeric and four monomeric
RT forms of metallothionein from the edible mussel Mytilus edulis.";
RL Eur. J. Biochem. 218:183-194(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Digestive gland;
RX MEDLINE=99206055; PubMed=10190057;
RA Barsyte D., White K.N., Lovejoy D.A.;
RT "Cloning and characterization of metallothionein cDNAs in the mussel
RT Mytilus edulis L. digestive gland.";
RL Comp. Biochem. Physiol. 122C:287-296(1999).
CC -!- FUNCTION: The metallothioneins are involved in the cellular
CC sequestration of toxic metal ions.
CC -!- SUBUNIT: Monomer.
CC -!- INDUCTION: By cadmium.
CC -!- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 2.
CC
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CC
DR EMBL; AJ005451; CAA06548.1; --
DR PIR; S39416; S39416.
DR InterPro; IPR003019; Metallthion_
DR Pfam; PF00131; metalthio; 1.
DR PRINTS; PR00875; MTWOLLUSC.
KW Metal-binding; Metal-thiolate cluster; Cadmium.
FT INIT MET 0
SQ SEQUENCE 72 AA; 7105 MW; 3EA99D959AEBB3B2 CRC64;

Query Match 49.3%; Score 36; DB 1; Length 72;
Best Local Similarity 75.0%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 EGCRCGEA 10
Db 21 EGCRCGDA 28

RESULT 23
MT1B MYTED STANDARD; PRT; 72 AA.
AC O62554;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Metallothionein 10-1b (MT-10-1b).
OS Mytilus edulis (Blue mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
OC Mytiloidea; Mytilidae; Mytilus.
OX NCBI_TaxID=6550;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Digestive gland;
RX MEDLINE=99206055; PubMed=10190057;
RA Barsyte D., White K.N., Lovejoy D.A.;
RT "Cloning and characterization of metallothionein cDNAs in the mussel

```

RT *Mytilus edulis* L. digestive gland.;  
RL Comp. Biochem. Physiol. 122C:287-296 (1999).  
CC -!- FUNCTION: The metallothioneins are involved in the cellular  
CC sequestration of toxic metal ions.  
CC -!- SUBUNIT: Monomer.  
CC -!- INDUCTION: By cadmium.  
CC -!- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 2.  
CC  
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CC  
CC EMBL; AJ005452; CAA06549.1; -.  
DR InterPro; IPR003019; Metallthion.  
DR Pfam; PF00131; metalthio; 1.  
DR PRINTS; PR00875; MTMOLLUSC.  
KW Metal-binding; Metal-thiolate cluster.  
FT INIT MET 0 0 By similarity.  
SQ SEQUENCE 72 AA; 7089 MW; 291F46EF9AEBB3B2 CRC64;  
  
Query Match 49.3%; Score 36; DB 1; Length 72;  
Best Local Similarity 75.0%; Pred. No. 12;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 3 EGCRCGEA 10  
||||| |:  
DB 21 EGCRCGDA 28  
  
RESULT 24  
MT PERVI STANDARD; PRT; 73 AA.  
AC Q9U568; O96388; Q9U569;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Metallothionein (MT).  
GN MT1 AND MT2.  
OS *Perna viridis* (Tropical green mussel).  
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;  
OC Mytiloidea; Mytilidae; Perna.  
OX NCBI\_TaxID=73031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99379847; PubMed=10451422;  
RA Khoo H.W., Patel K.H.;  
RT "Metallothionein cDNA, promoter, and genomic sequences of the tropical  
RT green mussel, *Perna viridis*.";  
RL J. Exp. Zool. 284:445-453 (1999).  
CC -!- FUNCTION: The metallothioneins are involved in the cellular  
CC sequestration of toxic metal ions.  
CC -!- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 2.  
CC  
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CC  
CC EMBL; AF092971; AAF22486.1; -.  
DR EMBL; AF092972; AAF22487.1; -.  
DR EMBL; AF036904; AAD02054.1; -.  
DR HSP; P05106; 1JUV2.  
DR InterPro; IPR003019; Metallthion.  
DR Pfam; PF001008; Metallthion\_2.  
DR Pfam; PF00131; metalthio; 1.

DR PRINTS; PR00875; MTMOLLUSC.  
KW Metal-binding; Metal-thiolate cluster; Cadmium.  
FT CONFLICT 38 C -> CGC (IN REF. 1; AAD02054).  
SQ SEQUENCE 73 AA; 7254 MW; 42293A9547DF5CA8 CRC64;  
  
Query Match 49.3%; Score 36; DB 1; Length 73;  
Best Local Similarity 75.0%; Pred. No. 12;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 3 EGCRCGEA 10  
||||| |:  
DB 22 EGCRCGDA 29  
  
RESULT 25  
YQJI ECOLI STANDARD; PRT; 207 AA.  
ID YQJI ECOLI  
AC Q46872;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Hypothetical protein yqji.  
GN YQJI OR B3071 OR SF3112 OR S3318.  
OS *Escherichia coli*, and  
OS *Shigella flexneri*.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; *Escherichia*.  
OX NCBI\_TaxID=562, 623;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX SPECIES=E.coli; STRAIN=K12 / MG1655;  
RX MEDLINE=97426617; PubMed=9278503;  
RA Blattner F.R.; Plunkett G. III; Bloch C.A.; Perna N.T.; Burland V.,  
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
RA Mau B., Shao Y.;  
RT "The complete genome sequence of *Escherichia coli* K-12.";  
RL Science 277:1453-1474 (1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;  
RX MEDLINE=2272406; PubMed=12384590;  
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,  
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,  
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding X., Chen S.,  
RA Cheng H., Yao Z., He B., Chen K., Ma D., Qiang B., Wen Y., Hou Y.,  
RA Xu J.;  
RT "Genome sequence of *Shigella flexneri* 2a: insights into pathogenicity  
RT through comparison with genomes of *Escherichia coli* K12 and O157.";  
RL Nucleic Acids Res. 30:4432-4441 (2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX SPECIES=S.flexneri; STRAIN=2457T / ATCC 700930 / Serotype 2a;  
RX MEDLINE=22590274; PubMed=12704152;  
RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,  
RA Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,  
RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,  
RA Schwartz D.C., Blattner F.R.;  
RT "Complete genome sequence and comparative genomics of *Shigella*  
RT flexneri serotype 2a strain 2457T.";  
RL Infect. Immun. 71:2775-2786 (2003).  
CC  
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CC  
CC EMBL; U28379; AAA89150.1; -.  
DR EMBL; AE000389; AAC76106.1; -.  
DR EMBL; AE015322; AAN44586.1; -.

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DR EMBL; AE016988; AAP18398.1; -.
DR PIR; D65095; D65095.
DR EcoGene; EG12954; YQJ1.
DR InterPro; IPR005149; PadR.
DR Pfam; PF03551; PadR; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 207 AA; 23401 MW; DD3D108D83E087F7 CRC64;

Query Match 49.3%; Score 36; DB 1; Length 207;
Best Local Similarity 75.0%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 HEGCRSGE 9
DB 17 HEGCKCKGE 24

RESULT 26
ID ISTB_PSEFL STANDARD; PRT; 231 AA.
AC Q51762;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Insertion sequence IS1162 putative ATP-binding protein.
OS Pseudomonas fluorescens.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=294;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ST;
RX MEDLINE=95212933; PubMed=7698671;
RA Solinas F., Marconi A.M., Ruzzi M., Zennaro E.;
RT "Characterization and sequence of a novel insertion sequence, IS1162,
from Pseudomonas fluorescens.";
RL Gene 155:77-82(1995).
CC -! SIMILARITY: BELONGS TO THE IS21/IS1162 PUTATIVE ATP-BINDING
PROTEIN FAMILY.
CC
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CC
CC EMBL; X79443; CAAS5960.1; -.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR002611; IstB_ATPbind.
DR Pfam; PF01695; IstB; 1.
DR SMART; SM00382; AAA; 1.
KW Transposable element; ATP-binding.
FT NP BIND 107 114 ATP (POTENTIAL).
SQ SEQUENCE 231 AA; 25997 MW; 341592AEA7DD794A CRC64;

Query Match 49.3%; Score 36; DB 1; Length 231;
Best Local Similarity 62.5%; Pred. No. 43;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHEGCRSG 8
DB 121 GHOACRQG 128

RESULT 27
ID DAPB_LISIN STANDARD; PRT; 263 AA.
AC Q92AA1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Dihydrodipicolinate reductase (EC 1.3.1.26) (DHPR).
GN DAPB OR LIN2021.
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1642;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIP 11262 / Serovar 6a;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaeser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
BA Quero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domant E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kref J., Kuhn M., Kunst F., Kurapkak G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehlant J., Cossart P.;
RL "Comparative genomics of Listeria species.";
SC Science 294:849-852(2001).
CC -! CATALYTIC ACTIVITY: 2.3.4.5-tetrahydrodipicolinate + NAD(P)(+) =
2,3-dihydrodipicolinate + NAD(P)H.
CC -! PATHWAY: Biosynthesis of diaminopimelate and lysine from aspartate
semialdehyde; second step.
CC -! SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -! SIMILARITY: Belongs to the dihydrodipicolinate reductase family.
CC
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CC
CC EMBL; AL596170; CAC97251.1; -.
DR PIR; AC1685; AC1685.
DR ListList; LIN02021; -.
DR HAMAP; MF_00102; -.
DR InterPro; IPR000846; DapB.
DR Pfam; PF05173; DapB_C; 1.
DR Pfam; PF01113; DapB_N; 1.
DR ProDom; PD004105; DapB; 1.
DR TIGRFAMs; TIGR00036; dapB; 1.
DR PROSITE; PS01298; DAPB; 1.
KW Diaminopimelate biosynthesis; Lysine biosynthesis; Oxidoreductase;
NADP; Complete proteome.
SQ SEQUENCE 263 AA; 28985 MW; 76550A4E0AA312D2 CRC64;

Query Match 49.3%; Score 36; DB 1; Length 263;
Best Local Similarity 70.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 EGCRSGEAG 12
DB 190 EGARGGEYEG 199

RESULT 28
ID IMD_STRCN STANDARD; PRT; 277 AA.
AC O33611;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Inhibition of morphological differentiation protein.
OS Streptomyces cyaneus (Streptomyces curvaci).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1904;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 14921 / PK100C;
RA Nishiyama T., Sakemi H., Doi K., Ogata S.;
RT "Analysis of chromosomal DNA fragment concerned with inhibition of
RL morphological differentiation in Streptomyces azureus.";
RL Submitted (JUN-1997) to the EMBL/GenBank/DDAJ databases.
CC -!- SIMILARITY: Belongs to the serB family.
CC -----
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CC -----
DR EMBL; AB004855; BAA21085.1; -.
DR InterPro; IPR006383; HAD_SF_IB.
DR InterPro; IPR006385; HAD_SF_IB_hyp2.
DR InterPro; IPR005834; Hydrolase.
DR Pfam; PF00702; Hydrolase; 1.
DR TIGRFAMs; TIGR01490; HAD-SF-IB-hyp1; 1.
DR TIGRFAMs; TIGR01488; HAD-SF-IB; 1.
KW Hydrolase.
SQ SEQUENCE 277 AA; 30275 MW; CA9BC322EBDF6A2 CRC64;

Query Match 49.3%; Score 36; DB 1; Length 277;
Best Local Similarity 54.5%; Pred. No. 52;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GHEGCRSGEAE 11
DB 151 GDGCGTGEVE 161

RESULT 29
PQOB BRAJA
ID PQOB BRAJA STANDARD; PRT; 309 AA.
AC Q89FG4;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Coenzyme PQQ synthetase protein B (Pyrroloquinoline quinone
DE biosynthesis protein B).
GN PQOB OR BLR6736.
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA 110;
RX MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA Sasamoto S., Watanabe A., Iidesawa K., Iriguchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimpō S., Teurouka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT Bradyrhizobium japonicum USDA110.";
RL DNA Res. 9:189-197(2002).
CC -!- FUNCTION: May be involved in the transport of PQQ or its precursor
CC to the periplasm (By similarity).
CC -!- PATHWAY: Pyrroloquinoline quinone (PQQ) biosynthesis.
CC -!- SIMILARITY: Belongs to the pqqB family.
CC -----
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DR EMBL; AP005959; BACS2001.1; -.
DR HAMAP; MF_00653; -. 1.
KW PQQ biosynthesis; Transport; Complete proteome.
SQ SEQUENCE 309 AA; 32725 MW; F9D9803E1E2B66CA CRC64;

Query Match 49.3%; Score 36; DB 1; Length 309;
Best Local Similarity 58.3%; Pred. No. 59;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GHEGCRSGEAEG 12
DB 21 CGCGCTARAIG 32

RESULT 30
SIFA CLOAB
ID SYFA CLOAB STANDARD; PRT; 339 AA.
AC Q97KG9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phenylalanyl-tRNA synthetase alpha chain (EC 6.1.1.20)
DE (Phenylalanyl-tRNA synthetase alpha chain) (PHERS).
GN PHERS OR CAC2357.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
RA Tatunov R.I., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA Bennett G.N., Koonin E.V., Smith D.R.;
RT "Genome sequence and comparative analysis of the solvent-producing
RT bacterium Clostridium acetobutylicum.";
RL J. Bacteriol. 183:4823-4838(2001).
CC -!- CATALYTIC ACTIVITY: ATP + L-phenylalanine + tRNA(Phe) = AMP +
CC diphosphate + L-phenylalanyl-tRNA(Phe).
CC -!- COFACTOR: Binds 2 magnesium ions per tetramer (By similarity).
CC -!- SUBUNIT: Tetramer of two alpha and two beta chains (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
CC Phe-tRNA synthetase alpha chain subfamily 1.
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CC -----
DR EMBL; AE007736; AAK80313.1; -.
DR PIR; F97190; F97190.
DR HAMAP; MF_00281; -. 1.
DR InterPro; IPR004188; Phe tRNA_synth_N.
DR InterPro; IPR004529; PheS.
DR InterPro; IPR002319; tRNA-synth_2d.
DR InterPro; IPR006195; tRNA_ligase_II.
DR Pfam; PF01409; tRNA-synth_N; 1.
DR Pfam; PF01409; tRNA-synth_2d; 1.
DR TIGRFAMs; TIGR00468; pheS; 1.
DR PROSITE; PS50862; AA tRNA_LIGASE II; 1.
DR Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW Metal-binding; Magnesium; Complete proteome.
FT METAL 254 254 MAGNESIUM (By SIMILARITY).
SQ SEQUENCE 339 AA; 38508 MW; 229E76449BE10918 CRC64;

Query Match 49.3%; Score 36; DB 1; Length 339;

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Best Local Similarity 58.3%; Pred. No. 65;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GHEGCRSRAEG 12
DB 267 GGGGCRVCKGEG 278

RESULT 31
ADH_MYCPN STANDARD; PRT; 351 AA.
AC P75214;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Probable NADP-dependent alcohol dehydrogenase (EC 1.1.1.2).
GN ADH OR MPN564 OR MP278.
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2104;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 29342 / ML29;
RX MEDLINE=97105885; PubMed=8948633;
RA Himmelreich R., Hilbert H., Plegens H., Pirkel E., Li B.-C.,
RT Herrmann R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
RL Nucleic Acids Res. 24:4420-4449(1996).
CC -!- CATALYTIC ACTIVITY: An alcohol + NADP(+) = an aldehyde + NADPH.
CC -!- COPACTOR: Binds 1 zinc ion per subunit (By similarity).
CC -!- SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
CC family.
CC
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CC
CC EMBL; AF0000027; AAB95926.1; -.
CC PIR; S73604; S73604.
CC HSSP; P14941; 1YKF.
CC InterPro; IPR0023328; ADH zinc.
CC InterPro; IPR002085; Adh_zn_family.
CC Pfam; PF00107; Adh_zinc_N; 1.
CC PROSITE; PS00059; ADH_ZINC; 1.
CC Oxidoreductase; Zinc; Metal-binding; NADP; Complete proteome.
FT METAL 37 37 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 59 59 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 60 60 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 150 150 ZINC (CATALYTIC) (BY SIMILARITY).
SQ SEQUENCE 351 AA; 37812 MW; 3153B93BFF64D2C CRC64;

Query Match 49.3%; Score 36; DB 1; Length 351;
Best Local Similarity 53.8%; Pred. No. 67;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 GHEGCRSRAEGS 13
DB 58 GHEGCGVDEVG 70

RESULT 32
KLFI_MOUSE STANDARD; PRT; 358 AA.
AC P46039; O70261;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Erythroid krueppel-like transcription factor (EKLF) (Erythroid

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DE transcription factor).
GN KLFI OR ELKF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=93233640; PubMed=7682653;
RA Miller I.J., Bieker J.J.;
RT "A novel, erythroid cell-specific murine transcription factor that
RT binds to the CACCC element and is related to the Kruppel family of
RT nuclear proteins.";
RL Mol. Cell. Biol. 13:2776-2786(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RA Jenkins N.A., Gilbert D.J., Copeland N.G., Gruzglin B., Bieker J.J.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RX MEDLINE=96025976; PubMed=7565748;
RA Anderson K.P., Kern C.B., Crable S.C., Lingrel J.B.;
RT "Isolation of a gene encoding a functional zinc finger protein
RT homologous to erythroid Kruppel-like factor: identification of a new
RT multigene family.";
RL Mol. Cell. Biol. 15:5957-5965(1995).
CC -!- FUNCTION: BINDS TO THE CACCC BOX IN THE BETA-GLOBIN GENE PROMOTER
CC AND ACTIVATES TRANSCRIPTION. PROBABLY SERVES AS A GENERAL SWITCH
CC FACTOR FOR ERYTHROID DEVELOPMENT.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: Erythroid specific. Only expressed in bone
CC marrow and spleen.
CC
CC -!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
CC FINGER PROTEINS.
CC
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CC
CC EMBL; M97200; AAA37546.1; ALT_INIT.
CC EMBL; AF019074; AAB87861.1; -.
CC EMBL; AF033102; AAC24497.1; -.
CC HSSP; P08047; 1SP2.
CC TRANSFAC; T01676; -.
CC MGD; MGI:1342771; Klfl.
CC InterPro; IPR007087; Znf_C2H2.
CC Pfam; PF00096; zf-C2H2; 3.
CC ProDom; PD000003; Znf_C2H2; 1.
CC SMART; SM00355; Znf_C2H2; 3.
CC PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
CC PROSITE; PS0157; ZINC_FINGER_C2H2_2; 3.
CC Transcription regulation; Activator; Zinc-finger; Metal-binding;
KW DNA-binding; Nuclear protein; Repeat.
FT DOMAIN 1 269 PRO-RICH.
FT DOMAIN 58 76 ASP/GLU-RICH (ACIDIC).
FT ZN_FING 275 299 C2H2-TYPE.
FT ZN_FING 305 329 C2H2-TYPE.
FT ZN_FING 335 357 C2H2-TYPE.
FT CONFLICT 94 94 C -> Y (IN REF. 3).
FT CONFLICT 116 116 A -> T (IN REF. 3).
FT CONFLICT 223 223 G -> P (IN REF. 3).
FT CONFLICT 287 287 S -> T (IN REF. 3).
SQ SEQUENCE 358 AA; 37757 MW; 6FD59F294DDA45D1 CRC64;

Query Match 49.3%; Score 36; DB 1; Length 358;
Best Local Similarity 46.2%; Pred. No. 69;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

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QY      1 GHEGCRSGEAGS 13
Db      278 GHEGCKSYKSS 290

RESULT 33
YPIA CAEEL
ID YPIA CAEEL STANDARD; PRT; 413 AA.
AC Q95000;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein C27F2.10 in chromosome III.
GN C27F2.10.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]_TaxID=6239;
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Kirsten J.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP REVISIONS.
RA Waterston R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO S.POMBE SPAC1B3.08.
CC -----
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CC -----
CC EMBL; U40419; AAL02444.1; -.
DR WormPep; C27F2.10; CE29189.
DR InterPro; IPR000717; PCI.
DR Pfam; PF01399; PCI; 1.
KW Hypothetical protein.
SQ SEQUENCE 413 AA; 47157 MW; C34F4CF20246F4D4 CRC64;

Query Match 49.3%; Score 36; DB 1; Length 413;
Best Local Similarity 58.3%; Pred. No. 80;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1 GHEGCRSGEAG 12
Db      130 GAECVSGDDEG 141

RESULT 34
TMS4 MOUSE
ID TMS4 MOUSE STANDARD; PRT; 435 AA.
AC Q8VCA5;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Transmembrane protease, serine 4 (EC 3.4.21.-) (Channel-activating
DE protease 2) (mCAP2).
GN TMRSS4 OR CAP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22144321; PubMed=12149280;
RA Vuagniaux G., Vallet V., Jaeger N.F., Hummler E., Rossier B.C.;
RT "Synergistic activation of ENaC by three membrane-bound channel-
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RT activating serine proteases (mCAP1, mCAP2, and mCAP3) and serum- and
RT glucocorticoid-regulated kinase (Sgk1) in Xenopus oocytes.";
RL J. Gen. Physiol. 120:191-201(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast tumor;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T.J., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prance C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
CC -!- FUNCTION: Probable protease. Seems to be capable of activating
CC ENaC.
CC -----
CC -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC -!- SIMILARITY: Belongs to peptidase family S1.
CC -!- SIMILARITY: Contains 1 LDL-receptor class A domain.
CC -!- SIMILARITY: Contains 1 SRCR domain.
CC -----
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CC -----
CC EMBL; AV043240; AAK85307.1; -.
DR HSPF; P00761; IAN1.
DR MEROPS; S01.034; -.
DR MGD; MGI:2384877; Tmprs4.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR002172; LDL_receptor_A.
DR InterPro; IPR01254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR001190; Srcr_receptor.
DR Pfam; PF00057; ldl_recept_a; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PROSITE; PS01209; LDLRA_1; FALSE_NEG.
DR PROSITE; PS50068; LDLRA_2; FALSE_NEG.
DR PROSITE; PS00420; SRCR_1; FALSE_NEG.
DR PROSITE; PS02287; SRCR_2; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Transmembrane; Signal-anchor.
FT DOMAIN 1 30 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 31 51 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT DOMAIN 52 435 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 59 101 LDL-RECEPTOR CLASS A.
FT DOMAIN 102 202 SRCR.
FT DOMAIN 203 435 SERINE PROTEASE.
FT ACT_SITE 243 243 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 288 288 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 385 385 CHARGE RELAY SYSTEM (BY SIMILARITY).
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FT SITE 202 203 CLEAVAGE (POTENTIAL).
FT DISULFID 62 81 BY SIMILARITY.
FT DISULFID 75 90 BY SIMILARITY.
FT DISULFID 125 181 BY SIMILARITY.
FT DISULFID 138 191 BY SIMILARITY.
FT DISULFID 194 308 BY SIMILARITY.
FT DISULFID 228 244 BY SIMILARITY.
FT DISULFID 354 370 BY SIMILARITY.
FT DISULFID 381 408 BY SIMILARITY.
FT CARBOHYD 128 128 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 435 AA; 47495 MW; DC52E45A43E01369 CRC64;

Query Match 49.3%; Score 36; DB 1; Length 435;
Best Local Similarity 63.6%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GHEGCRSGRAE 11
DB 77 GHLDCASGEDE 87

RESULT 35
NFS1 MOUSE
ID NFS1 MOUSE STANDARD; PRT; 451 AA.
AC Q9Z1J3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cysteine desulfurase, mitochondrial precursor (EC 4.4.1.-) (m-Nfs1).
GN NFS1 OR NIFS.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=Olfactory epithelium;
RX MEDLINE=98409329; PubMed=9738949;
RA Nakai Y., Yoshihara Y., Hayashi H., Kagamiyama H.;
RT "CDNA cloning and characterization of mouse Nifs-like protein, m-Nfs1:
RT mitochondrial localization of eukaryotic Nifs-like proteins.";
RL FEBS Lett. 433:143-148(1998).
CC -!- FUNCTION: Catalyzes the removal of elemental sulfur from cysteine
CC to produce alanine. It supplies the inorganic sulfur for iron-
CC sulfur (Fe-S) clusters.
CC -!- COPACITOR: Pyridoxal phosphate (By similarity).
CC -!- SUBCELLULAR LOCATION: Mitochondrial and cytoplasmic (By
CC similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative initiation;
CC Comment=2 isoforms, Mitochondrial (shown here) and Cytoplasmic,
CC may be produced by alternative initiation,
CC -!- TISSUE SPECIFICITY: Ubiquitous.
CC -!- SIMILARITY: Belongs to class-V of pyridoxal-phosphate-dependent
CC aminotransferases. Nifs/iscs subfamily.
CC
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CC
CC EMBL; AJ22660; CAA10916.1; ALT INIT.
CC MGD; MGI:1316706; Nfs1.
CC GO; GO:0005759; C:mitochondrial matrix; IDA.
CC InterPro; IPR000192; Aminotrans V.
CC Pfam; PF00266; aminotran 5; 1.
CC PROSITE; PS00595; AA_TRANSFER CLASS 5; 1.
CC Lyase; Pyridoxal phosphate; Mitochondrion; Transit peptide;
CC Alternative initiation.
KW

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FT TRANSIT 1 ? MITOCHONDRION (POTENTIAL).
FT CHAIN ? 451 CYSTEINE DESULFURASE, ISOFORM
FT CHAIN 55 451 MITOCHONDRIAL.
FT CHAIN 55 451 CYSTEINE DESULFURASE, ISOFORM
FT INIT MET 55 55 CYTOPLASMIC.
FT BINDING 252 252 FOR ISOFORM CYTOPLASMIC.
FT ACT SITE 375 375 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ SEQUENCE 451 AA; 50001 MW; 6BE5F3200A967B20 CRC64;

Query Match 49.3%; Score 36; DB 1; Length 451;
Best Local Similarity 70.0%; Pred. No. 88;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 ECGRSGEARG 12
DB 155 DSCRSLERAG 164

RESULT 36
NFS1 RAT
ID NFS1 RAT STANDARD; PRT; 451 AA.
AC Q9P3I9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cysteine desulfurase, mitochondrial precursor (EC 4.4.1.-).
GN NFS1 OR NIFS.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Hsu S.-C., Liew Y.-F., Shaw N.-S.;
RT "cDNA cloning of cysteine desulfurase (Nifs) protein in rat liver.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Catalyzes the removal of elemental sulfur from cysteine
CC to produce alanine. It supplies the inorganic sulfur for iron-
CC sulfur (Fe-S) clusters.
CC -!- COPACITOR: Pyridoxal phosphate (By similarity).
CC -!- SUBCELLULAR LOCATION: Mitochondrial and cytoplasmic (By
CC similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative initiation;
CC Comment=2 isoforms, Mitochondrial (shown here) and Cytoplasmic,
CC may be produced by alternative initiation;
CC -!- TISSUE SPECIFICITY: Ubiquitous.
CC -!- SIMILARITY: Belongs to class-V of pyridoxal-phosphate-dependent
CC aminotransferases. Nifs/iscs subfamily.
CC
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CC
CC EMBL; AF336041; AAK12337.1; -.
CC InterPro; IPR000192; Aminotrans V.
CC Pfam; PF00266; aminotran 5; 1.
CC PROSITE; PS00595; AA_TRANSFER CLASS 5; 1.
CC Lyase; Pyridoxal phosphate; Mitochondrion; Transit peptide;
CC Alternative initiation.
KW
FT TRANSIT 1 ? MITOCHONDRION (POTENTIAL).
FT CHAIN ? 451 CYSTEINE DESULFURASE, ISOFORM
FT CHAIN 55 451 MITOCHONDRIAL.
FT CHAIN 55 451 CYSTEINE DESULFURASE, ISOFORM
FT INIT MET 55 55 CYTOPLASMIC.
FT BINDING 252 252 FOR ISOFORM CYTOPLASMIC.
FT BINDING 252 252 PYRIDOXAL PHOSPHATE (BY SIMILARITY).

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FT ACT SITE 375 375 BY SIMILARITY.
SQ SEQUENCE 451 AA; 50012 MW; 8E9083D6222F3087 CRC64;

Query Match 49.3%; Score 36; DB 1; Length 451;
Best Local Similarity 70.0%; Pred. No. 88;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGCGRGEAEG 12
DB 155 DSCRSLEAEG 164

: ||| ||||
: ||| ||||

RESULT 37
NFS1_HUMAN
ID NFS1_HUMAN STANDARD; PRT; 457 AA.
AC Q9Y697; Q9NTZ5; Q9Y481;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cysteine desulfurase, mitochondrial precursor (EC 4.4.1.-) (HUSSY-08).
GN NFS1 OR NIFS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=99102954; PubMed=9885568;
RL Land T., Rouault T.A.;
RT "Targeting of a human iron-sulfur cluster assembly enzyme, nifs, to
RT different subcellular compartments is regulated through alternative
RT AUG utilization.";
RL Mol. Cell 2:807-815 (1998).
RN [2]
REVIEWS TO 380-402.
RP Land T., Rouault T.A.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
SEQUENCE OF 140-457 FROM N.A.
RP MEDLINE=21064499; PubMed=11124703;
RL Stanchi F., Bertocco E., Toppo S., Dioguardi R., Simionati B.,
RA Canata N., Zimbello R., Lanfranchi G., Valle G.;
RT "Characterization of 16 novel human genes showing high similarity to
RT yeast sequences.";
RL Yeast 18:69-80 (2001).
RN [4]
SEQUENCE OF 137-457 FROM N.A.
RL Laird G.;
RP Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Catalyzes the removal of elemental sulfur from cysteine
CC to produce alanine. It supplies the inorganic sulfur for iron-
CC sulfur (Fe-S) clusters.
CC -!- COPACTOR: Pyridoxal phosphate (By similarity).
CC -!- SUBCELLULAR LOCATION: Mitochondrial and cytoplasmic.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative initiation;
CC Comment=2 isoforms, Mitochondrial (shown here) and Cytoplasmic,
CC are produced by alternative initiation;
CC -!- TISSUE SPECIFICITY: Predominantly expressed in heart and skeletal
CC muscle. Also found in brain, liver and pancreas.
CC -!- SIMILARITY: Belongs to class-V of pyridoxal-phosphate-dependent
CC aminotransferases. Nifs/lscs subfamily.
CC -----
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CC -----
DR EMBL; AF097025; AAD09187.2; -
DR EMBL; AJ010952; CAA09424.1; -

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DR EMBL; AL109827; CAB87612.1; -
DR Genew; HGNC:15910; NFS1.
DR MIM; 603485; -
DR GO; GO:0005829; C:cytosol; TAS.
DR GO; GO:0005739; C:mitochondrion; TAS.
DR GO; GO:0005634; C:nucleus; TAS.
DR GO; GO:0006461; P:protein complex assembly; TAS.
DR GO; GO:0000096; P:sulfur amino acid metabolism; TAS.
DR InterPro; IPR000192; Aminotrans_V.
DR Pfam; PF00266; aminotran_5; 1.
DR PROSITE; PS00595; AA_TRANSFER_CLASS_5; 1.
KW Lyase; Pyridoxal phosphate; Mitochondrion; Transit peptide;
KW Alternative initiation.
FT TRANSIT 1 ? MITOCHONDRION (POTENTIAL).
FT CHAIN ? 457 CYSTEINE DESULFURASE, ISOFORM
FT CHAIN 61 457 MITOCHONDRIAL.
FT CHAIN 61 457 CYSTEINE DESULFURASE, ISOFORM
FT INIT MET 61 61 CYTOPLASMIC.
FT BINDING 258 258 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
FT ACT_SITE 381 381 BY SIMILARITY.
FT CONFLICT 412 412 R -> A (IN REF. 1).
FT CONFLICT 431 431 K -> N (IN REF. 1).
SQ SEQUENCE 457 AA; 50253 MW; 03FDBFFCA0089669 CRC64;

Query Match 49.3%; Score 36; DB 1; Length 457;
Best Local Similarity 70.0%; Pred. No. 89;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGCGRGEAEG 12
DB 161 DSCRSLEAEG 170

: ||| ||||
: ||| ||||

RESULT 38
Y410_ARATH
ID Y410_ARATH STANDARD; PRT; 594 AA.
AC P16128; Q9S882;
DT 01-APR-1990 (Rel. 14, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical protein At4g18490.
GN AT4G18490 OR F28J12.150.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Scrophophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=cv. Columbia;
RC MEDLINE=20083488; PubMed=10617198;
RX Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Voickaert G.,
RA Pohl T., Dueterhoeft A., Stiekema W., Entian K.-D., Terryn N.,
RA Harris B., Ansoerge W., Brandt P., Grivell L.A., Rieger M.,
RA Weichselgartner M., de Simone V., Obermaier B., Maché R., Mueller M.,
RA Kreits M., Delenly M., Puigdomenech P., Watson M., Schmidtheini T.,
RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
RA Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P.,
RA Latham S.-A., McCullagh B., Bilham L., Robben J.,
RA Van der Schueren J., Grymoprez B., Chuang Y.-J., Vandenbussche F.,
RA Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,
RA Weitzenecker T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
RA Mooljman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
RA Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
RA De Keyser A., Buyssehaert C., Gielen J., Villarroel R., De Clercq R.,
RA Van Montagu M., Rogers J., Cronin A., Quail M.A., Bray-Allen S.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McIlay K., Mayes R.,
RA Pettrét D., Bloecker H., Scharfe M., Lynne M., Benes V., Reckmann S.,
RA Borkova D., Bloecker H., Scharfe M., Lynne M., Benes V., Reckmann S.,
RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A.,

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RA Neumann S., Argirion A., Vitale D., Liguori R., Piravandi E.,  
RA Massenot O., Quigley P., Clabaud G., Muehlenle A., Felber R.,  
RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,  
RA Chedro F., Coeber R., Berger C., Monfort A., Casacuberta E.,  
RA Gibbons T., Weber N., Vandenbol M., Barges M., Terol J., Torres A.,  
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,  
RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bielke C.,  
RA Prisman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,  
RA Zaccaria P., Devian M., Wilson R.K., de la Bastide M., Habermann K.,  
RA Parnell L., Bedha N., Gnoj L., Schutz K., Huang E., Spiegel L.,  
RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,  
RA Stonking T., Kalicki J., Graves T., Harmon G., Edwards J.,  
RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,  
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,  
RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.W.,  
RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,  
RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,  
RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,  
RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,  
RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,  
RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,  
RA Chen E., Maria M.A., Martienssen R., McCombie W.R.,  
RA "Sequence and analysis of chromosome 4 of the plant Arabidopsis  
RT thaliana".  
RT Nature 402:769-777(1999).  
RL Nature 402:769-777(1999).  
RN [2]  
RP SEQUENCE OF 1-290 FROM N.A.  
RC STRAIN=cv. Columbia;  
RX MEDLINE=9028329; PubMed=2158442;  
RA Konec C., Mayerhofer R., Konec-Kalman Z., Nevrath C., Reiss B.,  
RA Redel G.P., Schnell J.;  
RT "Isolation of a gene encoding a novel chloroplast protein by T-DNA  
RT tagging in Arabidopsis thaliana".  
RL EMBO J. 9:1337-1346(1990).  
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CC -----  
CC EMBL; AL021710; CAA16729.1; -;  
DR EMBL; AL161548; CAB78851.1; -;  
DR EMBL; X51799; CAA36096.1; -;  
DR PIR; T04545; T04545.  
KW Hypothetical protein.  
SQ SEQUENCE 594 AA; 65822 MW; 39618E936AC3C34E CRC64;  
  
Query Match 49.3%; Score 36; DB 1; Length 594;  
Best Local Similarity 70.0%; Pred. No. 1.2e+02;  
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 HEGCRSGEAE 11  
||| ||| |  
Db 180 HELCRSGTKE 189  
  
RESULT 39  
GIDA BACAA STANDARD; PRT; 629 AA.  
ID GIDA BACAA  
AC Q81JH3;  
DT 15-MAR-2004 (Rel. 43, Created)  
DT 15-MAR-2004 (Rel. 43, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Glucose inhibited division protein A.  
GN GIDA OR BA5733.  
OS Bacillus anthracis (strain Ames).  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=198094;  
RN [1]  
RP SEQUENCE FROM N.A.

RX MEDLINE=22508414; PubMed=12721629;  
RA Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,  
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,  
RA Holzapfel E.K., Okstad O.A., Helgason E., Rillstone J., Wu M.,  
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.,  
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,  
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,  
RA Benton J.L., Mahmoud Y., Jiang L., Hance I.R., Weidman J.F.,  
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,  
RA Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,  
RA Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,  
RA Fraser C.M.;  
RT "The genome sequence of Bacillus anthracis Ames and comparison to  
RT closely related bacteria".  
RL Nature 423:81-86(2003).  
CC -!- SIMILARITY: Not known.  
CC -!- FUNCTION: Belongs to the gida family.  
CC -----  
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CC -----  
CC EMBL; AE017041; AAP29364.1; -;  
DR TIGR; BA5733; -;  
DR HAMAP; MF 00129; -; 1.  
DR InterPro; IPR001327; FAD\_pyr\_redox.  
DR InterPro; IPR002218; GIDA.  
DR InterPro; IPR004416; GIDA\_sub.  
DR InterPro; IPR001100; Pyr\_redox.  
DR Pfam; PF01134; GIDA; 1.  
DR PRINTS; PR00368; FADPNR.  
DR PRINTS; PR00411; PNDRDTASEI.  
DR ProDom; PD003738; GIDA; 1.  
DR TIGRFAMs; TIGR00136; GIDA; 1.  
DR PROSITE; PS01280; GIDA\_1; 1.  
DR PROSITE; PS01281; GIDA\_2; 1.  
KW Complete proteome.  
SQ SEQUENCE 629 AA; 70334 MW; 5471811C406E059D CRC64;  
  
Query Match 49.3%; Score 36; DB 1; Length 629;  
Best Local Similarity 60.0%; Pred. No. 1.3e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 HEGCRSGEAE 10  
||| ||| |  
Db 16 GHAGCEAGLA 25  
  
RESULT 40  
GIDA BACCR STANDARD; PRT; 629 AA.  
ID GIDA BACCR  
AC Q814F7;  
DT 15-MAR-2004 (Rel. 43, Created)  
DT 15-MAR-2004 (Rel. 43, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Glucose inhibited division protein A.  
GN GIDA OR BC5485.  
OS Bacillus cereus (strain ATCC 14579 / DSM 31).  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=226900;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22508415; PubMed=12721630;  
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,  
RA Kapral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,  
RA Chu L., Mazur M., Goltzman E., Larsen N., D'Souza M., Walunas T.,  
RA Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,  
RA Overbeek R., Kyrpides N.;  
RT "Genome sequence of Bacillus cereus and comparative analysis with

```

RT Bacillus anthracis.";
RL Nature 423:87-91(2003).
CC -!- FUNCTION: Not known.
CC -!- SIMILARITY: Belongs to the gida family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF017015; RAP12339.1; -.
DR HAMAP; MF_00129; -.
DR InterPro; IPR001327; FAD_Pyr_redox.
DR InterPro; IPR002218; GIDA.
DR InterPro; IPR004416; GIDA_sub.
DR InterPro; IPR001100; Pyr_redox.
DR Pfam; PF01134; GIDA; 1.
DR PRINTS; PR00368; FADENR.
DR PRINTS; PR00411; FNDRTASEI.
DR ProDom; PD003738; GIDA; 1.
DR TIGRFAMs; TIGR00136; gida; 1.
DR PROSITE; PS01280; GIDA_1; 1.
DR PROSITE; PS01281; GIDA_2; 1.
KW Complete proteome.
SQ SEQUENCE 629 AA; 70305 MW; BF989B8791BF422A CRC64;

Query Match 49.3%; Score 36; DB 1; Length 629;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GHEGCRSGEA 10
DB 16 GHAGCEAGLA 25

RESULT 41
GIDA_CLOPE
ID GIDA_CLOPE STANDARD; PRT; 630 AA.
AC Q8XH31;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glucose inhibited division protein A.
GN GIDA OR CPE2654.
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=13 / Type A;
RX MEDLINE=21664373; PubMed=11792842;
RA Shinizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
CC -!- FUNCTION: Not known.
CC -!- SIMILARITY: Belongs to the gida family.
CC -----
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CC -----
DR EMBL; AF003194; BAB82360.1; -.
DR HAMAP; MF_00129; -.

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DR InterPro; IPR002218; GIDA.
DR InterPro; IPR004416; GIDA_sub.
DR Pfam; PF01134; GIDA; 1.
DR ProDom; PD003738; GIDA; 1.
DR TIGRFAMs; TIGR00136; gida; 1.
DR PROSITE; PS01280; GIDA_1; 1.
DR PROSITE; PS01281; GIDA_2; 1.
KW Complete proteome.
SQ SEQUENCE 630 AA; 70624 MW; 159131D51F0DCF2C CRC64;

Query Match 49.3%; Score 36; DB 1; Length 630;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GHEGCRSGEA 10
DB 16 GHAGCEAGLA 25

RESULT 42
PCPM_CHICK
ID PCPM_CHICK STANDARD; PRT; 640 AA.
AC P21642;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Phosphoenolpyruvate carboxykinase, mitochondrial precursor [GTP]
DE (EC 4.1.1.32) (Phosphoenolpyruvate carboxylase) (PEPCK-M).
GN PCK2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=90237025; PubMed=2110163;
RA Weldon S.L., Rando A., Matathias A.S., Hod Y., Kalonick P.A.,
RA Savon S., Cook J.S., Hanson R.W.;
RT "Mitochondrial phosphoenolpyruvate carboxykinase from the chicken.
RT Comparison of the cdna and protein sequences with the cytosolic
RT isozyme.";
RL J. Biol. Chem. 265:7308-7317(1990).
CC -!- FUNCTION: In birds PEPCK-M facilitates the recycling of lactate
CC carbon in the liver.
CC -!- CATALYTIC ACTIVITY: GTP + oxaloacetate = GDP + phosphoenolpyruvate
CC + CO(2).
CC -!- COFACTOR: Requires manganese.
CC -!- ENZYME REGULATION: Activity appears to be constitutive.
CC -!- PATHWAY: Rate-limiting gluconeogenic enzyme.
CC -!- SUBCELLULAR LOCATION: Mitochondrial.
CC -!- TISSUE SPECIFICITY: In birds, PEPCK-M is the sole form of hepatic
CC PEPCK, but it constitutes 60% of the enzyme in the kidney.
CC -!- MISCELLANEOUS: In eukaryotes there are two isozymes: a cytoplasmic
CC one and a mitochondrial one.
CC -!- SIMILARITY: Belongs to the phosphoenolpyruvate carboxykinase [GTP]
CC family.
CC -----
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CC -----
DR EMBL; J05419; AAA49006.1; ALT_SEQ.
DR PIR; A35191; QYCHGM.
DR InterPro; IPR008209; PEP_carboxykin.
DR InterPro; IPR008210; PEPCK_N.
DR Pfam; PF00821; PEPCK; 1.
DR ProDom; PD004738; PEPCK_N; 1.

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DR PROSITE; PS00505; PEPCCK\_GTP; 1.  
 KW Glucuronogenesis; Lyase; Decarboxylase; GTP-binding; Mitochondrion;  
 TRANSIT peptide; Manganese.  
 FT CHAIN 1 33  
 FT CHAIN 34 640  
 FT NP BIND 255 262  
 FT ACT SITE 306 306  
 SQ SEQUENCE 640 AA; 70971 MW; 0F43AE3AFCEFD546 CRC64;  
 Query Match 49.3%; Score 36; DB 1; Length 640;  
 Best Local Similarity 54.5%; Pred. NO. 1.3e+02;  
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 GHEGCRSGEAE 11  
 DB 7 GAQSCRGGETE 17  
 RESULT 43  
 CL16\_HUMAN STANDARD; PRT; 704 AA.  
 ID Q96NV7; Q81X31;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 15-MAR-2004 (Rel. 43, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Chloride intracellular channel 6.  
 GN CL16 OR CLIC1L.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RX MEDLINE=22395649; PubMed=14597386;  
 RA Friedli M., Guipponi M., Bertrand S., Bertrand D., Neerman-Arbez M.,  
 RA Scott H.S., Antonarakis S.E., Raymond A.;  
 RT "Identification of a novel member of the CLIC family, CLIC6, mapping  
 to 21q22.12.";  
 RL Gene 320:31-40(2003).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM A), AND TISSUE SPECIFICITY.  
 RX MEDLINE=2213786; PubMed=12226712;  
 RA Strippoli P., D'Addabbo P., Lenzi L., Giannone S., Canaider S.,  
 RA Casadei R., Vitale L., Carinci P., Zannotti M.;  
 RT "Segmental paralogy in the human genome: a large-scale triplication on  
 1p, 6p, and 21q.";  
 RL Mamm. Genome 13:456-462(2002).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM A).  
 RX MEDLINE=20289799; PubMed=10830953;  
 RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,  
 RA Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Groner Y.,  
 RA Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,  
 RA Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,  
 RA Reichwald A., Rump J., Schillhabel M., Schudy A., Zimmermann W.,  
 RA Rosenthal K., Kudo J., Shibuya K., Kawasaki K., Asakawa S.,  
 RA Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,  
 RA Minoshima S., Shimizu N., Nordiek G., Hornischer K., Brandt P.,  
 RA Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloeker H.,  
 RA Ramer J., Beck A., Klages S., Hennig S., Rieseemann L., Degand E.,  
 RA Wehmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,  
 RA Lehrach H., Reinhardt R., Yaspo M.-L.;  
 RT "The DNA sequence of human chromosome 21.";  
 RL Nature 405:311-319(2000).  
 RN [4]  
 RP SEQUENCE OF 530-704 FROM N.A.  
 RC TISSUE=Small intestine;  
 RA Ninomiya K., Wagatsuna M., Kanda K., Kondo H., Yokoi T., Kodaira H.,  
 RA Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K.,  
 RA Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R.,  
 RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,  
 RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,  
 RA Mateuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K.,

RA Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,  
 RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;  
 RT "NEBO human cDNA sequencing project.";  
 RN Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
 RP [5]  
 RC SEQUENCE OF 279-704 FROM N.A. (ISOFORM A).  
 RX TISSUE=Brain;  
 MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -!- FUNCTION: Probable chloride ion channel. May play a critical role  
 in water-secreting cells, possibly through the regulation of  
 chloride ion transport (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (predominantly). Upon chloride  
 ion efflux from the cell, it is translocated to the plasma  
 membrane (By similarity).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event-Alternative splicing. Named isoforms-2;  
 CC Name=B;  
 CC IsoId=Q96NV7-1; Sequence=Displayed;  
 CC Name=A;  
 CC IsoId=Q96NV7-2; Sequence=VSP\_008963;  
 CC -!- TISSUE SPECIFICITY: Expressed in brain, placenta, pancreas and  
 liver.  
 CC -!- PTM: Phosphorylated (By similarity).  
 CC -!- SIMILARITY: Belongs to the chloride channel CLIC family.  
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 DR EMBL; AF448439; AAN76730.1; -;  
 DR EMBL; AF448438; AAN76729.1; -;  
 DR EMBL; AF426169; AAL24813.1; -;  
 DR EMBL; AP001720; -; NOT ANNOTATED CDS.  
 DR EMBL; AK092733; BAC03959.1; ALT\_INIT.  
 DR EMBL; BC040196; AHA40196.1; -;  
 DR Genew; HGNC:2065; CLIC6.  
 DR InterPro; IPR004046; GST\_Cterm.  
 DR InterPro; IPR002946; Int\_C1\_channel.  
 DR Pfam; PF00043; GST\_C; 1.  
 DR PRINTS; PR01263; INTCLCHANNEL.  
 DR TIGRPFAMs; TIGR00862; O-CLC; 1.  
 KW Ionic channel; Ion transport; Chloride channel; Chloride;  
 KW Voltage-gated channel; Repeat; Polymorphism; Alternative splicing.  
 DOMAIN 157 282 13 X 10 AA TANDEM REPEAT OF G-D-[SNG]-  
 [VIM]-[DEQ]-A-[EAG]-[GDVE]-[PRG]-[LAVP].  
 FT REPEAT 157 166  
 FT REPEAT 167 176  
 FT REPEAT 177 186  
 FT REPEAT 187 196

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FT REPEAT 197 206 5.
FT REPEAT 207 216 6.
FT REPEAT 217 226 7.
FT REPEAT 227 236 8.
FT REPEAT 237 246 9.
FT REPEAT 247 256 10.
FT REPEAT 257 266 11.
FT REPEAT 267 276 12.
FT REPEAT 277 286 13.
FT VARSPLIC 459 476
Missing (in isoform A).
FT FTID=VSP 008963.
FT VARIANT 632 632 D -> G (in dbSNP:3171439).
FT FTID=VAR 014139.
SQ SEQUENCE 704 AA; 73011 MW; A58F30E099BF357 CRC64;

Query Match 49.3%; Score 36; DB 1; Length 704;
Best Local Similarity 58.3%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GHEGCRSGEAG 12
Db 29 GEFGAGGGEAG 40

RESULT 44
FBL1 CHICK STANDARD; PRT; 704 AA.
ID FBL1 CHICK STANDARD; PRT; 704 AA.
AC 073775; 073774;
DT 16-OCT-2001 (Rel. 40, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fibulin-1 precursor.
GN FBLN1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN (1)_TaxID=9031;
RP SEQUENCE FROM N.A. (ISOFORMS C AND D).
RC TISSUE=Embryo;
RX MEDLINE=99120531; PubMed=9923656;
RA Barth J.L., Atgraves K.M., Roark E.F., Little C.D., Atgraves W.S.;
RT "Identification of chicken and C. elegans fibulin-1 homologs and
characterization of the C. elegans fibulin-1 gene.";
RL Matrix Biol. 17:635-646(1998).
CC -!- FUNCTION: Incorporated into fibronectin-containing matrix fibers.
CC May play a role in cell adhesion and migration along protein
CC fibers within the extracellular matrix (ECM). Could be important
CC for certain developmental processes and contribute to the
CC supramolecular organization of ECM architecture, in particular to
CC those of basement membranes.
CC -!- SUBUNIT: Interacts with itself and with various extracellular
CC matrix components (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-alternative splicing; Named isoforms=2;
CC Name=D;
CC IsoId=O73775-2; Sequence=Displayed;
CC Name=C;
CC IsoId=O73775-1; Sequence=VSP 007378;
CC -!- SIMILARITY: Belongs to the fibulin family.
CC -!- SIMILARITY: Contains 3 anaphylatoxin-like domains.
CC -!- SIMILARITY: Contains 9 EGF-like domains.
CC -----
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DR EMBL; AF051399; AAC05387.1; -.
DR EMBL; AF051400; AAC05388.1; -.
DR HSP; P00742; IHCG.
DR InterPro; IPR000020; Anaphylatoxin.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR001881; EGF Ca.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR006210; IEGF.
DR Pfam; PF01821; ANATO; 2.
DR Pfam; PF00008; EGF; 6.
DR SMART; SM00104; ANATO; 3.
DR SMART; SM00181; EGF; 9.
DR SMART; SM00179; EGF CA; 8.
DR PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
DR PROSITE; PS01178; ANAPHYLATOXIN_2; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; 5.
DR PROSITE; PS00022; EGF_1; FALSE_NEG.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS00026; EGF_3; 5.
DR PROSITE; PS01187; EGF CA; 8.
KW Signal; Alternative splicing; Glycoprotein; Extracellular matrix;
KW Repeat; EGF-like domain; Calcium-binding.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 704 FIBULIN-1.
FT DOMAIN 33 74 ANAPHYLATOXIN-LIKE 1.
FT DOMAIN 75 109 ANAPHYLATOXIN-LIKE 2.
FT DOMAIN 110 142 ANAPHYLATOXIN-LIKE 3.
FT DOMAIN 177 216 EGF-LIKE 1.
FT DOMAIN 217 262 EGF-LIKE 2.
FT DOMAIN 263 308 EGF-LIKE 3.
FT DOMAIN 309 356 EGF-LIKE 4.
FT DOMAIN 357 399 EGF-LIKE 5.
FT DOMAIN 400 441 EGF-LIKE 6.
FT DOMAIN 442 481 EGF-LIKE 7.
FT DOMAIN 482 525 EGF-LIKE 8.
FT DOMAIN 526 579 EGF-LIKE 9.
FT DOMAIN 357 441 SELF-ASSOCIATION AND FN1-BINDING (BY SIMILARITY).
FT DISULFID 33 59 BY SIMILARITY.
FT DISULFID 34 66 BY SIMILARITY.
FT DISULFID 47 67 BY SIMILARITY.
FT DISULFID 76 107 BY SIMILARITY.
FT DISULFID 89 108 BY SIMILARITY.
FT DISULFID 110 134 BY SIMILARITY.
FT DISULFID 111 141 BY SIMILARITY.
FT DISULFID 124 142 BY SIMILARITY.
FT DISULFID 181 191 BY SIMILARITY.
FT DISULFID 187 200 BY SIMILARITY.
FT DISULFID 202 215 BY SIMILARITY.
FT DISULFID 221 234 BY SIMILARITY.
FT DISULFID 228 243 BY SIMILARITY.
FT DISULFID 249 261 BY SIMILARITY.
FT DISULFID 267 280 BY SIMILARITY.
FT DISULFID 274 289 BY SIMILARITY.
FT DISULFID 295 307 BY SIMILARITY.
FT DISULFID 313 326 BY SIMILARITY.
FT DISULFID 320 335 BY SIMILARITY.
FT DISULFID 342 355 BY SIMILARITY.
FT DISULFID 361 374 BY SIMILARITY.
FT DISULFID 368 383 BY SIMILARITY.
FT DISULFID 385 398 BY SIMILARITY.
FT DISULFID 404 416 BY SIMILARITY.
FT DISULFID 412 425 BY SIMILARITY.
FT DISULFID 427 440 BY SIMILARITY.
FT DISULFID 446 455 BY SIMILARITY.
FT DISULFID 451 464 BY SIMILARITY.
FT DISULFID 466 480 BY SIMILARITY.
FT DISULFID 486 499 BY SIMILARITY.
FT DISULFID 495 508 BY SIMILARITY.
FT DISULFID 510 524 BY SIMILARITY.
FT DISULFID 530 543 BY SIMILARITY.
FT DISULFID 537 552 BY SIMILARITY.
FT DISULFID 557 578 BY SIMILARITY.

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FT CARBOHYD 96 96 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 536 536 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 540 540 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 568 704 VRLKTDITIRKICRPNVNCVLDVHTISHTVISLPTFR
FT FT EPTREPIITFLRAITPTYPANQADIIIFDITGNLRESFDII
FT FT KRYMDGMTVGVVRPIVGPFAHLKLENNYVMGVVSHR
FT FT NIYNVHIFVSEYWF -> RCELPNENKECSLPIRIYY
FT FT HUSFPTNIQVPTDIFRMGPSNAVPGDKILLISISGNQEGFF
FT FT TTKKNNHSGIVVMQRIITEPRDLGLTIQMLTRHGTVNTF
FT FT IAKLFVSAQL (in isoform C).
SQ SEQUENCE 704 AA; 78137 MW; D47D5A30D5E42932 CRC64;
Query Match 49.3%; Score 36; DB 1; Length 704;
Best Local Similarity 71.4%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 HEGCRSG 8
DB 178 HDGCRGG 184
RESULT 45
VP4_RDVA
ID VP4_RDVA STANDARD; PRT; 727 AA.
AC P22474;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Nonstructural protein Pns4.
GN S4.
OS Rice dwarf virus (isolate Akita) (RDV).
OC Viruses; dsRNA viruses; Reoviridae; Phytoreovirus.
OX NCBI_TaxID=142803;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91021049; PubMed=2219732;
RA Suzuki N., Watanabe Y., Kusano T., Kitagawa Y.;
RT "Sequence analysis of rice dwarf phytoreovirus genome segments S4,
RT S5, and S6; comparison with the equivalent wound tumor virus
RT segments.";
RL Virology 179:446-454(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91037950; PubMed=2230727;
RA Uyeda I., Kudo H., Yamada N., Matsumura T., Shikata E.;
RT "Nucleotide sequence of rice dwarf virus genome segment 4.";
RL J. Gen. Virol. 71:2217-2222(1990).
CC -!- FUNCTION: MAY INDUCE DWARFISM OF RICE.
CC -!- SIMILARITY: TO WOUND TUMOR VIRUS S4.
CC -----
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CC -----
CC EMBL; X54622; CAA38442.1; -.
CC DR EMBL; D00608; BAA00483.1; -.
CC DR PIR; A45342; A45342.
CC KW Nonstructural protein.
CC FT CONFLICT 417 417 L -> A (IN REF. 2).
CC FT CONFLICT 421 421 A -> T (IN REF. 2).
CC FT CONFLICT 497 497 E -> G (IN REF. 2).
CC FT CONFLICT 663 663 Q -> R (IN REF. 2).
SQ SEQUENCE 727 AA; 79836 MW; 7AA2FA737FCA8DE9 CRC64;
Query Match 49.3%; Score 36; DB 1; Length 727;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 GHEGCRSG 8
DB 331 GHHCRSG 338
RESULT 46
MEN_DROME
ID MEN_DROME STANDARD; PRT; 796 AA.
AC P52302;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Lethal(3)malignant blood neoplasm-1 protein (Mbn(83)).
GN L(3)MBN OR L(3)MEN-1.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Oregon-R;
RX MEDLINE=94229362; PubMed=8174791;
RA Konrad L., Becker G., Schmidt A., Kloeckner T.;
RA Kauter-Stiller G., Dreschers S., Edstroem J.-E., Gateff E.;
RT "Cloning, structure, cellular localization, and possible function of
RT the tumor suppressor gene lethal(3)malignant blood neoplasm-1 of
RT Drosophila melanogaster.";
RL Dev. Biol. 163:98-111(1994).
CC -!- FUNCTION: Required for differentiation of the phagocytic blood-
CC cell type, the plasmatocyte.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic; mainly around the nucleus.
CC -!- TISSUE SPECIFICITY: Blood cells and other tissues.
CC -----
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CC -----
CC EMBL; Z47722; CAA87654.1; -.
CC DR PIR; S57844; S57844.
CC DR FlyBase; FBgn0002440; l(3)mbn.
CC DR InterPro; IPR000618; Insect cuticle.
CC DR Pfam; PF00379; Chitin_bind_4; 1.
CC Repeat.
CC FT DOMAIN 225 314 2 X 37 AA REPEATS.
CC FT REPEAT 225 261 1-1.
CC FT REPEAT 278 314 1-2.
CC FT DOMAIN 471 512 2 X 21 AA REPEATS.
CC FT REPEAT 471 491 2-1.
CC FT REPEAT 482 512 2-2.
CC FT DOMAIN 576 711 7 X APPROXIMATE TANDEM REPEATS,
CC GLY-SER-RICH.
CC FT REPEAT 576 598 3-1.
CC FT REPEAT 599 618 3-2.
CC FT REPEAT 619 640 3-3.
CC FT REPEAT 641 658 3-4.
CC FT REPEAT 659 676 3-5.
CC FT REPEAT 677 694 3-6.
CC FT REPEAT 695 711 3-7.
SQ SEQUENCE 796 AA; 83348 MW; 6B1D593961FF370 CRC64;
Query Match 49.3%; Score 36; DB 1; Length 796;
Best Local Similarity 53.3%; Pred. No. 1.6e+02;
Matches 8; Conservative 3; Mismatches 2; Indels 2; Gaps 1;
QY 1 GHE--GCRSGEAGS 13
DB 728 GHEETGGRNGDKQS 742

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RESULT 47
NKX1 RAT
ID NKX1 RAT STANDARD; PRT; 1181 AA.
AC Q9QZM6; Q62932;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Sodium/potassium/calcium exchanger 1 precursor (Na(+)/K(+)/Ca(2+)-
exchange protein 1) (Retinal rod Na-Ca+K exchanger).
GN SLC24A1 OR NKX1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC STRAIN=Sprague-Dawley; TISSUE=Eye;
RX MEDLINE=2017335; PubMed=10751314;
RA Poon S., Leach S., Li X.-F., Tucker J.E., Schnetkamp P.P.M.,
RA Lytton J.,
RT "Alternatively spliced isoforms of the rat eye
sodium/calcium-potassium exchanger NKX1.";
RL Am. J. Physiol. 278:C651-C660(2000).
RN [2]
SEQUENCE OF 1067-1155 FROM N.A.
RA White K.E., Geesek P.A., Friedman P.A.;
RA Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Critical component of the visual transduction cascade,
controlling the calcium concentration of outer segments during
light and darkness. Light causes a rapid lowering of cytosolic
free calcium in the outer segment of both retinal rod and cone
photoreceptors, and the light-induced lowering of calcium is caused
by extrusion via this protein which plays a key role in the
process of light adaptation. Transports one Ca(2+) and one K(+) in
exchange for four Na(+).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC -!- Event=Alternative splicing; Named isoforms=4;
CC Name=1;
CC IsoId=Q9QZM6-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9QZM6-2; Sequence=VSP_006161;
CC Name=3;
CC IsoId=Q9QZM6-3; Sequence=VSP_006162;
CC Name=4;
CC IsoId=Q9QZM6-4; Sequence=VSP_006163;
CC -!- TISSUE SPECIFICITY: Highly expressed in the eye.
CC -!- SIMILARITY: BELONGS TO THE SLC24A FAMILY OF TRANSPORTERS.
CC
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CC
CC -----
DR EMBL; AF176688; AAD53121.1; -.
DR EMBL; U49235; AAB37753.1; -.
DR InterPro; IPR004817; K NaCaexchang.
DR InterPro; IPR004481; K NaCaexchang.
DR InterPro; IPR004837; NaCa Exmemb.
DR Pfam; PF01699; Na_Ca_Ex; 2.
DR TIGRFAMs; TIGR00367; TIGR00367; 1.
DR TIGRFAMs; TIGR00927; 2A1904; 1.
DR Vision; Transport; Antiport; Symport; Calcium transport;
KW Transmembrane; Glycoprotein; Phosphorylation; Signal; Repeat;
KW Alternative splicing.
FT SIGNAL 1 38 POTENTIAL.
FT CHAIN 39 1181 SODIUM/POTASSIUM/CALCIUM EXCHANGER 1.
FT DOMAIN 39 419 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 420 440 POTENTIAL.

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FT DOMAIN 441 464 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 465 485 POTENTIAL.
FT DOMAIN 486 491 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 492 512 POTENTIAL.
FT DOMAIN 513 519 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 520 544 POTENTIAL.
FT DOMAIN 545 552 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 553 569 POTENTIAL.
FT DOMAIN 570 589 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 590 1010 POTENTIAL.
FT DOMAIN 1011 1017 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1018 1038 POTENTIAL.
FT DOMAIN 1039 1053 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 1054 1074 POTENTIAL.
FT DOMAIN 1075 1092 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1093 1113 POTENTIAL.
FT DOMAIN 1114 1121 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 1122 1142 POTENTIAL.
FT DOMAIN 1143 1150 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1151 1171 POTENTIAL.
FT DOMAIN 1172 1181 CYTOPLASMIC (POTENTIAL).
FT REPEAT 461 501 ALPHA-1.
FT REPEAT 1061 1092 ALPHA-2.
FT DOMAIN 730 741 14 X APPROXIMATE TANDEM REPEATS.
FT REPEAT 742 754 1.
FT REPEAT 755 766 2.
FT REPEAT 767 778 3.
FT REPEAT 779 791 4.
FT REPEAT 792 804 5.
FT REPEAT 805 817 6.
FT REPEAT 818 830 7.
FT REPEAT 831 843 8.
FT REPEAT 844 856 9.
FT REPEAT 857 869 10.
FT REPEAT 870 881 11.
FT REPEAT 882 893 12.
FT REPEAT 894 905 13.
FT DOMAIN 952 974 14.
FT MOD_RES 625 POLY-GLU.
FT CARBOHYD 271 271 PHOSPHORYLATION (POTENTIAL).
FT VARSPLIC 598 710 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARSPLIC 616 710 Missing (in isoform 2).
FT VARSPLIC 652 679 /FTId=VSP_006161.
FT VARSPLIC 652 679 Missing (in isoform 3).
FT VARSPLIC 652 679 /FTId=VSP_006162.
FT VARSPLIC 652 679 Missing (in isoform 4).
FT VARSPLIC 652 679 /FTId=VSP_006163.
SQ SEQUENCE 1181 AA; 129980 MW; B063C1C119369GAB CRC64;
Query Match 49.3%; Score 36; DB 1; Length 1181;
Best Local Similarity 66.7%; Pred No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY QY 1 GHEGCRSGEAG 12
Db 724 GEGEREETEAG 735
RESULT 48
MT SYNNU
ID MT SYNNU STANDARD; PRT; 56 AA.
AC P30565;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Metallothionein (MT).
GN MTNA.
OS Synchococcus vulcanus (Thermosynchococcus vulcanus).
OC Bacteria; Cyanobacteria; Chroococcales; Thermosynchococcus.
OX NCBI_TaxID=32053;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=93043047; PubMed=1421159;

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RA Shimizu T., Hiyama T., Ikeuchi M., Inoue Y.;
RT "Nucleotide sequence of a metallothionein gene of the thermophilic
RL cyanobacterium Synechococcus vulcanus.";
RR Plant Mol. Biol. 20:565-567(1992).
CC -!- FUNCTION: This protein complexes cadmium, zinc and copper.
CC -!- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 14.
CC -----
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CC -----
DR EMBL; X53839; CAA37832.1; -.
DR InterPro; IPR000518; Metallothio_Pro.
DR Pfam; PF02069; Metallothio_Pro; 1.
DR PRINTS; PR00859; MTPROKARYOTE.
DR ProDom; PD019076; Metallothio_Pro; 1.
DR Metal-binding; Metal-thiolate_cluster; Zinc; Cadmium; Copper.
DR INIT_MET 0 0 BY SIMILARITY.
DR SEQUENCE 56 AA; 5643 MW; C0653389F3FB7C85 CRC64;
DR
DR Query Match 47.9%; Score 35; DB 1; Length 56;
DR Best Local Similarity 60.0%; Pred. No. 14;
DR Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
DR
DR QY 1 GHEGCRSGEA 10
DR || || || ||
DR DB 47 GHAGCGCGSA 56
DR
DR
DR RESULT 49
DR TUBE_MYCTU STANDARD; PRT; 89 AA.
DR ID TUBE_MYCTU
DR AC P02944;
DR DT 21-JUL-1986 (Rel. 01, Created)
DR DT 21-JUL-1986 (Rel. 01, Last sequence update)
DR DT 01-NOV-1988 (Rel. 09, Last annotation update)
DR DE Tuberculin-active protein.
DR OS Mycobacterium tuberculosis.
DR OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
DR OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
DR NCBI_TaxID=1773;
DR [1]_RN [1]
DR RP SEQUENCE.
DR STRAIN=Human type Aoyama/B;
DR MEDLINE=75133468; PubMed=804477;
DR RA Kuwabara S.;
DR RT "Amino acid sequence of tuberculin-active protein from Mycobacterium
DR RT tuberculosis.";
DR RL J. Biol. Chem. 250:2563-2568(1975).
DR CC -!- FUNCTION: TUBERCULIN IS THE SOLUBLE, PROTEINACEOUS CELL SUBSTANCE
DR CC OF THE BACTERIUM, TO WHICH INFECTED ANIMALS BECOME HYPERSENSITIVE
DR CC AND REACT CHARACTERISTICALLY TO DERMAL INJECTIONS.
DR CC -!- MISCELLANEOUS: THIS PROTEIN IS THE MOST POTENT COMPONENT WITH
DR CC TUBERCULIN ACTIVITY SO FAR PURIFIED AND CHARACTERIZED.
DR PIR; A03444; TKMYT.
DR DISULFID 27 59
DR SEQUENCE 89 AA; 9493 MW; 91DA5E8B044660F1 CRC64;
DR
DR Query Match 47.9%; Score 35; DB 1; Length 89;
DR Best Local Similarity 61.5%; Pred. No. 23;
DR Matches 8; Conservative 1; Mismatches 2; Indels 2; Gaps 1;
DR
DR QY 2 HEGCRSG--BAEG 12
DR || || || ||
DR bB 56 HEICRDGSGSEG 68

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CBFA_MAIZE STANDARD; PRT; 179 AA.
P25209;
01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
CCAAT-binding transcription factor subunit A (CBF-A) (NF-Y protein
chain B) (NF-YB) (CAAT-box DNA binding protein subunit B).
NFY2.
Zea mays (Maize).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACMAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
[1]_RN
SEQUENCE FROM N.A.
MEDLINE=92195809; PubMed=1549471;
Li X.-Y.; Mantovani R.; Hooft van Huysduijn R., Andre I.,
Benoit C., Mathis D.;
"Evolutionary variation of the CCAAT-binding transcription factor
NF-Y.";
RL Nucleic Acids Res. 20:1087-1091(1992).
CC -!- FUNCTION: Stimulates the transcription of various genes by
CC recognizing and binding to a CCAAT motif in promoters, for example
CC in type 1 collagen, albumin and beta-actin genes.
CC -!- SUBUNIT: Heterotrimeric transcription factor composed of three
CC components, A, B and C. NF-YB and NF-YC must interact and
CC dimerize for NF-YA association and DNA binding.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DOMAIN: Can be divided into three domains: the weakly conserved A
CC domain, the highly conserved B domain thought to be involved in
CC subunit interaction and DNA binding, and the Glu-rich C domain.
CC -!- SIMILARITY: Belongs to the CBF-A subunit family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X59714; CAA42234.1; -.
CC FIR; S22820; S22820.
CC DR HSSP; P48781; I167.
CC DR TRANSFAC; T05212; -.
CC DR MaizeDB; 69282; -.
CC DR InterPro; IPR003956; CBFA_NFYB
CC DR InterPro; IPR003958; CBFA_NFYB_domain.
CC DR InterPro; IPR003957; CBFA_NFYB_copls.
CC DR InterPro; IPR007124; Hist_TAF.
CC DR Pfam; PF08088; CBFD_NFYB_HMF; 1.
CC DR PRINTS; PR00615; CCAATSUBUNTA.
CC DR PROSITE; PS00685; CBFA_NFYB; 1.
CC DR Transcription regulation; DNA-binding; Activator; Nuclear protein.
KW DOMAIN 1 29 A DOMAIN.
FT FT 30 119 B DOMAIN.
FT DOMAIN 120 179 C DOMAIN.
FT FT 36 42 BY SIMILARITY.
FT DNA BIND
FT SEQUENCE 179 AA; 18995 MW; 30621316CB469454 CRC64;
SQ
Query Match 47.9%; Score 35; DB 1; Length 179;
Best Local Similarity 58.3%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 GHEGCRSGEAG 12
DB 142 GHVGASSSNAEG 153

```

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 19, 2004, 17:08:00 ; Search time 58.0806 Seconds  
(without alignments)  
63.242 Million cell updates/sec

Title: US-10-726-692-20

Perfect score: 73

Sequence: 1 GHEGCRSGEAGS 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : A\_Geneseq\_29Jan04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	64.4	338	4	ABG15398 Novel hum
2	45	61.6	1385	7	ADC86871 Human GPC
3	44	60.3	740	3	AAY99411 Human PRO
4	44	60.3	740	4	AAB66160 Protein o
5	44	60.3	802	3	AAB40501 Human ORF
6	44	60.3	802	4	AAT29179 Human PRO
7	44	60.3	802	6	ABU58555 Human PRO
8	44	60.3	802	6	ABU88103 Novel hum
9	44	60.3	802	6	ABU84418 Human sec
10	44	60.3	802	6	ABR62292 Human sec
11	44	60.3	802	6	ABR65682 Human sec
12	44	60.3	802	6	ABU95622 Human sec
13	44	60.3	802	6	ABU82861 Human PRO
14	44	60.3	802	6	ABU89982 Novel hum
15	44	60.3	802	6	ABR68231 Human sec
16	44	60.3	802	6	ABU09342 Human cho
17	44	60.3	802	6	ABU96284 Novel hum
18	44	60.3	802	6	ABU92715 Human sec
19	44	60.3	802	6	ABO08792 Human sec
20	44	60.3	802	6	ABO02844 Human sec
21	44	60.3	802	6	ABR74998 Human sec
22	44	60.3	802	6	ABR94760 Human sec
23	44	60.3	802	6	ABU85733 Human PRO
24	44	60.3	802	6	ABU98893 Novel hum
25	44	60.3	802	6	ABU98108 Novel hum

26	44	60.3	802	6	ABU91814	Novel hum
27	44	60.3	802	6	ABU89507	Human PRO
28	44	60.3	802	6	ABU86348	Human sec
29	44	60.3	802	6	ABU67561	Human sec
30	44	60.3	802	6	ABU80589	Human PRO
31	44	60.3	802	6	ABR99507	Human sec
32	44	60.3	802	6	ABR98897	Human sec
33	44	60.3	802	6	ABO16420	Human sec
34	44	60.3	802	6	ABR92320	Human sec
35	44	60.3	802	6	ABO18961	Human sec
36	44	60.3	802	6	ABR78382	Human sec
37	44	60.3	802	6	ABU85118	Novel hum
38	44	60.3	802	6	ABO00257	Novel hum
39	44	60.3	802	6	ABO11589	Human sec
40	44	60.3	802	6	ABO02234	Human sec
41	44	60.3	802	6	ABU88808	Novel hum
42	44	60.3	802	6	ABU83503	Human sec
43	44	60.3	802	6	ABO06304	Novel hum
44	44	60.3	802	6	ABR59340	Human sec
45	44	60.3	802	6	ABO09402	Human sec
46	44	60.3	802	6	ABO19266	Novel hum
47	44	60.3	802	6	ABO11284	Human sec
48	44	60.3	802	6	ABR66902	Human sec
49	44	60.3	802	6	ABO16115	Human sec
50	44	60.3	802	6	ABO13821	Human sec

ALIGNMENTS

RESULT 1

ABG15398

ID ABG15398 standard; protein; 338 AA.

XX

AC ABG15398;

DT 18-FEB-2002 (first entry)

XX

DE Novel human diagnostic protein #15389.

XX

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder.

XX

OS Homo sapiens.

XX

PN WO200175067-A2.

XX

PD 11-OCT-2001.

XX

PF 30-MAR-2001; 2001WO-US008631.

XX

PR 31-MAR-2000; 2000US-00540217.

PR

23-AUG-2000; 2000US-00649167.

XX

(HYSE-) HYSEQ INC.

PA

Drmanac RT, Liu C, Tang YT;

XX

WPI; 2001-639362/73.

XX

N-PSDB; AAS79585.

XX

PT New isolated polynucleotide and encoded polypeptides, useful in

diagnostics, forensics, gene mapping, identification of mutations

PT responsible for genetic disorders or other traits and to assess

PT biodiversity.

XX

Claim 20; SEQ ID NO 45757; 103pp; English.

XX

CC The invention relates to isolated polynucleotide (I) and polypeptide (II)

sequences. (I) is useful as hybridisation probes, polymerase chain

reaction (PCR) primers, oligomers, and for chromosome and gene mapping,

and in recombinant production of (II). The polynucleotides are also used

in diagnostics as expressed sequence tags for identifying expressed

CC genes. (I) is useful in gene therapy techniques to restore normal  
 CC activity of (II) or to treat disease states involving (II). (II) is  
 CC useful for generating antibodies against it, detecting or quantitating a  
 CC polypeptide in tissue, as molecular weight markers and as a food  
 CC supplement. (II) and its binding partners are useful in medical imaging  
 CC of sites expressing (II). (I) and (II) are useful for treating disorders  
 CC involving aberrant protein expression or biological activity. The  
 CC polypeptide and polynucleotide sequences have application in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic  
 CC amino acid sequences of the invention. Note: The sequence data for this  
 CC patent did not appear in the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 338 AA;

Query Match 64.4%; Score 47; DB 4; Length 338;  
 Best Local Similarity 72.7%; Pred. No. 25;  
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GHEGCRSGEAE 11  
 |||||  
 DB 202 GHRGCSFGAE 212

# RESULT 2

ADC86871  
 ID ADC86871 standard; protein; 1385 AA.

XX AC ADC86871;

XX DT 01-JAN-2004 (first entry)

XX DE Human GPCR protein SEQ ID NO:1324.

XX KW human; GPCR; guanosine triphosphate-binding protein coupled receptor;  
 gene therapy.

XX OS Homo sapiens.

XX PN EP1270724-A2.

XX PD 02-JAN-2003.

XX PF 18-JUN-2002; 2002EP-00013517.

XX PR 18-JUN-2001; 2001JP-00246789.

XX PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
 (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.

XX PI Suwa M, Aesai K, Akiyama Y, Aburatani H;

XX WPI; 2003-315783/31.

XX DR N-PSDB; ADC86870.

XX PT New polynucleotide, useful for preparing a composition for treating a  
 patient in need of increased or suppressed activity or expression of the  
 PT guanosine triphosphate-binding protein coupled receptor.

XX PS Claim 2; SEQ ID NO 1324; 28pp; English.

XX CC The invention relates to a novel polynucleotide encoding a guanosine  
 CC triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of  
 CC the invention may have a use in gene therapy. The polynucleotide and  
 CC polypeptide are useful for preparing a composition for treating a patient  
 CC in need of increased or suppressed activity or expression of the  
 CC guanosine triphosphate-binding protein coupled receptor. The protein  
 CC sequences shown in ADC85549-ADC87617 represent GPCR's of the invention.

XX

SQ Sequence 1385 AA;

Query Match 61.6%; Score 45; DB 7; Length 1385;  
 Best Local Similarity 69.2%; Pred. No. 2.2e+02;  
 Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GHEGCRSGEAE 13

DB 797 GHRGAPGEAE 809

# RESULT 3

AA99411

ID AA99411 standard; protein; 740 AA.

XX AC AA99411;

XX DT 08-AUG-2000 (first entry)

XX DE Human PRO1487 (UNQ756) amino acid sequence SEQ ID NO:260.

XX KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;  
 transmembrane; secretion; immunoadhesion; pharmaceutical; screening.

XX OS Homo sapiens.

XX PN WO200012708-A2.

XX PD 09-MAR-2000.

XX PF 01-SEP-1999; 99WO-US020111.

XX PR 01-SEP-1998; 98US-0098716P.

XX PR 01-SEP-1998; 98US-0098749P.

XX PR 01-SEP-1998; 98US-0098750P.

XX PR 02-SEP-1998; 98US-0098803P.

XX PR 02-SEP-1998; 98US-0098821P.

XX PR 02-SEP-1998; 98US-0098843P.

XX PR 09-SEP-1998; 98US-0098536P.

XX PR 09-SEP-1998; 98US-0098596P.

XX PR 09-SEP-1998; 98US-0098602P.

XX PR 09-SEP-1998; 98US-0098642P.

XX PR 10-SEP-1998; 98US-0098741P.

XX PR 10-SEP-1998; 98US-0098754P.

XX PR 10-SEP-1998; 98US-0098763P.

XX PR 10-SEP-1998; 98US-0098792P.

XX PR 10-SEP-1998; 98US-0098812P.

XX PR 10-SEP-1998; 98US-0098815P.

XX PR 10-SEP-1998; 98US-0098816P.

XX PR 15-SEP-1998; 98US-0100385P.

XX PR 15-SEP-1998; 98US-0100388P.

XX PR 15-SEP-1998; 98US-0100390P.

XX PR 16-SEP-1998; 98US-0100584P.

XX PR 16-SEP-1998; 98US-0100627P.

XX PR 16-SEP-1998; 98US-0100661P.

XX PR 16-SEP-1998; 98US-0100662P.

XX PR 16-SEP-1998; 98US-0100664P.

XX PR 17-SEP-1998; 98US-0100683P.

XX PR 17-SEP-1998; 98US-0100684P.

XX PR 17-SEP-1998; 98US-0100710P.

XX PR 17-SEP-1998; 98US-0100711P.

XX PR 17-SEP-1998; 98US-0100919P.

XX PR 17-SEP-1998; 98US-0100930P.

XX PR 18-SEP-1998; 98US-0100848P.

XX PR 18-SEP-1998; 98US-0100849P.

XX PR 18-SEP-1998; 98US-0101014P.

XX PR 18-SEP-1998; 98US-0101068P.

XX PR 18-SEP-1998; 98US-0101071P.

XX PR 22-SEP-1998; 98US-0101279P.

XX PR 23-SEP-1998; 98US-0101471P.

XX PR 23-SEP-1998; 98US-0101472P.

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PR 23-SEP-1998; 98US-0101474P.
PR 23-SEP-1998; 98US-0101475P.
PR 23-SEP-1998; 98US-0101476P.
PR 23-SEP-1998; 98US-0101477P.
PR 23-SEP-1998; 98US-0101478P.
PR 23-SEP-1998; 98US-0101479P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101741P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101915P.
PR 24-SEP-1998; 98US-0101916P.
PR 29-SEP-1998; 98US-0102207P.
PR 29-SEP-1998; 98US-0102240P.
PR 29-SEP-1998; 98US-0102307P.
PR 29-SEP-1998; 98US-0102330P.
PR 29-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102484P.
PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.
PR 02-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.
PR 06-OCT-1998; 98US-0103449P.
PR 07-OCT-1998; 98US-0103314P.
PR 07-OCT-1998; 98US-0103315P.
PR 07-OCT-1998; 98US-0103328P.
PR 07-OCT-1998; 98US-0103395P.
PR 07-OCT-1998; 98US-0103396P.
PR 07-OCT-1998; 98US-0103401P.
PR 08-OCT-1998; 98US-0103633P.
PR 08-OCT-1998; 98US-0103678P.
PR 08-OCT-1998; 98US-0103679P.
PR 08-OCT-1998; 98US-0103711P.
PR 14-OCT-1998; 98US-0104257P.
PR 20-OCT-1998; 98US-0104987P.
PR 20-OCT-1998; 98US-0105000P.
PR 21-OCT-1998; 98US-0105104P.
PR 22-OCT-1998; 98US-0105169P.
PR 22-OCT-1998; 98US-0105266P.
PR 26-OCT-1998; 98US-0105693P.
PR 26-OCT-1998; 98US-0105694P.
PR 27-OCT-1998; 98US-0105807P.
PR 27-OCT-1998; 98US-0105881P.
PR 27-OCT-1998; 98US-0105882P.
PR 27-OCT-1998; 98US-010602P.
PR 28-OCT-1998; 98US-0106023P.
PR 28-OCT-1998; 98US-0106029P.
PR 28-OCT-1998; 98US-0106030P.
PR 28-OCT-1998; 98US-0106032P.
PR 28-OCT-1998; 98US-0106033P.
PR 28-OCT-1998; 98US-0106178P.
PR 29-OCT-1998; 98US-0106248P.
PR 29-OCT-1998; 98US-0106384P.
PR 29-OCT-1998; 98US-0108500P.
PR 30-OCT-1998; 98US-0106464P.
PR 03-NOV-1998; 98US-0106856P.
PR 03-NOV-1998; 98US-0106902P.
PR 03-NOV-1998; 98US-0106905P.
PR 03-NOV-1998; 98US-0106919P.
PR 03-NOV-1998; 98US-0106932P.
PR 03-NOV-1998; 98US-0106934P.
PR 10-NOV-1998; 98US-0107783P.
PR 17-NOV-1998; 98US-0108775P.
PR 17-NOV-1998; 98US-0108779P.
PR 17-NOV-1998; 98US-0108788P.
PR 17-NOV-1998; 98US-0108801P.
PR 17-NOV-1998; 98US-0108802P.
PR 17-NOV-1998; 98US-0108806P.
PR 17-NOV-1998; 98US-0108807P.
PR 17-NOV-1998; 98US-0108867P.

PR 17-NOV-1998; 98US-0108925P.
PR 18-NOV-1998; 98US-0108848P.
PR 18-NOV-1998; 98US-0108849P.
PR 18-NOV-1998; 98US-0108850P.
PR 18-NOV-1998; 98US-0108851P.
PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108858P.
PR 18-NOV-1998; 98US-0108904P.
XX (GETH ) GENENTECH INC.
XX Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;
XX WPI; 2000-237871/20.
XX N-PSDB; AAA37093.
XX New mammalian DNA sequences encoding transmembrane, receptor or secreted
XX PRO polypeptides, useful for screening of potential peptide or small
XX molecule inhibitors of the relevant receptor/ligand interactions.
XX Claim 12; Fig 144; 773pp; English.
XX AAA37022 to AAA37144 encode the new isolated human transmembrane
XX receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The
XX transmembrane and receptor PRO proteins can be used for screening of
XX potential peptide or small molecule inhibitors of the relevant
XX receptor/ligand interactions. The polypeptides and nucleotide sequences
XX encoding then have various industrial applications, including uses as
XX pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR
XX primers and hybridisation probes used in the isolation of the PRO
XX polypeptides from the present invention
XX Sequence 740 AA;

Query Match 60.3%; Score 44; DB 3; Length 740;
Best Local Similarity 72.7%; Pred. NO. 1.7e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 EGCGRSGAEGS 13
Db 46 EGCGRSGQAAS 56
|||||:|
|||||:|

RESULT 4
AAB66160
ID AAB66160 standard; protein; 740 AA.
XX
XX AAB66160;
XX
XX 02-APR-2001 (first entry)
XX
XX Protein of the invention #72.
XX
XX Secreted; transmembrane; gene therapy.
XX
XX Unidentified.
XX
XX WO200078961-A1.
XX
XX 28-DEC-2000.
XX
XX 18-FEB-2000; 2000WO-US004342.
XX
XX 23-JUN-1999; 98US-0141037P.
XX 20-JUL-1999; 98US-0144758P.
XX 26-JUL-1999; 98US-0145698P.
XX 01-SEP-1999; 99WO-US020111.
XX 29-OCT-1999; 99US-0162506P.
XX 30-NOV-1999; 99WO-US028313.
XX 02-DEC-1999; 99WO-US028551.
XX 16-DEC-1999; 99WO-US030095.
XX 05-JAN-2000; 2000WO-US000219.
XX 06-JAN-2000; 2000WO-US000376.
```

XX (GETH ) GENENTECH INC.  
 PA Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
 PI Gao W, Goddard A, Godowski PJ, Grimaldi CU, Gurney AL, Hillan KJ;  
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;  
 PI Williams PW, Wood WI;  
 XX WPI; 2001-0711395/08.  
 DR Secreted and transmembrane proteins and nucleic acids designated PRO,  
 PT useful as hybridization probes, in chromosome and gene mapping and gene  
 PT therapy.  
 XX Claim 1; Fig 144; 787pp; English.  
 XX The present invention relates to secreted and transmembrane proteins.  
 CC These proteins and the DNA encoding them may be used as hybridization  
 CC probes, in chromosome and gene mapping and in the generation of anti-  
 CC sense RNA and DNA. They may also be used to generate either  
 CC transgenic animals or knockout animals which are in turn useful for  
 CC development and screening of therapeutically useful reagents. The nucleic  
 CC acids may also be used in gene therapy  
 XX Sequence 740 AA;  
 SQ  
 Query Match 60.3%; Score 44; DB 4; Length 740;  
 Best Local Similarity 72.7%; Pred. No. 1.7e+02;  
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 3 EGCGRSGEARGS 13  
 Db 46 EGCGRSGQAAS 56  
 |||||:|  
 RESULT 5  
 AAB40501  
 ID AAB40501 standard; protein; 802 AA.  
 XX AAB40501;  
 XX 08-FEB-2001 (first entry)  
 DT Human ORFX ORF265 polypeptide sequence SEQ ID NO:530.  
 DE  
 XX Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;  
 KW vulnery; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;  
 KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;  
 KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;  
 KW hypotensive; dermatological; immunosuppressive; antinflammatory;  
 KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;  
 KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;  
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease;  
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;  
 KW cholesterol ester storage; systemic lupus erythematosus; infection;  
 KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;  
 KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;  
 KW bone damage; cartilage damage; antinflammatory disease; coagulation;  
 KW thrombosis; contraceptive.  
 XX Homo sapiens.  
 OS  
 XX WO200058473-A2.  
 PN  
 XX 05-OCT-2000.  
 PD  
 XX 31-MAR-2000; 2000WO-US008621.  
 PF  
 XX 31-MAR-1999; 99US-0127607P.  
 PR 02-APR-1999; 99US-0127636P.  
 PR 05-APR-1999; 99US-0127728P.  
 PR 30-MAR-2000; 2000US-00540763.  
 XX

PA (CURA-) CURAGEN CORP.  
 XX Shinkets RA, Leach M;  
 XX WPI; 2000-60362/57.  
 DR N-PSDB; AAC74710.  
 XX Novel nucleic acids and peptides derived from open reading frame X,  
 PT useful for treating e.g. cancers, proliferative disorders,  
 PT neurodegenerative disorders and cardiovascular disease.  
 XX Claim 11; Page 699-700; 5507pp; English.  
 PS AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,  
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX  
 CC sequences have activities such as: cytostatic; hepatotropic; vulnery;  
 CC antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic;  
 CC anticonvulsant; antiarthritic; immunosuppressant; immunostimulant;  
 CC cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;  
 CC dermatological; immunosuppressive; antinflammatory; antibacterial;  
 CC antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The  
 CC sequences can be used for determining the presence of or predisposition  
 CC to, or preventing or treating pathological conditions associated with an  
 CC ORFX-associated disorder. The nucleic acids can be used to express ORFX  
 CC proteins in gene therapy vectors. The proteins and nucleic acids may be  
 CC used to treat cancers, proliferative disorders, neurodegenerative  
 CC disorders, osteoarthritis, graft vs host disease, cardiovascular disease,  
 CC diabetes mellitus, hypertension, hypothyroidism, cholesterol ester  
 CC storage, systemic lupus erythematosus, severe combined immunodeficiency  
 CC (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune  
 CC disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and  
 CC cartilage damage, nocturnal haemoglobinuria, antinflammatory disease; to  
 CC enhance coagulation; to inhibit thrombosis; and as a contraceptive  
 XX Sequence 802 AA;  
 SQ  
 Query Match 60.3%; Score 44; DB 3; Length 802;  
 Best Local Similarity 72.7%; Pred. No. 1.8e+02;  
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 3 EGCGRSGEARGS 13  
 Db 46 EGCGRSGQAAS 56  
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 XX 18-DEC-2001 (first entry)  
 DT Human PRO polypeptide sequence #156.  
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 XX PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;  
 KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;  
 KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;  
 KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.  
 XX Homo sapiens.  
 OS  
 XX WO200168848-A2.  
 PN  
 XX 20-SEP-2001.  
 PD  
 XX 28-FEB-2001; 2001WO-US006520.  
 PF  
 XX 01-MAR-2000; 2000WO-US005601.  
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PR 14-MAR-2000; 2000US-0189328P.  
 PR 15-MAR-2000; 2000WO-US006884.  
 PR 21-MAR-2000; 2000US-0190828P.  
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 PR 03-MAY-2000; 2000US-0201516P.  
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 PR 22-MAY-2000; 2000WO-US014042.  
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 PR 02-JUN-2000; 2000WO-US015264.  
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 PR 28-JUL-2000; 2000WO-US020710.  
 PR 22-AUG-2000; 2000US-00644848.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 08-NOV-2000; 2000WO-US030952.  
 PR 01-DEC-2000; 2000WO-US032678.  
 PR 20-DEC-2000; 2000WO-US034955.  
 XX  
 PA (GETH ) GENENTECH INC.

XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;  
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;  
 XX  
 DR WPI; 2001-602746/68.  
 DR N-PSDB; AAS46080.  
 XX  
 PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the  
 PT presence of tumors, such as prostate and breast tumors, in mammals and to  
 PT screen for modulators of the compounds.  
 XX  
 PS Claim 11; Fig 312; 774pp; English.

XX Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.  
 CC The PRO polypeptides and their associated nucleic acids can be used to  
 CC detect the presence of a tumour in a mammal by comparing the level of  
 CC expression of a PRO polypeptide in a test sample of cells from the animal  
 CC and a control sample of normal cells, whereby a higher level of  
 CC expression in the test sample indicates the presence of a tumour in the  
 CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats  
 CC and rabbits but are preferably human. The polypeptides can be used to  
 CC stimulate tumour necrosis factor (TNF) alpha release from human blood,  
 CC when contacted with it. A specific polypeptide can be used to stimulate  
 CC the proliferation or differentiation of chondrocyte cells. The PRO  
 CC proteins can be used to determine the presence of tumours and also  
 CC susceptibility to tumour development, particularly adrenal, lung, colon,  
 CC breast, prostate, rectal, cervical, or liver tumours, in mammalian  
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids  
 CC can be used for genetic analysis of individuals with genetic disorders

XX Sequence 802 AA;

Query Match 60.3%; Score 44; DB 4; Length 802;  
 Best Local Similarity 72.7%; Pred. No. 1.8e+02;  
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 ECGRSGEAGS 13

Db	RESULT 7	46 ECGRSGQAAAS 56
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XX AC	ABUS8555;	
XX DT	15-APR-2003 (first entry)	
XX DE	Human PRO polypeptide #156.	
XX KW	Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;	
XX KW	dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;	
XX KW	antibody-dependent enzyme mediated prodrug therapy.	
XX OS	Homo sapiens.	
XX PN	US2003027272-A1.	
XX PD	06-FEB-2003.	
XX PF	21-JUN-2002; 2002US-00176492.	
XX PR	18-SEP-1997; 97US-0059263P.	
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PR 07-OCT-1998; 98US-00168978.

Query Match 60.3%; Score 44; DB 6; Length 802;

Best Local Similarity 72.7%; Pred. No. 1.8e+02;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGCRCGEAEGS 13

Db 46 EGCRCGQAAS 56

RESULT 8

ABU88103

ID ABU88103 standard; protein; 802 AA.



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 PR 06-OCT-1998; 98US-0103258P.  
 Query Match 60.3%; Score 44; DB 6; Length 802;  
 Best Local Similarity 72.7%; Pred.No. 1.8e+02;  
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 3 EGCRCGEAGS 13  
 Db 46 EGCRCGQAAAS 56  
 RESULT 9  
 ID ABU84418  
 XX ABU84418 standard; protein; 802 AA.  
 AC ABU84418;  
 XX 02-AUG-2003 (first entry)  
 DT 02-AUG-2003 (first entry)  
 XX Human secreted/transmembrane protein (PRO) #156.  
 DE  
 XX

KW Human; secreted and transmembrane protein; PRO; TNF-alpha;  
 KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;  
 XX tissue typing.  
 OS Homo sapiens.  
 XX US2003032112-A1.  
 XX PD 13-FEB-2003.  
 XX PF 21-JUN-2002; 2002US-00176756.  
 XX PR 18-SEP-1997; 97US-0059263P.  
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XX PN US2003036159-A1.
XX XX 20-FEB-2003.
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Query Match 60.3%; Score 44; DB 6; Length 802;  
Best Local Similarity 72.7%; Pred. No. 1.8e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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ABU99622  
ID ABU99622 standard; protein; 802 AA.

XX AC ABU99622;

XX 09-AUG-2003 (first entry)

XX Human secreted/transmembrane protein (PRO) #156.

XX Human; secreted and transmembrane protein; PRO; TNF-alpha;  
KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;  
tissue typing.

XX OS Homo sapiens.

XX US2003040070-A1.

XX 27-FEB-2003.

XX 27-JUN-2002; 2002US-00184627.

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Query Match 60.3%; Score 44; DB 6; Length 802;

Best Local Similarity 72.7%; Pred. No. 1.8e+02;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Db |||||:|  
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RESULT 13

ABU82861

ID ABU82861 standard; protein; 802 AA.

XX AC ABU82861;

XX 27-JUN-2003 (first entry)

XX DE Human PRO polypeptide #156.

XX Human; PRO polypeptide; secreted and transmembrane protein; tumour;

KW chromosome mapping; gene mapping; cytostatic.

XX OS Homo sapiens.

XX PN US2003032113-A1.

XX PD 13-FEB-2003.

XX 20-JUN-2002; 2002US-00176911.

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Query Match 60.3%; Score 44; DB 6; Length 802;
Best Local Similarity 72.7%; Pred. No. 1.8e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGCRCGEAGS 13
DB 46 EGCRCGQAAAS 56

RESULT 14
ABU89982
ID ABU89982 standard; protein; 802 AA.
XX AC ABU89982;
XX DT 11-AUG-2003 (first entry)
XX DE Novel human secreted and transmembrane protein PRO1487.
XX KW Human; gene therapy; tissue typing; tumour; chondrocyte proliferation;
XX KW chondrocyte differentiation; tumour necrosis factor-alpha release;
XX OS Homo sapiens.
XX US2003036147-A1.
XX PD 20-FEB-2003.
XX PF 02-JUL-2002; 2002US-00187741.
XX PR 18-SEP-1997; 97US-0059263P.
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RESULT 15
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ID ABR68231 standard; protein; 802 AA.
XX AC ABR68231;
XX DT 11-AUG-2003 (first entry)
XX DE Human secreted polypeptide PRO1487, SEQ ID NO:312.
XX KW Human; PRO; secreted protein; transmembrane protein;
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnery; gene therapy.
XX OS Homo sapiens.
XX PN US2003027264-A1.
XX PD 06-FEB-2003.
XX PF 18-JUN-2002; 2002US-00174579.
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Query Match 60.3%; Score 44; DB 6; Length 802;
Best Local Similarity 72.7%; Pred. No. 1.8e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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RESULT 16
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ID ABU09342 standard; protein; 802 AA.
XX
AC ABU09342;
XX
DT 01-JUL-2003 (first entry)
XX
DE Human chondroitin synthase.
XX
KW Human; chondroitin synthase; vector; sugar chain production;
KW chondroitin disaccharide repetitive unit; enzyme.
XX
OS Homo sapiens.
XX
PN WO2003012099-A1.
XX
PD 13-FEB-2003.
XX
PF 01-AUG-2002; 2002WO-JP007859.
XX
PR 01-AUG-2001; 2001JP-00234112.
PA (NEWI-) NEW IND RES ORG.
XX
PI Sugahara K, Kitagawa H;
XX
WPI; 2003-248181/24.
DR N-PSDB; ABX95723.
XX
PT New vector for use in producing human chondroitin synthase applicable in
PT production of sugar chains and having a disaccharide repetitive unit of
chondroitin.
XX
PS Claim 1; Fig 1; 61pp; Japanese.
XX
CC The present invention relates to a vector containing DNA that encodes
CC human chondroitin synthase. The vector is useful for producing
CC chondroitin synthase which may be used in the production of a sugar chain
CC having a disaccharide repetitive unit of chondroitin. The polynucleotide
CC sequence encoding chondroitin synthase is useful as a hybridisation probe
CC for chondroitin synthase. The present sequence represents human
CC chondroitin synthase
SQ Sequence 802 AA;

Query Match 60.3%; Score 44; DB 6; Length 802;
Best Local Similarity 72.7%; Pred. No. 1.8e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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RESULT 17
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ID ABU96284 standard; protein; 802 AA.
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AC ABU96284;  
XX DT 25-JUL-2003 (first entry)  
XX DE Novel human secreted and transmembrane protein PRO1487.  
XX KW Human; secreted and transmembrane protein; PRO; transgenic animal;  
KW knockout; chromosome identification; tissue typing; tumour;  
KW chondrocyte proliferation; chondrocyte differentiation;  
KW tumor necrosis factor-alpha release stimulator.  
XX OS Homo sapiens.  
XX PN US2003036144-A1.  
XX PD 20-FEB-2003.  
XX PF 01-JUL-2002; 2002US-00187601.  
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Best Local Similarity 72.7%; Pred. No. 1.8e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Db 46 EGCRCGQAAAS 56

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AC ABU92715;  
DT 18-JUL-2003 (first entry)  
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DE Human secreted/transmembrane protein (PRO) #156.  
XX  
KW Human; secreted protein; transmembrane protein; PRO; tumour;

KW proliferation; differentiation; chondrocyte cell; TNF-alpha;  
KW tumour necrosis factor-alpha; gene therapy.  
XX Homo sapiens.  
OS  
XX US2003036149-A1.  
PN  
XX 20-FEB-2003.  
PD  
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PF 02-JUL-2002; 2002US-00187746.  
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Best Local Similarity 72.7%; Pred. No. 1.8e+02;  
Matches 8; Conservative. 1; Mismatches 2; Indels 0; Gaps 0;

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RESULT 19

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ID ABO08792 standard; protein; 802 AA.

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AC ABO08792;  
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DT 17-AUG-2003 (first entry)

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KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;

KW tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour;

KW prostate tumour; rectal tumour; cervical tumour; liver tumour.

XX Homo sapiens.

OS Homo sapiens.

XX US2003044923-A1.

PN

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PF 24-JUN-2002; 2002US-00179522.  
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KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour.
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XX KW Human; PRO; secreted protein; transmembrane protein; extracellular domain; tumour necrosis factor-alpha; TNF-alpha; chondrocyte; proliferation; differentiation; cartilage disorder; bone disorder; arthritis; sports injury; cancer; tumour; diagnosis; adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix; liver; drug screening; transgenic animal; genetic analysis; antiarthritic; vulnery; gene therapy.  
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XX US2003040056-A1.  
XX PN 27-FEB-2003.  
XX PD 21-JUN-2002; 2002US-00176916.  
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Query Match 60.3%; Score 44; DB 6; Length 802;
Best Local Similarity 72.7%; Pred. NO. 1.9e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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RESULT 22
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ID ABR94760 standard; protein; 802 AA.
XX AC ABR94760;
XX DT 13-SEP-2003 (first entry)
XX DE Human secreted polypeptide PRO1487, SEQ ID NO:312.
XX KW Human; PRO; secreted protein; transmembrane protein;
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulneryary; gene therapy.
XX OS Homo sapiens.
XX PN US2003044926-A1.
XX PD 06-MAR-2003.
XX PF 26-JUN-2002; 2002US-00183015.
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Query Match 60.3%; Score 44; DB 6; Length 802;
Best Local Similarity 72.7%; Pred. No. 1.8e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGRSGEAEGRS 13
DB 46 EGRSGQAAS 56

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ID ABU85733 standard; protein; 802 AA.
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AC ABU85733;
XX
DT 02-JUL-2003 (first entry)
XX
DE Human PRO polypeptide #156.
XX
KW Human; PRO; secreted polypeptide; transmembrane polypeptide;
KW tumour necrosis factor alpha; TNF-alpha; chondrocyte cell; tumour;
XX cytostatic.
XX
OS Homo sapiens.
XX
PN US2003036140-A1.
XX
PD 20-FEB-2003.
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PF 01-JUL-2002; 2002US-00187588.
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PR 04-SEP-2001; 2001US-00946374.  
PR 15-JAN-2002; 2002US-00052586.  
XX

(GETH ) GENENTECH INC.

PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;  
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

XX WPI; 2003-332028/31.  
XX N-PSDB; ACA72926.

PT Three hundred and five nucleic acids encoding PRO polypeptides, useful  
PT for the manufacture of a medicament for diagnosing or treating tumor.

XX Claim 11; Fig 312; 707pp; English.

CC The invention relates to human PRO polypeptides (secreted and  
CC transmembrane polypeptides) and the PRO polynucleotides encoding them.  
CC The invention also relates to a method for stimulating the release of  
CC tumour necrosis factor alpha (TNF-alpha) from human blood by contacting  
CC the blood with a sequence of the invention, a method for stimulating the  
CC proliferation or differentiation of chondrocyte cells by contacting the  
CC cells with a PRO polypeptide and a method for detecting the presence of a  
CC tumour in a mammal. The polypeptides and polynucleotides are useful for  
CC the manufacture of a medicament for diagnosing or treating a tumour in a  
CC mammal. Sequences ABU85578-ABU85882 represent human PRO polypeptides of  
CC the invention. Note: The sequence data for this patent is also available  
CC in electronic format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)

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Query Match 60.3%; Score 44; DB 6; Length 802;  
Best Local Similarity 72.7%; Pred. NO. 1.8e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGCRRSGAEAGS 13  
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Db 46 EGCRRSGQAAS 56

RESULT 24  
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XX AC ABU98893;  
XX DT 01-AUG-2003 (first entry)  
XX DE Novel human secreted and transmembrane protein PRO1487.  
XX KW Human; secreted and transmembrane protein; PRO; cytostatic; gene therapy;  
KW chondrocyte stimulator; tumour; adrenal tumour; lung tumour;  
KW colon tumour; breast tumour; prostate tumour; rectal tumour;  
KW cervical tumour; liver tumour; TNF-alpha release;  
KW tumour necrosis factor alpha release; chondrocyte cell proliferation;  
KW chondrocyte cell differentiation; pharmaceutical; diagnostic; biosensor;  
KW bioreactor.  
XX OS Homo sapiens.  
XX PN US2003013153-A1.  
XX PD 16-JAN-2003.  
XX PF 19-JUN-2002; 2002US-00175737.  
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Best Local Similarity 72.7%; Pred. No. 1.8e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGCGRSGAEGS 13  
Db 46 EGCGRSGQAAS 56

RESULT 25

ABU98108  
ID ABU98108 standard; protein; 802 AA.  
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AC ABU98108;  
XX  
DT 30-JUL-2003 (first entry)  
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XX Human; secreted and transmembrane protein; PRO; cytosolic; gene therapy;  
KW chondrocyte stimulator; tumour; adrenal tumour; lung tumour;  
KW colon tumour; breast tumour; prostate tumour; rectal tumour;  
KW cervical tumour; liver tumour; chromosome identification.  
XX  
OS Homo sapiens.  
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Best Local Similarity 72.7%; Pred. No. 1.8e+02;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGCGRSGAEGS 13  
Db 46 EGCGRSQMAAS 56

RESULT 26

ABU91814

ID ABU91814 standard; protein; 802 AA.

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AC ABU91814;

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DT 11-AUG-2003 (first entry)

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XX Human; gene therapy; chromosome identification; tissue typing.  
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XX 06-FEB-2003.  
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PR 24-SEP-1998; 98US-0101743P.  
PR 24-SEP-1998; 98US-0101922P.  
PR 25-SEP-1998; 98US-0101786P.  
PR 29-SEP-1998; 98US-0102207P.  
PR 29-SEP-1998; 98US-0102240P.  
PR 29-SEP-1998; 98US-0102330P.  
PR 29-SEP-1998; 98US-0102331P.  
PR 30-SEP-1998; 98US-0102487P.  
PR 30-SEP-1998; 98US-0102570P.  
PR 30-SEP-1998; 98US-0102571P.  
PR 01-OCT-1998; 98US-0102684P.  
PR 01-OCT-1998; 98US-0102687P.  
PR 02-OCT-1998; 98US-0102965P.  
PR 06-OCT-1998; 98US-0103258P.  
PR 06-OCT-1998; 98US-0103449P.  
PR 07-OCT-1998; 98US-00168978.  
PR 07-OCT-1998; 98US-0103395P.  
PR 07-OCT-1998; 98US-0103401P.

Query Match 60.3%; Score 44; DB 6; Length 802;  
Best Local Similarity 72.7%; Pred. No. 1.8e+02;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGRSGEAGS 13  
|||||:  
Db 46 EGRSGQAAS 56

RESULT 27

ABU89507

ID ABU89507 standard; protein; 802 AA.

XX ABU89507;

DT 09-JUL-2003 (first entry)

DE Human PRO polypeptide #156.

KW Human; PRO polypeptide; secreted protein; transmembrane protein;  
KW chromosome mapping; gene mapping; tumour; adrenal; lung; colon; breast;  
KW prostate; rectal; cervical; liver; cancer; TNF-alpha;  
KW tumour necrosis factor-alpha; proliferation; differentiation;  
KW chondrocyte cell; bone disorder; cartilage disorder; sports injury;

KW arthritis; cytostatic; antiarthritic; osteopathic.

XX Homo sapiens.

XX US2003036141-A1.

XX 20-FEB-2003.

XX 01-JUL-2002; 2002US-00187597.

XX 18-SEP-1997; 97US-0059263P.

XX 18-SEP-1997; 97US-0059266P.

XX 21-OCT-1997; 97US-0062250P.

XX 21-OCT-1997; 97US-0063486P.

XX 24-OCT-1997; 97US-0063120P.

XX 24-OCT-1997; 97US-0063121P.

XX 28-OCT-1997; 97US-0063540P.

XX 28-OCT-1997; 97US-0063541P.

XX 28-OCT-1997; 97US-0063544P.

XX 28-OCT-1997; 97US-0063564P.

XX 29-OCT-1997; 97US-0063734P.

XX 31-OCT-1997; 97US-0063870P.

XX 31-OCT-1997; 97US-0064103P.

XX 13-NOV-1997; 97US-0065311P.

XX 21-NOV-1997; 97US-0066120P.

XX 24-NOV-1997; 97US-0066466P.

XX 24-NOV-1997; 97US-0066772P.

XX 11-DEC-1997; 97US-0069335P.

XX 12-DEC-1997; 97US-0069425P.

XX 17-DEC-1997; 97US-0069870P.

XX 18-DEC-1997; 97US-0068017P.

XX 10-MAR-1998; 98US-0077450P.

XX 11-MAR-1998; 98US-0077632P.

XX 11-MAR-1998; 98US-0077649P.

XX 20-MAR-1998; 98US-0078886P.

XX 20-MAR-1998; 98US-0078939P.

XX 27-MAR-1998; 98US-0079664P.

XX 27-MAR-1998; 98US-0079786P.

XX 31-MAR-1998; 98US-0080107P.

XX 31-MAR-1998; 98US-0080194P.

XX 01-APR-1998; 98US-0080327P.

XX 01-APR-1998; 98US-0080333P.

XX 08-APR-1998; 98US-0081049P.

XX 08-APR-1998; 98US-0081070P.

XX 09-APR-1998; 98US-0081195P.

XX 15-APR-1998; 98US-0081838P.

98US-0088028P.

98US-0088029P.

98US-0088033P.

98US-0088326P.

98US-0088167P.

98US-0088202P.

98US-0088212P.

98US-0088217P.

98US-0088655P.

98US-0088722P.

98US-0088738P.

98US-0088740P.

98US-0088811P.

98US-0088824P.

98US-0088825P.

98US-0088826P.

98US-0088861P.

98US-0088863P.

98US-0088876P.

98US-0089090P.

98US-0089105P.

98US-0089512P.

98US-0089514P.

98US-0089538P.

98US-0089598P.

98US-0089598P.

98US-0090246P.

98US-0090252P.

98US-0090254P.

98US-0090429P.

98US-0090435P.

98US-0090444P.

98US-0090461P.

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98US-0090540P.

98US-0090676P.

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98US-0090690P.

98US-0090694P.

98US-0090695P.

04-JUN-1998;

04-JUN-1998;

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10-JUN-1998;

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10-JUN-1998;

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10-AUG-1998;

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26-AUG-1998;

26-AUG-1998;

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PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-009602P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099812P.
PR 15-SEP-1998; 98US-0100388P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 16-SEP-1998; 98US-0101751P.
PR 16-SEP-1998; 98US-0101933P.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101068P.
PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101475P.
PR 23-SEP-1998; 98US-0101477P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101739P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101922P.
PR 25-SEP-1998; 98US-0101786P.
PR 25-SEP-1998; 98US-0102207P.
PR 29-SEP-1998; 98US-0102240P.
PR 29-SEP-1998; 98US-0102330P.
PR 29-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.
PR 02-OCT-1998; 98US-0102965P.
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Query Match 60.3%; Score 44; DB 6; Length 802;

Best Local Similarity 72.7%; Pred.No. 1.8e+02;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY      3  EGCRCGEARGS 13
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Db      46  EGCRCGQAAAS 56
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RESULT 28
ABU86348
ID  ABU86348 standard; protein; 802 AA.
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XX AC

XX ABU86348;

XX DT 01-JUL-2003 (first entry)

XX DE Human secreted/transmembrane protein (PRO) #156.

XX KW Human; immunogen; secreted protein; transmembrane protein; PRO; tumour;  
proliferation; differentiation; chondrocyte cells;

XX KW tumour necrosis factor-alpha; TNF-alpha; blood; gene therapy.

XX OS Homo sapiens.

XX PN US2003036146-A1.

XX PD 20-FEB-2003.

XX PF 02-JUL-2002; 2002US-00187603.

XX XX

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PR 26-JUN-1998; 98US-00105413.
PR 16-SEP-1998; 98WO-US019330.
PR 07-OCT-1998; 98US-00168978.
PR 07-OCT-1998; 98WO-US021141.
PR 06-NOV-1998; 98US-00187368.
PR 01-DEC-1998; 98WO-US025108.
PR 07-DEC-1998; 98US-00202054.
PR 03-MAR-1999; 99US-00254311.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028551.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 30-JUL-2001; 2001US-00918585.
PR 06-AUG-2001; 2001US-00924419.
PR 13-AUG-2001; 2001US-00929404.
PR 16-AUG-2001; 2001US-00931836.
PR 28-AUG-2001; 2001US-00941992.
PR 29-AUG-2001; 2001WO-US027099.
PR 04-SEP-2001; 2001US-00946374.
PR 15-JAN-2002; 2002US-00052586.
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(GETH ) GENENTECH INC.

BAker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;

PI Fan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

XX WPI; 2003-332034/31.

DR N-PSDB; ACA73540.

XX Three hundred and five nucleic acids encoding PRO polypeptides, useful in  
PT gene therapy, chromosome identification, tissue typing, and for detecting  
PT the presence of tumor in a mammal.

XX Claim 11; Fig 312; 707pp; English.

PS The invention relates to three hundred and five nucleic acids encoding  
CC PRO polypeptides (secreted and transmembrane), sequences 80% identical to  
CC them, or encoding a PRO polypeptide lacking its associated signal peptide  
CC or an extracellular domain of the PRO polypeptide, with or lacking its  
CC associated signal peptide. Also included are the encoded PRO proteins,  
CC PRO expression vectors, host cells transformed with the vector (used to  
CC produce PRO proteins), a chimeric molecule comprising the PRO  
CC polypeptide fused to a heterologous amino acid sequence, an anti-PRO  
CC antibody, a method for stimulating the release of tumor necrosis factor  
CC alpha (TNF-alpha) from human blood (by contacting the blood with PRO1079,  
CC PRO827, PRO791, PRO1131, PRO1316, PRO1183, PRO1343, PRO1760, PRO1567 or  
CC PRO4333), a method for stimulating the proliferation or differentiation  
CC of chondrocyte cells by contacting the cells with a PRO6029 polypeptide,  
CC a method for detecting the presence of tumor in a mammal and an  
CC oligonucleotide probe derived from any of the nucleotide sequences cited  
CC above. The PRO polypeptide or anti-PRO antibody is useful for preparing a  
CC medicament for treating a condition that is responsive to the PRO  
CC polypeptide or anti-PRO antibody. The PRO nucleotide sequences are useful  
CC as hybridisation probes in chromosome and gene mapping, or in generating  
CC antisense RNA and DNA. PRO nucleic acids are also useful in preparing PRO  
CC polypeptides, in assays to identify other proteins or molecules involved  
CC in a binding reaction, to generate transgenic animals or knockout  
CC animals, which in turn are useful in the development and screening of  
CC therapeutically useful reagents, for chromosome identification, and  
CC tissue typing. The PRO polypeptides and nucleic acid molecules are also  
CC useful for detecting the presence of a tumour in a mammal, stimulating  
CC proliferation or differentiation of chondrocyte cells, stimulating the  
CC release of tumour necrosis factor-alpha from human blood, in gene  
CC therapy, or as molecular weight markers for protein electrophoresis  
CC purposes. The anti-PRO antibodies may be used in diagnostic assays for  
CC PRO, or for the affinity purification of PRO from recombinant cell  
CC culture or natural sources. The present sequence represents a PRO protein

SQ Sequence 802 AA;

Query Match 60.3%; Score 44; DB 6; Length 802;  
Best Local Similarity 72.7%; Pred. No. 1.8e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGCRCGEAEGS 13  
|||||:|  
Db 46 EGCRCGQAAS 56

RESULT 29

ABU67561  
ID ABU67561 standard; protein; 802 AA.

AC ABU67561;

DT 29-MAY-2003 (first entry)

DE Human secreted/transmembrane protein (PRO) #156.

KW Human; secreted and transmembrane protein; PRO; TNF-alpha;  
KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;  
KW tissue typing.

OS Homo sapiens.

XX US2003036162-A1.

XX 20-FEB-2003.

XX 12-JUL-2002; 2002US-00194423.

XX

PR 26-JUN-1998; 98US-00105413.  
PR 16-SEP-1998; 98WO-US019330.  
PR 07-OCT-1998; 98US-00168978.  
PR 06-NOV-1998; 98WO-US021141.  
PR 01-DEC-1998; 98US-00187368.  
PR 07-DEC-1998; 98WO-US025108.  
PR 03-MAR-1999; 98US-00202054.  
PR 08-MAR-1999; 99US-00254311.  
PR 14-MAY-1999; 99WO-US005028.  
PR 02-JUN-1999; 99US-00311832.  
PR 12-JUN-1999; 99WO-US010733.  
PR 25-AUG-1999; 99US-00380137.  
PR 25-AUG-1999; 99US-00380138.  
PR 25-AUG-1999; 99US-00380139.  
PR 01-SEP-1999; 99US-00380142.  
PR 15-SEP-1999; 99WO-US020111.  
PR 18-OCT-1999; 99US-00403297.  
PR 12-NOV-1999; 99US-00423844.  
PR 02-DEC-1999; 99WO-US028301.  
PR 01-DEC-1999; 99WO-US028551.  
PR 30-DEC-1999; 99WO-US031274.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 01-MAR-2000; 2000WO-US005601.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 22-AUG-2000; 2000US-00644848.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 18-SEP-2000; 2000US-00664610.  
PR 08-SEP-2000; 2000US-00665350.  
PR 08-NOV-2000; 2000US-00705238.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000US-00747259.  
PR 20-DEC-2000; 2000WO-US034956.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 22-MAR-2001; 2001US-00816744.  
PR 10-MAY-2001; 2001US-00854208.  
PR 25-MAY-2001; 2001US-00854280.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 05-JUN-2001; 2001US-00874503.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 18-JUL-2001; 2001US-00908827.  
PR 30-JUL-2001; 2001US-00918585.  
PR 06-AUG-2001; 2001US-00924419.  
PR 13-AUG-2001; 2001US-00929404.  
PR 16-AUG-2001; 2001US-00931836.  
PR 28-AUG-2001; 2001US-00941992.  
PR 29-AUG-2001; 2001WO-US027099.  
PR 04-SEP-2001; 2001US-00946374.  
PR 15-JAN-2002; 2002US-00052586.

(GETH ) GENENTECH INC.

XX

XX

PI Baker, J. Chen J., Desnoyers L.,

PI Pan J., Smith V., Watanabe CK,

DR WPI; 2003-332039/31.

DR N-PSDB; ACA05855.

Goddard A., Godowski PJ, Gurney AL;  
Wood WI, Zhang Z;

XX New secreted and transmembrane PRO polypeptides and nucleic acids, useful  
 PT in gene therapy, in chromosome and gene mapping, as chromosome markers,  
 PT in tissue typing, and in chromosome identification.

PS Claim 11; Fig 312; 706pp; English.

XX The invention discloses human nucleic acids encoding secreted and  
 CC transmembrane (PRO) polypeptides. Also disclosed is an antibody that  
 CC specifically binds to the PRO polypeptide, a method for stimulating the  
 CC release of tumour necrosis factor alpha (TNF-alpha) from human blood by  
 CC contacting the blood a PRO polypeptide, a method for stimulating the  
 CC proliferation or differentiation of chondrocyte cells by contacting the  
 CC cells with a PRO polypeptide, a method for detecting the presence of a  
 CC tumour in a mammal and an oligonucleotide probe derived from any of the  
 CC PRO nucleotide sequences. The nucleotide sequences are useful as probes,  
 CC in chromosome and gene mapping, in generating antisense RNA and DNA, in  
 CC preparing PRO polypeptides by recombinant techniques and in gene therapy  
 CC (e.g. for replacement of defective gene). The PRO polypeptides are useful  
 CC as molecular weight markers for protein electrophoresis purposes, for  
 CC chromosome identification, as chromosome markers, as therapeutic agents,  
 CC for stimulating the release of TNF-alpha from human blood, for  
 CC stimulating the proliferation or differentiation of chondrocytes and  
 CC detecting the presence of a tumour. The PRO polypeptides and nucleic  
 CC acids may also be used diagnostically for tissue typing. The sequences  
 CC presented in ABU67406-ABU67710 are the PRO polypeptides of the invention  
 XX Sequence 802 AA;

Query Match 60.3%; Score 44; DB 6; Length 802;  
 Best Local Similarity 72.7%; Pred. No. 1.8e+02;  
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGCGRSGEAGS 13  
 |||||:  
 Db 46 EGCGRSQAAAS 56

RESULT 30  
 ABU80589  
 ID ABU80589 standard; protein; 802 AA.

XX ABU80589;

XX 23-JUN-2003 (first entry)

XX Human PRO protein #156.

XX Human; tumour; adrenal; lung; colon; breast; prostate; rectal; cervical;  
 KW liver; PRO; gene therapy.

XX Homo sapiens.

XX US2003036137-A1.

XX 20-FEB-2003.

XX 27-JUN-2002; 2002US-00184640.

XX 26-JUN-1998; 98US-00105413.

XX 16-SEP-1998; 98WO-US019330.

XX 07-OCT-1998; 98US-00168978.

XX 07-OCT-1998; 98WO-US021141.

XX 01-DEC-1998; 98WO-US025108.

XX 07-DEC-1998; 98US-00202054.

XX 03-MAR-1999; 99US-00254311.

XX 08-MAR-1999; 99WO-US005028.

XX 14-MAY-1999; 99US-00311832.

XX 14-MAY-1999; 99WO-US010733.

XX 02-JUN-1999; 99WO-US012252.

XX 25-AUG-1999; 99US-00380137.

XX 25-AUG-1999; 99US-00380138.

PR 25-AUG-1999; 99US-00380139.  
 PR 25-AUG-1999; 99US-00380142.  
 PR 01-SEP-1999; 99WO-US020111.  
 PR 15-SEP-1999; 99WO-US021090.  
 PR 18-OCT-1999; 99US-00403237.  
 PR 12-NOV-1999; 99US-00423844.  
 PR 01-DEC-1999; 99WO-US028301.  
 PR 02-DEC-1999; 99WO-US028551.  
 PR 30-DEC-1999; 99WO-US031274.  
 PR 05-JAN-2000; 2000WO-US000219.  
 PR 18-FEB-2000; 2000WO-US004341.  
 PR 18-FEB-2000; 2000WO-US004342.  
 PR 22-FEB-2000; 2000WO-US004414.  
 PR 24-FEB-2000; 2000WO-US005004.  
 PR 01-MAR-2000; 2000WO-US005601.  
 PR 02-MAR-2000; 2000WO-US005841.  
 PR 15-MAR-2000; 2000WO-US006884.  
 PR 30-MAR-2000; 2000WO-US008439.  
 PR 17-MAY-2000; 2000WO-US013705.  
 PR 22-MAY-2000; 2000WO-US014042.  
 PR 30-MAY-2000; 2000WO-US014941.  
 PR 02-JUN-2000; 2000WO-US015284.  
 PR 28-JUN-2000; 2000WO-US020710.  
 PR 22-AUG-2000; 2000US-00644848.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 18-SEP-2000; 2000US-00664610.  
 PR 18-SEP-2000; 2000US-00665350.  
 PR 08-NOV-2000; 2000US-00709238.  
 PR 08-NOV-2000; 2000WO-US030952.  
 PR 01-DEC-2000; 2000WO-US032678.  
 PR 20-DEC-2000; 2000US-00747259.  
 PR 20-DEC-2000; 2000WO-US034956.  
 PR 28-FEB-2001; 2001WO-US006520.  
 PR 22-MAR-2001; 2001US-00816744.  
 PR 10-MAY-2001; 2001US-00854208.  
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 PR 04-SEP-2001; 2001US-00946374.  
 PR 15-JAN-2002; 2002US-00052586.

(GETH ) GENENTECH INC.

Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;

Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-342038/32.

N-PSDB; ACA66689.

Three hundred and five nucleic acids encoding secreted and transmembrane  
 PRO polypeptides, useful for the diagnosis, prevention and/or treatment  
 of tumors, such as adrenal, lung, colon, breast, prostate, rectal,  
 cervical or liver tumors.

Claim 11; Fig 312; 708pp; English.

The invention relates to three hundred and five nucleic acids encoding  
 PRO polypeptides (secreted and transmembrane). Methods and compositions  
 of the present invention are useful for the diagnosis, prevention and/or  
 treatment of tumors, such as adrenal, lung, colon, breast, prostate,  
 rectal, cervical or liver tumors. The PRO polypeptides are also useful  
 as molecular weight markers, or for chromosome identification. The PRO





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Best Local Similarity 72.7%; Pred. NO. 1.8e+02;
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Db 46 EGCGRSGQAAS 56

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ID ABR78382 standard; protein; 802 AA.
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AC ABR78382;
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DT 19-SEP-2003 (first entry)
XX
DE Human secreted polypeptide PRO1487, SEQ ID NO:312.
XX
KW Human; PRO; secreted protein; transmembrane protein;
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnery; gene therapy.
XX
OS Homo sapiens.

XX US2003054474-A1.
XX 20-MAR-2003.
XX 22-JUL-2002; 2002US-00201530.
XX 22-JUN-1998; 98US-0090254P.
XX 02-JUN-1999; 99WO-US012252.
XX 25-AUG-1999; 99US-00380137.
XX 28-FEB-2001; 2001WO-US006520.
XX 15-JAN-2002; 2002US-00052586.
XX (GETH ) GENENTECH INC.
XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
XX Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-503631/47.
XX N-PSDB; ACF00255.
XX New secreted and transmembrane PRO polypeptides and nucleic acids, useful
XX in gene therapy, or for preparing a medicament for treating a condition
XX that is responsive to the PRO polypeptide or anti-PRO antibody.
XX Claim 11; Fig 312; 700pp; English.
XX The invention relates to human PRO secreted/transmembrane polypeptides
XX (ABR78227-ABR78531) and nucleic acids encoding them (ACF00100-00404). The
XX invention also relates to sequences at least 80% identical to the PRO
XX nucleic acid and polypeptide sequences of the invention, recombinant
XX vectors and host cells comprising a PRO nucleic acid, a method for the
XX recombinant production of a PRO polypeptide, antibodies against a PRO
XX polypeptide, and fusion proteins comprising a PRO polypeptide. Nucleic
XX acids encoding PRO polypeptides of the invention were initially
XX identified via homology screening using consensus sequences based on the
XX extracellular domain sequences from known secreted proteins. Human CDNA
XX libraries containing sequences of interest were identified using
XX oligonucleotides based on the consensus sequences, and cDNA clones were
XX isolated and characterised. The PRO polypeptides are useful for
XX stimulating release of tumour necrosis factor-alpha (TNF-alpha) from
XX human blood and may thus be used in the treatment of conditions in which
XX enhanced TNF-alpha release would be beneficial. They are also useful for
XX stimulating the proliferation or differentiation of chondrocytes and as
XX such may be used in the treatment of various bone and/or cartilage
XX disorders such as arthritis and sports injuries. The PRO polypeptides may
XX be used in a method for detecting the presence of a tumour (e.g., an
XX adrenal tumour, lung tumour, colon tumour, breast tumour, prostate
XX tumour, rectal tumour, cervical tumour or liver tumour) in a mammal. This
XX method involves comparing the level of expression of the PRO polypeptide
XX in test and control samples, where a higher level of expression of PRO
XX polypeptide in the test sample as compared to the control sample is
XX indicative of the presence of a tumour. The PRO polypeptides are
XX additionally useful for in drug screening to identify agonists and
XX antagonists of PRO polypeptides. PRO nucleic acids are useful as
XX hybridisation probes (for isolation of cDNA molecules), in chromosome
XX gene mapping, in the generation of antisense RNA and DNA and in gene
XX therapy. The nucleic acids can also be used for mapping genes encoding
XX PRO polypeptides, for genetic analysis of individuals with genetic
XX disorders, and for generating either transgenic animals or knock-out
XX animals which are useful in the development and screening of
XX therapeutically useful compounds. Sequences ABR78227-ABR78531 represent
XX the human PRO secreted/transmembrane polypeptides of the invention. Note:
XX The sequence data for this patent is also available in electronic format
XX from USPTO at seqdata.uspto.gov/sequence.html
XX Sequence 802 AA;
XX Query Match 60.3%; Score 44; DB 6; Length 802;
XX Best Local Similarity 72.7%; Pred. No. 1.8e+02;
XX Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 3 EGCGRSGEAGS 13
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RESULT 37
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AC  ABU85118;
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DT  30-JUN-2003 (first entry)
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DE  Novel human secreted and transmembrane protein PRO1487.
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XX  Human; secreted and transmembrane protein; PRO; cytostatic; gene therapy;
KW  chondrocyte stimulator; chromosome mapping; gene mapping;
KW  transgenic animal; knock-out animal; tumour.
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XX  Homo sapiens.
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XX  US2003032114-A1.
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XX  13-FEB-2003.
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XX  20-JUN-2002; 2002US-00176919.
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Query Match 60.3%; Score 44; DB 6; Length 802;  
Best Local Similarity 72.7%; Pred. No. 1.9e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 EGCRCGEAGCS 13  
Db 46 EGCRCGQAAS 56

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XX ABO00257;  
XX AC 06-AUG-2003 (first entry)  
XX DT Novel human secreted and transmembrane protein PRO1487.  
XX DE Human; gene therapy; tumour necrosis factor alpha; TNF-alpha;  
XX KW chondrocyte stimulation; tumour; tissue typing.  
XX OS Homo sapiens.  
XX PN US2003032101-A1.  
XX PD 13-FEB-2003.  
XX PF 17-JUN-2002; 2002US-00173695.  
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Query Match 60.3%; Score 44; DB 6; Length 802;  
Best Local Similarity 72.7%; Pred. No. 1.8e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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DB 46 ECGRSGQAAS 56

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ABO11589  
ID ABO11589 standard; protein; 802 AA.

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AC ABO11589;

XX  
DT 26-AUG-2003 (first entry)

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DE Human secreted/transmembrane protein (PRO) #156.  
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KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;  
KW tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour;  
KW prostate tumour; rectal tumour; cervical tumour; liver tumour.

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Query Match 60.3%; Score 44; DB 6; Length 802;
Best Local Similarity 72.7%; Pred. No. 1.8e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGRSGEAGSGS 13
Db 46 EGRSGQAAS 56

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XX KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
XX KW tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour;
XX KW prostate tumour; rectal tumour; cervical tumour; liver tumour.
XX OS Homo sapiens.
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Db 46 ECSRSGQAAS 56
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Query Match 60.3%; Score 44; DB 6; Length 802;  
Best Local Similarity 72.7%; Pred. No. 1.8e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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KW Human; secreted and transmembrane protein; PRO; chromosome mapping;  
KW gene mapping; gene therapy; tumour necrosis factor alpha; TNF-alpha;  
KW chondrocyte; tumour.  
XX  
OS Homo sapiens.  
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PN US2003036134-A1.  
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Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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XX AC ABO06304;

XX DT 13-AUG-2003 (first entry)

XX DE Novel human secreted and transmembrane protein PRO1487.

XX KW Human; secreted and transmembrane protein; PRO; gene therapy;  
XX KW chondrocyte stimulator; chromosome mapping; gene mapping;  
XX KW transgenic animal; knockout animal; tissue typing;  
XX KW chondrocyte proliferation; chondrocyte differentiation;  
XX KW tumour necrosis factor-alpha stimulation; TNF-alpha stimulation.

XX OS Homo sapiens.

XX PN US2003022294-A1.

XX PD 30-JAN-2003.

XX PF 19-JUN-2002; 2002US-00175738.

XX PR 18-SEP-1997; 97US-0059263P.

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XX DT 28-JUL-2003 (first entry)

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XX KW Human; PRO; secreted protein; transmembrane protein;

XX KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;

XX KW chondrocyte; proliferation; differentiation; cartilage disorder;

XX KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;

XX KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;

XX KW liver; drug screening; transgenic animal; genetic analysis;

XX KW antiarthritic; vulnery; gene therapy.

XX OS Homo sapiens.

XX PN US2003027275-A1.

XX PD 06-FEB-2003.

XX PF 20-JUN-2002; 2002US-00176918.

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Query Match 60.3%; Score 44; DB 6; Length 802;
Best Local Similarity 72.7%; Pred No. 1.8e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Db 46 EGCRRSGAAGS 56

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DT 17-AUG-2003 (first entry)
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KW Human; secreted and transmembrane protein; PRO; TNF-alpha;
KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour.
XX
OS Homo sapiens.
XX
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PD 06-FEB-2003.
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PR 29-SEP-1998; 98US-0102207P.  
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PR 30-SEP-1998; 98US-0102487P.  
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PR 30-SEP-1998; 98US-0102571P.  
PR 01-OCT-1998; 98US-0102684P.

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 PR 06-OCT-1998; 98US-0103449P.

Query Match 60.3%; Score 44; DB 6; Length 802;  
 Best Local Similarity 72.7%; Pred. No. 1.8e+02;  
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGRSGEAGS 13  
 DB 46 EGRSGQAAS 56

## RESULT 46

ABO19266  
 ID ABO19266 standard; protein; 802 AA.

AC ABO19266;

DT 27-AUG-2003 (first entry)

DE Novel human secreted and transmembrane protein PRO1487.

XX Human; secreted and transmembrane protein; PRO; chromosome mapping;  
 KW gene mapping; transgenic animal; knockout animal; tissue typing;  
 KW chromosome identification; tumour; chondrocyte proliferation;  
 KW chondrocyte differentiation; tumour necrosis factor-alpha release;  
 KW gene therapy.

XX Homo sapiens.

XX US2003036118-A1.

XX 20-FEB-2003.

XX 21-JUN-2002; 2002US-00176760.

XX 26-JUN-1998; 98US-00105413.  
 PR 16-SEP-1998; 98WO-US019330.  
 PR 07-OCT-1998; 98US-00168978.  
 PR 07-OCT-1998; 98WO-US021141.  
 PR 06-NOV-1998; 98US-00187368.  
 PR 01-DEC-1998; 98WO-US025108.  
 PR 07-DEC-1998; 98US-00202054.  
 PR 03-MAR-1999; 99US-00254311.  
 PR 08-MAR-1999; 99WO-US005028.  
 PR 14-MAY-1999; 99US-00311832.  
 PR 14-MAY-1999; 99WO-US010733.  
 PR 02-JUN-1999; 99WO-US012252.  
 PR 25-AUG-1999; 99US-00380137.  
 PR 25-AUG-1999; 99US-00380138.  
 PR 25-AUG-1999; 99US-00380139.  
 PR 25-AUG-1999; 99US-00380142.  
 PR 01-SEP-1999; 99WO-US020111.  
 PR 15-SEP-1999; 99WO-US021090.  
 PR 18-OCT-1999; 99US-00403297.  
 PR 12-NOV-1999; 99US-00423844.  
 PR 01-DEC-1999; 99WO-US028301.  
 PR 02-DEC-1999; 99WO-US028551.  
 PR 30-DEC-1999; 99WO-US031274.  
 PR 05-JAN-2000; 2000WO-US000219.  
 PR 18-FEB-2000; 2000WO-US004341.  
 PR 18-FEB-2000; 2000WO-US004342.  
 PR 22-FEB-2000; 2000WO-US004414.  
 PR 24-FEB-2000; 2000WO-US005004.  
 PR 01-MAR-2000; 2000WO-US005601.  
 PR 02-MAR-2000; 2000WO-US005841.  
 PR 15-MAR-2000; 2000WO-US006884.  
 PR 30-MAR-2000; 2000WO-US008439.  
 PR 17-MAY-2000; 2000WO-US013705.  
 PR 22-MAY-2000; 2000WO-US014042.  
 PR 30-MAY-2000; 2000WO-US014941.

PR 02-JUN-2000; 2000WO-US015264.  
 PR 28-JUL-2000; 2000WO-US020710.  
 PR 22-AUG-2000; 2000US-00644848.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 18-SEP-2000; 2000US-00664610.  
 PR 18-SEP-2000; 2000US-00665350.  
 PR 08-NOV-2000; 2000US-00709238.  
 PR 08-NOV-2000; 2000WO-US030952.  
 PR 01-DEC-2000; 2000WO-US032678.  
 PR 20-DEC-2000; 2000US-00747259.  
 PR 20-DEC-2000; 2000WO-US034956.  
 PR 28-FEB-2001; 2001WO-US006520.  
 PR 22-MAR-2001; 2001US-00816744.  
 PR 10-MAY-2001; 2001US-00854208.  
 PR 10-MAY-2001; 2001US-00854280.  
 PR 25-MAY-2001; 2001US-00866028.  
 PR 01-JUN-2001; 2001WO-US017800.  
 PR 05-JUN-2001; 2001US-00874503.  
 PR 20-JUN-2001; 2001WO-US019692.  
 PR 29-JUN-2001; 2001WO-US021066.  
 PR 09-JUL-2001; 2001WO-US021735.  
 PR 18-JUL-2001; 2001US-00908827.  
 PR 30-JUL-2001; 2001US-00918585.  
 PR 06-AUG-2001; 2001US-00924419.  
 PR 13-AUG-2001; 2001US-00929404.  
 PR 16-AUG-2001; 2001US-00931836.  
 PR 28-AUG-2001; 2001US-00941992.  
 PR 29-AUG-2001; 2001WO-US027099.  
 PR 04-SEP-2001; 2001US-00946374.  
 PR 15-JAN-2002; 2002US-00052586.

XX (GETH ) GENENTECH INC.

XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;  
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

XX WPI: 2003-402071/38.

XX N-PSDB; ACD25513.

XX New secreted and transmembrane PRO polypeptides and nucleic acids, useful  
 PT in gene therapy, chromosome identification, tissue typing, for detecting  
 PT the presence of tumor in a mammal, or as hybridization probes in gene  
 PT mapping.

XX Claim 11; SEQ ID NO 312; 707pp; English.

XX The invention describes a novel isolated PRO polypeptide. The PRO  
 CC polypeptide or anti-PRO antibody is useful for preparing a medicament for  
 CC treating a condition that is responsive to the PRO polypeptide or anti-  
 CC PRO antibody. The PRO nucleotide sequences are useful as hybridisation  
 CC probes in chromosome and gene mapping, or in generating antisense RNA and  
 CC DNA. PRO nucleic acids are also useful in preparing PRO polypeptides, in  
 CC assays to identify other proteins or molecules involved in binding  
 CC reaction, to generate transgenic animals or knockout animals, which in  
 CC turn are useful in the development and screening of therapeutically  
 CC useful reagents, for chromosome identification, and tissue typing. The  
 CC PRO polypeptides and nucleic acid molecules are also useful for detecting  
 CC the presence of tumour in a mammal, stimulating proliferation or  
 CC differentiation of chondrocyte cells, stimulating the release of tumour  
 CC necrosis factor-alpha from human blood, in gene therapy, or as molecular  
 CC weight markers for protein electrophoresis purposes. The anti-PRO  
 CC antibodies may be used in diagnostic assays for PRO, or for the affinity  
 CC purification of PRO from recombinant cell culture or natural sources.  
 CC This is the amino acid sequence of a novel human secreted and  
 CC transmembrane PRO polypeptide

XX Sequence 802 AA;

Query Match 60.3%; Score 44; DB 6; Length 802;  
 Best Local Similarity 72.7%; Pred. No. 1.8e+02;  
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGRSGEAGS 13

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PR 07-MAY-1998; 98US-0084639P.  
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PR 15-MAY-1998; 98US-0085579P.  
PR 15-MAY-1998; 98US-0085580P.  
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PR 02-JUN-1998; 98US-0087759P.  
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PR 26-JUN-1998; 98US-0090862P.  
PR 26-JUN-1998; 98US-0090863P.  
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PR 24-JUL-1998; 98US-0094006P.

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46 EGRSGQAAS 56

RESULT 47  
ABO11284  
ID ABO11284 standard; protein; 802 AA.  
XX ABO11284;  
AC ABO11284;  
XX 25-AUG-2003 (first entry)  
DT Human secreted/transmembrane protein (PRO) #156.  
DE Human secreted and transmembrane protein; PRO; TNF-alpha;  
XX Human secreted and transmembrane protein; PRO; TNF-alpha;  
KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;  
KW tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour;  
KW prostate tumour; rectal tumour; cervical tumour; liver tumour.  
XX  
OS Homo sapiens.  
XX  
XX US2003036123-A1.  
PN  
XX  
XX 20-FEB-2003.  
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XX  
XX 25-JUN-2002; 2002US-00180551.  
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PR 18-SEP-1997; 97US-0059263P.  
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PR 28-OCT-1997; 97US-0063540P.  
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PR 28-OCT-1997; 97US-0063564P.  
PR 29-OCT-1997; 97US-0063734P.  
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PR 13-NOV-1997; 97US-0065311P.  
PR 21-NOV-1997; 97US-0066120P.  
PR 24-NOV-1997; 97US-0066466P.  
PR 24-NOV-1997; 97US-0066772P.  
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PR 17-DEC-1997; 97US-0069870P.  
PR 18-DEC-1997; 97US-0068017P.  
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PR 15-APR-1998; 98US-0081838P.  
PR 21-APR-1998; 98US-0082568P.  
PR 21-APR-1998; 98US-0082569P.  
PR 22-APR-1998; 98US-0082704P.  
PR 22-APR-1998; 98US-0082797P.  
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PR 30-SEP-1998; 98US-0102487P.  
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PR 01-OCT-1998; 98US-0102684P.  
PR 01-OCT-1998; 98US-0102687P.  
PR 02-OCT-1998; 98US-0102965P.  
PR 06-OCT-1998; 98US-0103258P.  
PR 06-OCT-1998; 98US-0103449P.

Query Match 60.3%; Score 44; DB 6; Length 802;  
Best Local Similarity 72.7%; Pred. No. 1.8e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGCGRSGAEGS 13  
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Db 46 EGCGRSQQAAS 56

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ABR66902  
ID ABR66902 standard; protein; 802 AA.

XX ABR66902;  
XX 05-AUG-2003 (first entry)  
XX Human secreted polypeptide PRO1487, SEQ ID NO:312.  
XX Human; PRO; secreted protein; transmembrane protein;  
XX extracellular domain; tumour necrosis factor-alpha; TNF-alpha;  
XX chondrocyte; proliferation; differentiation; cartilage disorder;  
XX bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;  
XX adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;  
XX liver; drug screening; transgenic animal; genetic analysis;  
XX antiarthritic; vulnery; gene therapy.  
XX Homo sapiens.  
XX US2003036148-A1.  
XX 20-FEB-2003.  
XX 02-JUL-2002; 2002US-00187743.  
XX 18-SEP-1997; 97US-0059263P.  
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

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45	44	60.3	802	12	Sequence 312, App
46	44	60.3	802	12	Sequence 312, App
47	44	60.3	802	12	Sequence 312, App
48	44	60.3	802	12	Sequence 312, App
49	44	60.3	802	12	Sequence 312, App
50	44	60.3	802	12	Sequence 260, App

ALIGNMENTS

RESULT 1  
US-10-292-798-1324  
; Sequence 1324, Application US/10292798  
; Publication No. US20030235833A1  
; GENERAL INFORMATION:  
; APPLICANT: SUWA, MAKIKO  
; APPLICANT: ASAI, KIYOSHI  
; APPLICANT: AKIYAMA, YUTAKA  
; APPLICANT: ABURATANI, HIROYUKI  
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS  
; FILE REFERENCE: 084335/166  
; CURRENT APPLICATION NUMBER: US/10/292,798  
; CURRENT FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: 10/017,161  
; PRIOR FILING DATE: 2001-12-18  
; PRIOR APPLICATION NUMBER: JP 2001-246789  
; PRIOR FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 2070  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 1324  
; TYPE: PRT  
; LENGTH: 1385  
; ORGANISM: Homo sapiens  
US-10-292-798-1324

Query Match 61.6%; Score 45; DB 15; Length 1385;  
Best Local Similarity 69.2%; Pred. No. 26+02;  
Matches: 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 GHEGCRSGEAGS 13  
DB 797 GHRGPAPGEAGS 809

RESULT 2  
US-09-946-374-260  
; Sequence 260, Application US/09946374  
; Publication No. US20030073129A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2830P1C1  
; CURRENT APPLICATION NUMBER: US/09/946,374  
; CURRENT FILING DATE: 2001-09-04  
; PRIOR APPLICATION NUMBER: 60/098716  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098723  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098749  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098750  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098803  
; PRIOR FILING DATE: 1998-09-02  
; PRIOR APPLICATION NUMBER: 60/098821  
; PRIOR FILING DATE: 1998-09-02  
; PRIOR APPLICATION NUMBER: 60/098843  
; PRIOR FILING DATE: 1998-09-02  
; PRIOR APPLICATION NUMBER: 60/099536  
; PRIOR FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: 60/099596  
; PRIOR FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: 60/099598  
; PRIOR FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: 60/099602  
; PRIOR FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: 60/099642  
; PRIOR FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: 60/099741  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099754  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099763  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099792  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099808  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099812  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099815  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099816  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/100385  
; PRIOR FILING DATE: 1998-09-15  
; PRIOR APPLICATION NUMBER: 60/100388  
; PRIOR FILING DATE: 1998-09-15  
; PRIOR APPLICATION NUMBER: 60/100390  
; PRIOR FILING DATE: 1998-09-15  
; PRIOR APPLICATION NUMBER: 60/100584  
; PRIOR FILING DATE: 1998-09-16  
; PRIOR APPLICATION NUMBER: 60/100627  
; PRIOR FILING DATE: 1998-09-16  
; PRIOR APPLICATION NUMBER: 60/100661  
; PRIOR FILING DATE: 1998-09-16  
; PRIOR APPLICATION NUMBER: 60/100662  
; PRIOR FILING DATE: 1998-09-16  
; PRIOR APPLICATION NUMBER: 60/100664  
; PRIOR FILING DATE: 1998-09-16  
; PRIOR APPLICATION NUMBER: 60/100683  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/100684  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/100710  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/100711  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/100848  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/100849  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/100919  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/100930  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/101014  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/101068  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/101071  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/101279  
; PRIOR FILING DATE: 1998-09-22  
; PRIOR APPLICATION NUMBER: 60/101471  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101472  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101474  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101475  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101476  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101477  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101479  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101738  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/101741  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/101743  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/101915  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/101916  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/102207  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 60/102240  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 60/102307  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 60/102330  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 60/102331  
; PRIOR FILING DATE: 1998-09-29

;; PRIOR APPLICATION NUMBER: 60/102484  
;; PRIOR FILING DATE: 1998-09-30  
;; PRIOR APPLICATION NUMBER: 60/102487  
;; PRIOR FILING DATE: 1998-09-30  
;; PRIOR APPLICATION NUMBER: 60/102570  
;; PRIOR FILING DATE: 1998-09-30  
;; PRIOR APPLICATION NUMBER: 60/102571  
;; PRIOR FILING DATE: 1998-09-30  
;; PRIOR APPLICATION NUMBER: 60/102684  
;; PRIOR FILING DATE: 1998-10-01  
;; PRIOR APPLICATION NUMBER: 60/102687  
;; PRIOR FILING DATE: 1998-10-01  
;; PRIOR APPLICATION NUMBER: 60/102965  
;; PRIOR FILING DATE: 1998-10-02  
;; PRIOR APPLICATION NUMBER: 60/103258  
;; PRIOR FILING DATE: 1998-10-06  
;; PRIOR APPLICATION NUMBER: 60/103314  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103315  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103328  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103395  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103396  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103401  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103449  
;; PRIOR FILING DATE: 1998-10-06  
;; PRIOR APPLICATION NUMBER: 60/103633  
;; PRIOR FILING DATE: 1998-10-08  
;; PRIOR APPLICATION NUMBER: 60/103678  
;; PRIOR FILING DATE: 1998-10-08  
;; PRIOR APPLICATION NUMBER: 60/103679  
;; PRIOR FILING DATE: 1998-10-08  
;; PRIOR APPLICATION NUMBER: 60/103711  
;; PRIOR FILING DATE: 1998-10-08  
;; PRIOR APPLICATION NUMBER: 60/104257  
;; PRIOR FILING DATE: 1998-10-14  
;; PRIOR APPLICATION NUMBER: 60/104987  
;; PRIOR FILING DATE: 1998-10-20  
;; PRIOR APPLICATION NUMBER: 60/105000  
;; PRIOR FILING DATE: 1998-10-20  
;; PRIOR APPLICATION NUMBER: 60/105002  
;; PRIOR FILING DATE: 1998-10-20  
;; PRIOR APPLICATION NUMBER: 60/105104  
;; PRIOR FILING DATE: 1998-10-21  
;; PRIOR APPLICATION NUMBER: 60/105169  
;; PRIOR FILING DATE: 1998-10-22  
;; PRIOR APPLICATION NUMBER: 60/105266  
;; PRIOR FILING DATE: 1998-10-22  
;; PRIOR APPLICATION NUMBER: 60/105693  
;; PRIOR FILING DATE: 1998-10-26  
;; PRIOR APPLICATION NUMBER: 60/105694  
;; PRIOR FILING DATE: 1998-10-26  
;; PRIOR APPLICATION NUMBER: 60/105807

Query Match 60.3%; Score 44; DB 10; Length 802;  
Best Local Similarity 72.7%; Pred. No. 1.7e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGCRRSGAEGS 13  
DB 46 EGCRRSGAAGS 56

## RESULT 3

US-10-206-915-312  
; Sequence 312, Application US/10206915  
; Publication No. US20040029221A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.

;; APPLICANT: Chen, Jian  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Pan, James  
;; APPLICANT: Smith, Victoria  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
;; FILE REFERENCE: P3430RIC513  
;; CURRENT APPLICATION NUMBER: US/10/206,915  
;; CURRENT FILING DATE: 2002-07-26  
;; PRIOR APPLICATION NUMBER: 10/052586  
;; PRIOR FILING DATE: 2002-01-15  
;; PRIOR APPLICATION NUMBER: 60/059263  
;; PRIOR FILING DATE: 1997-09-18  
;; PRIOR APPLICATION NUMBER: 60/059266  
;; PRIOR FILING DATE: 1997-09-18  
;; PRIOR APPLICATION NUMBER: 60/062250  
;; PRIOR FILING DATE: 1997-10-17  
;; PRIOR APPLICATION NUMBER: 60/063120  
;; PRIOR FILING DATE: 1997-10-24  
;; PRIOR APPLICATION NUMBER: 60/063121  
;; PRIOR FILING DATE: 1997-10-24  
;; PRIOR APPLICATION NUMBER: 60/063486  
;; PRIOR FILING DATE: 1997-10-21  
;; PRIOR APPLICATION NUMBER: 60/063540  
;; PRIOR FILING DATE: 1997-10-28  
;; PRIOR APPLICATION NUMBER: 60/063541  
;; PRIOR FILING DATE: 1997-10-28  
;; PRIOR APPLICATION NUMBER: 60/063544  
;; PRIOR FILING DATE: 1997-10-28  
;; PRIOR APPLICATION data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 612  
;; SEQ ID NO 312  
;; LENGTH: 802  
;; TYPE: PRT  
;; ORGANISM: Homo Sapien  
US-10-206-915-312

Query Match 60.3%; Score 44; DB 12; Length 802;  
Best Local Similarity 72.7%; Pred. No. 1.7e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGCRRSGAEGS 13  
DB 46 EGCRRSGAAGS 56

## RESULT 4

US-10-199-670-312  
; Sequence 312, Application US/10199670  
; Publication No. US20040033560A1  
; GENERAL INFORMATION:

;; APPLICANT: Baker, Kevin P.  
;; APPLICANT: Chen, Jian  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Pan, James  
;; APPLICANT: Smith, Victoria  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
;; FILE REFERENCE: P3430RIC401  
;; CURRENT APPLICATION NUMBER: US/10/199,670  
;; CURRENT FILING DATE: 2002-07-19

; PRIOR APPLICATION NUMBER: 10/052586  
; PRIOR FILING DATE: 2002-01-15  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059266  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063120  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063121  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063486  
; PRIOR FILING DATE: 1997-10-21  
; PRIOR APPLICATION NUMBER: 60/063540  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063541  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063544  
; PRIOR FILING DATE: 1997-10-28  
; Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 312  
; LENGTH: 802  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-199-670-312

Query Match 60.3%; Score 44; DB 12; Length 802;  
Best Local Similarity 72.7%; Pred. No. 1.7e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGCRCGEAEGS 13  
|||||:|  
DB 46 EGCRCGQAAS 56

RESULT 5  
US-10-201-858-312  
; Sequence 312, Application US/10201858  
; Publication No. US20040038337A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P34301C464  
; CURRENT APPLICATION NUMBER: US/10/201,858  
; CURRENT FILING DATE: 2002-07-23  
; PRIOR APPLICATION NUMBER: 10/052586  
; PRIOR FILING DATE: 2002-01-15  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059266  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063120  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063121  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063486  
; PRIOR FILING DATE: 1997-10-21  
; PRIOR APPLICATION NUMBER: 60/063540  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063541  
; PRIOR FILING DATE: 1997-10-28  
; Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 312  
; LENGTH: 802  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-199-670-312

; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063541  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063544  
; PRIOR FILING DATE: 1997-10-28  
; Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 312  
; LENGTH: 802  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-201-858-312

Query Match 60.3%; Score 44; DB 12; Length 802;  
Best Local Similarity 72.7%; Pred. No. 1.7e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGCRCGEAEGS 13  
|||||:|  
DB 46 EGCRCGQAAS 56

RESULT 6  
US-10-205-890-312  
; Sequence 312, Application US/10205890  
; Publication No. US20040048334A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P34301C519  
; CURRENT APPLICATION NUMBER: US/10/205,890  
; CURRENT FILING DATE: 2002-07-26  
; PRIOR APPLICATION NUMBER: 10/052586  
; PRIOR FILING DATE: 2002-01-15  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059266  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063120  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063121  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063486  
; PRIOR FILING DATE: 1997-10-21  
; PRIOR APPLICATION NUMBER: 60/063540  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063541  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063544  
; PRIOR FILING DATE: 1997-10-28  
; Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 312  
; LENGTH: 802  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-205-890-312

Query Match 60.3%; Score 44; DB 12; Length 802;  
Best Local Similarity 72.7%; Pred. No. 1.7e+02;



Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGRSGEARGS 13  
|||||:|  
Db 46 EGRSGQAAAS 56

## RESULT 7

US-10-208-024-312  
; Sequence 312, Application US/10208024

; Publication No. US20040048335A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430R1C538

; CURRENT APPLICATION NUMBER: US/10/208,024

; CURRENT FILING DATE: 2002-07-29

; PRIOR APPLICATION NUMBER: 10/052586

; PRIOR FILING DATE: 2002-01-15

; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059266

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/063120

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063121

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063486

; PRIOR FILING DATE: 1997-10-21

; PRIOR APPLICATION NUMBER: 60/063540

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063541

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063544

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 312

; LENGTH: 802

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-208-024-312

Query Match 60.3%; Score 44; DB 12; Length 802;

Best Local Similarity 72.7%; Pred. No. 1.7e+02;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGRSGEARGS 13  
|||||:|  
Db 46 EGRSGQAAAS 56

## RESULT 8

US-10-201-853-312

; Sequence 312, Application US/10201853

; Publication No. US20040053358A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430R1C465

; CURRENT APPLICATION NUMBER: US/10/201,853

; CURRENT FILING DATE: 2002-07-23

; PRIOR APPLICATION NUMBER: 10/052586

; PRIOR FILING DATE: 2002-01-15

; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059266

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/063120

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063121

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063486

; PRIOR FILING DATE: 1997-10-21

; PRIOR APPLICATION NUMBER: 60/063540

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063541

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063544

; PRIOR FILING DATE: 1997-10-28

; Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 312

; LENGTH: 802

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-201-853-312

Query Match 60.3%; Score 44; DB 12; Length 802;

Best Local Similarity 72.7%; Pred. No. 1.7e+02;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGRSGEARGS 13  
|||||:|

Db 46 EGRSGQAAAS 56

## RESULT 9

US-10-174-581-312

; Sequence 312, Application US/10174581

; Publication No. US20030017540A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430R1C41

; CURRENT APPLICATION NUMBER: US/10/174,581

; CURRENT FILING DATE: 2002-06-18

; PRIOR APPLICATION NUMBER: 10/052586

; PRIOR FILING DATE: 2002-01-15

1	PRIOR FILING DATE: 1998-04-21	
2	PRIOR APPLICATION NUMBER: 60/082569	
3	PRIOR FILING DATE: 1998-04-21	
4	PRIOR APPLICATION NUMBER: 60/082704	
5	PRIOR FILING DATE: 1998-04-22	
6	PRIOR APPLICATION NUMBER: 60/082797	
7	PRIOR FILING DATE: 1998-04-22	
8	PRIOR APPLICATION NUMBER: 60/083322	
9	PRIOR FILING DATE: 1998-04-28	
10	PRIOR APPLICATION NUMBER: 60/083495	
11	PRIOR FILING DATE: 1998-04-29	
12	PRIOR APPLICATION NUMBER: 60/083496	
13	PRIOR FILING DATE: 1998-04-29	
14	PRIOR APPLICATION NUMBER: 60/083499	
15	PRIOR FILING DATE: 1998-04-29	
16	PRIOR APPLICATION NUMBER: 60/083559	
17	PRIOR FILING DATE: 1998-04-29	
18	PRIOR APPLICATION NUMBER: 60/084366	
19	PRIOR FILING DATE: 1998-05-05	
20	PRIOR APPLICATION NUMBER: 60/084414	
21	PRIOR FILING DATE: 1998-05-06	
22	PRIOR APPLICATION NUMBER: 60/084639	
23	PRIOR FILING DATE: 1998-05-07	
24	PRIOR APPLICATION NUMBER: 60/084640	
25	PRIOR FILING DATE: 1998-05-07	
26	PRIOR APPLICATION NUMBER: 60/084643	
27	PRIOR FILING DATE: 1998-05-07	
28	PRIOR APPLICATION NUMBER: 60/085573	
29	PRIOR FILING DATE: 1998-05-15	
30	PRIOR APPLICATION NUMBER: 60/085579	
31	PRIOR FILING DATE: 1998-05-15	
32	PRIOR APPLICATION NUMBER: 60/085580	
33	PRIOR FILING DATE: 1998-05-15	
34	PRIOR APPLICATION NUMBER: 60/085582	
35	PRIOR FILING DATE: 1998-05-15	
36	PRIOR APPLICATION NUMBER: 60/085700	
37	PRIOR FILING DATE: 1998-05-15	
38	PRIOR APPLICATION NUMBER: 60/086023	
39	PRIOR FILING DATE: 1998-05-18	
40	PRIOR APPLICATION NUMBER: 60/087098	
41	PRIOR FILING DATE: 1998-05-28	
42	PRIOR APPLICATION NUMBER: 60/086392	
43	PRIOR FILING DATE: 1998-05-22	
44	PRIOR APPLICATION NUMBER: 60/086486	
45	PRIOR FILING DATE: 1998-05-22	
46	PRIOR APPLICATION NUMBER: 60/087098	
47	PRIOR FILING DATE: 1998-05-28	
48	PRIOR APPLICATION NUMBER: 60/087208	
49	PRIOR FILING DATE: 1998-05-28	
50	PRIOR APPLICATION NUMBER: 60/087609	
51	PRIOR FILING DATE: 1998-06-02	
52	PRIOR APPLICATION NUMBER: 60/087759	
53	PRIOR FILING DATE: 1998-06-02	
54	PRIOR APPLICATION NUMBER: 60/087827	
55	PRIOR FILING DATE: 1998-06-03	
56	PRIOR APPLICATION NUMBER: 60/088025	
57	PRIOR FILING DATE: 1998-06-04	
58	PRIOR APPLICATION NUMBER: 60/088028	
59	PRIOR FILING DATE: 1998-06-04	
60	PRIOR APPLICATION NUMBER: 60/088029	
61	PRIOR FILING DATE: 1998-06-04	
62	PRIOR APPLICATION NUMBER: 60/088033	
63	PRIOR FILING DATE: 1998-06-04	
64	PRIOR APPLICATION NUMBER: 60/088167	
65	PRIOR FILING DATE: 1998-06-05	
66	PRIOR APPLICATION NUMBER: 60/088202	
67	PRIOR FILING DATE: 1998-06-05	
68	PRIOR APPLICATION NUMBER: 60/088212	
69	PRIOR FILING DATE: 1998-06-05	
70	PRIOR APPLICATION NUMBER: 60/088217	
71	PRIOR FILING DATE: 1998-06-05	
72	PRIOR APPLICATION NUMBER: 60/088326	
73	PRIOR FILING DATE: 1998-06-04	
74	PRIOR APPLICATION NUMBER: 60/088555	
75	PRIOR FILING DATE: 1998-06-09	

; PRIOR APPLICATION NUMBER: 60/088722  
 ; PRIOR FILING DATE: 1998-06-10  
 ; PRIOR APPLICATION NUMBER: 60/088738  
 ; PRIOR FILING DATE: 1998-06-10  
 ; PRIOR APPLICATION NUMBER: 60/088740  
 ; PRIOR FILING DATE: 1998-06-10  
 ; PRIOR APPLICATION NUMBER: 60/088811  
 ; PRIOR FILING DATE: 1998-06-10  
 ; PRIOR APPLICATION NUMBER: 60/088824  
 ; PRIOR FILING DATE: 1998-06-10  
 ; PRIOR APPLICATION NUMBER: 60/088825  
 ; PRIOR FILING DATE: 1998-06-10  
 ; PRIOR APPLICATION NUMBER: 60/088826  
 ; PRIOR FILING DATE: 1998-06-10  
 ; PRIOR APPLICATION NUMBER: 60/088861  
 ; PRIOR FILING DATE: 1998-06-11  
 ; PRIOR APPLICATION NUMBER: 60/088863  
 ; PRIOR FILING DATE: 1998-06-11  
 ; PRIOR APPLICATION NUMBER: 60/088876  
 ; PRIOR FILING DATE: 1998-06-11  
 ; PRIOR APPLICATION NUMBER: 60/089090  
 ; PRIOR FILING DATE: 1998-06-12  
 ; PRIOR APPLICATION NUMBER: 60/089105  
 ; PRIOR FILING DATE: 1998-06-12  
 ; PRIOR APPLICATION NUMBER: 60/089512  
 ; PRIOR FILING DATE: 1998-06-16  
 ; PRIOR APPLICATION NUMBER: 60/089514  
 ; PRIOR FILING DATE: 1998-06-16  
 ; PRIOR APPLICATION NUMBER: 60/089538  
 ; PRIOR FILING DATE: 1998-06-17  
 ; PRIOR APPLICATION NUMBER: 60/089598  
 ; PRIOR FILING DATE: 1998-06-17  
 ; PRIOR APPLICATION NUMBER: 60/089653

Query Match 60.3%; Score 44; DB 12; Length 802;

Best Local Similarity 72.7%; Pred. No. 1.7e+02; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGCRCGEAGS 13  
 |||||:|  
 DB 46 EGCRCGQAAS 56

# RESULT 10

; Sequence 312, Application US/10176483  
 ; Publication No. US20030017541A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Chen, Jian  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE REFERENCE: P34301C68

; CURRENT APPLICATION NUMBER: US/10/176,483  
 ; CURRENT FILING DATE: 2002-06-20

; Prior application removed - See File Wrapper or Palm  
 ; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 312  
 ; LENGTH: 802  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapien

US-10-176-483-312

Query Match 60.3%; Score 44; DB 12; Length: 802;

Best Local Similarity 72.7%; Pred. No. 1.7e+02; Mismatches 2; Indels 0; Gaps 0;  
 Matches: 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGCRCGEAGS 13  
 |||||:|  
 DB 46 EGCRCGQAAS 56

# RESULT 11

; Sequence 312, Application US/10176749  
 ; Publication No. US20030017542A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Chen, Jian  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE REFERENCE: P34301C76

; CURRENT APPLICATION NUMBER: US/10/176,749  
 ; CURRENT FILING DATE: 2002-06-20

; Prior application removed - See File Wrapper or Palm  
 ; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 312  
 ; LENGTH: 802  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapien

US-10-176-749-312

Query Match 60.3%; Score 44; DB 12; Length 802;

Best Local Similarity 72.7%; Pred. No. 1.7e+02; Mismatches 2; Indels 0; Gaps 0;  
 Matches: 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGCRCGEAGS 13  
 |||||:|  
 DB 46 EGCRCGQAAS 56

# RESULT 12

; Sequence 312, Application US/10176914  
 ; Publication No. US20030017543A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Chen, Jian  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE REFERENCE: P34301C83

; CURRENT APPLICATION NUMBER: US/10/176,914  
 ; CURRENT FILING DATE: 2002-06-20

; Prior application removed - See File Wrapper or Palm  
 ; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 312  
 ; LENGTH: 802  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapien

US-10-176-914-312

US-10-176-914-312

Query Match 60.3%; Score 44; DB 12; Length 802;  
 Best Local Similarity 72.7%; Pred. No. 1.7e+02;  
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGRSGEARGS 13  
 |||||:|  
 Db 46 EGRSGQAAAS 56

RESULT 13

US-10-176-915-312

; Sequence 312, Application US/10176915  
 ; Publication No. US20030017544A1  
 ; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Chen, Jian  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
 ; FILE REFERENCE: P3430R1C110  
 ; CURRENT APPLICATION NUMBER: US/10/176,915  
 ; CURRENT FILING DATE: 2002-06-21  
 ; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612  
 ; SEQ ID NO 312  
 ; LENGTH: 802  
 ; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-176-915-312

Query Match 60.3%; Score 44; DB 12; Length 802;  
 Best Local Similarity 72.7%; Pred. No. 1.7e+02;  
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGRSGEARGS 13  
 |||||:|  
 Db 46 EGRSGQAAAS 56

RESULT 14

US-10-006-485A-260

; Sequence 260, Application US/10006485A  
 ; Publication No. US20030064062A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan I.  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, Christopher J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Hillan, Kenneth J.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; TITLE OF INVENTION: Acids Encoding the Same  
 ; FILE REFERENCE: P2830P1C9  
 ; CURRENT APPLICATION NUMBER: US/10/006,485A  
 ; CURRENT FILING DATE: 2001-12-06

; PRIOR APPLICATION NUMBER: 60/098716  
 ; PRIOR FILING DATE: 1998-09-01  
 ; PRIOR APPLICATION NUMBER: 60/098723  
 ; PRIOR FILING DATE: 1998-09-01  
 ; PRIOR APPLICATION NUMBER: 60/098749  
 ; PRIOR FILING DATE: 1998-09-01  
 ; PRIOR APPLICATION NUMBER: 60/098750  
 ; PRIOR FILING DATE: 1998-09-01  
 ; PRIOR APPLICATION NUMBER: 60/098803  
 ; PRIOR FILING DATE: 1998-09-02  
 ; PRIOR APPLICATION NUMBER: 60/098821  
 ; PRIOR FILING DATE: 1998-09-02  
 ; PRIOR APPLICATION NUMBER: 60/098843  
 ; PRIOR FILING DATE: 1998-09-02  
 ; PRIOR APPLICATION NUMBER: 60/099536  
 ; PRIOR FILING DATE: 1998-09-09  
 ; PRIOR APPLICATION NUMBER: 60/099596  
 ; PRIOR FILING DATE: 1998-09-09  
 ; PRIOR APPLICATION NUMBER: 60/099598  
 ; PRIOR FILING DATE: 1998-09-09  
 ; PRIOR APPLICATION NUMBER: 60/099602  
 ; PRIOR FILING DATE: 1998-09-09  
 ; PRIOR APPLICATION NUMBER: 60/099642  
 ; PRIOR FILING DATE: 1998-09-09  
 ; PRIOR APPLICATION NUMBER: 60/099741  
 ; PRIOR FILING DATE: 1998-09-10  
 ; PRIOR APPLICATION NUMBER: 60/099754  
 ; PRIOR FILING DATE: 1998-09-10  
 ; PRIOR APPLICATION NUMBER: 60/099763  
 ; PRIOR FILING DATE: 1998-09-10  
 ; PRIOR APPLICATION NUMBER: 60/099792  
 ; PRIOR FILING DATE: 1998-09-10  
 ; PRIOR APPLICATION NUMBER: 60/099808  
 ; PRIOR FILING DATE: 1998-09-10  
 ; PRIOR APPLICATION NUMBER: 60/099812  
 ; PRIOR FILING DATE: 1998-09-10  
 ; PRIOR APPLICATION NUMBER: 60/099815  
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 ; PRIOR FILING DATE: 1998-09-10  
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 ; PRIOR FILING DATE: 1998-09-15  
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 ; PRIOR APPLICATION NUMBER: 60/100584  
 ; PRIOR FILING DATE: 1998-09-16  
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 ; PRIOR APPLICATION NUMBER: 60/100661  
 ; PRIOR FILING DATE: 1998-09-16  
 ; PRIOR APPLICATION NUMBER: 60/100662  
 ; PRIOR FILING DATE: 1998-09-16  
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 ; PRIOR FILING DATE: 1998-09-16  
 ; PRIOR APPLICATION NUMBER: 60/100683  
 ; PRIOR FILING DATE: 1998-09-17  
 ; PRIOR APPLICATION NUMBER: 60/100684  
 ; PRIOR FILING DATE: 1998-09-17  
 ; PRIOR APPLICATION NUMBER: 60/100710  
 ; PRIOR FILING DATE: 1998-09-17  
 ; PRIOR APPLICATION NUMBER: 60/100711  
 ; PRIOR FILING DATE: 1998-09-17  
 ; PRIOR APPLICATION NUMBER: 60/100848  
 ; PRIOR FILING DATE: 1998-09-18  
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 ; PRIOR APPLICATION NUMBER: 60/100919  
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 ; PRIOR APPLICATION NUMBER: 60/100930  
 ; PRIOR FILING DATE: 1998-09-17  
 ; PRIOR APPLICATION NUMBER: 60/101014

;; PRIOR FILING DATE: 1998-09-18  
;; PRIOR APPLICATION NUMBER: 60/101068  
;; PRIOR FILING DATE: 1998-09-18  
;; PRIOR APPLICATION NUMBER: 60/101071  
;; PRIOR FILING DATE: 1998-09-18  
;; PRIOR APPLICATION NUMBER: 60/101279  
;; PRIOR FILING DATE: 1998-09-22  
;; PRIOR APPLICATION NUMBER: 60/101471  
;; PRIOR FILING DATE: 1998-09-23  
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;; PRIOR FILING DATE: 1998-09-23  
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;; PRIOR FILING DATE: 1998-09-23  
;; PRIOR APPLICATION NUMBER: 60/101475  
;; PRIOR FILING DATE: 1998-09-23  
;; PRIOR APPLICATION NUMBER: 60/101476  
;; PRIOR FILING DATE: 1998-09-23  
;; PRIOR APPLICATION NUMBER: 60/101477  
;; PRIOR FILING DATE: 1998-09-23  
;; PRIOR APPLICATION NUMBER: 60/101479  
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;; PRIOR APPLICATION NUMBER: 60/101738  
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;; PRIOR APPLICATION NUMBER: 60/101741  
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;; PRIOR FILING DATE: 1998-09-24  
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;; PRIOR FILING DATE: 1998-09-24  
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;; PRIOR FILING DATE: 1998-10-02  
;; PRIOR APPLICATION NUMBER: 60/103258  
;; PRIOR FILING DATE: 1998-10-06  
;; PRIOR APPLICATION NUMBER: 60/103314  
;; PRIOR FILING DATE: 1998-10-07  
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;; PRIOR APPLICATION NUMBER: 60/103328  
;; PRIOR FILING DATE: 1998-10-07  
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;; PRIOR FILING DATE: 1998-10-07  
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;; PRIOR APPLICATION NUMBER: 60/103633  
;; PRIOR FILING DATE: 1998-10-08

;; PRIOR APPLICATION NUMBER: 60/103678  
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;; PRIOR FILING DATE: 1998-10-08  
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;; PRIOR APPLICATION NUMBER: 60/104987  
;; PRIOR FILING DATE: 1998-10-20  
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;; PRIOR FILING DATE: 1998-10-20  
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;; PRIOR APPLICATION NUMBER: 60/105169  
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;; PRIOR APPLICATION NUMBER: 60/105266  
;; PRIOR FILING DATE: 1998-10-22  
;; PRIOR APPLICATION NUMBER: 60/105693  
;; PRIOR FILING DATE: 1998-10-26  
;; PRIOR APPLICATION NUMBER: 60/105694  
;; PRIOR FILING DATE: 1998-10-26  
;; PRIOR APPLICATION NUMBER: 60/105807  
;; PRIOR FILING DATE: 1998-10-27  
;; PRIOR APPLICATION NUMBER: 60/105881  
;; PRIOR FILING DATE: 1998-10-27  
;; PRIOR APPLICATION NUMBER: 60/105882  
;; PRIOR FILING DATE: 1998-10-27  
;; PRIOR APPLICATION NUMBER: 60/106023  
;; PRIOR FILING DATE: 1998-10-28

Query Match 60.3%; Score 44; DB 12; Length 802;  
Best Local Similarity 72.7%; Pred. No. 1.7e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGCRRSGEAGGS 13  
|||||:  
Db 46 EGCRRSGQAAAS 56

RESULT 15  
US-10-013-907A-260  
; Sequence 260, Application US/10013907A  
; Publication No. US20030064925A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan I.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2830PIC34  
; CURRENT APPLICATION NUMBER: US/10/013,907A  
; CURRENT FILING DATE: 2001-12-10  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 477  
; SEQ ID NO 260  
; LENGTH: 802  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-013-907A-260

Query Match 60.3%; Score 44; DB 12; Length 802;  
Best Local Similarity 72.7%; Pred. No. 1.7e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGCRSGEAEAGS 13  
|||||:|  
Db 46 EGCRSGQAAAS 56

## RESULT 16

US-10-015-499A-260  
; Sequence 260, Application US/10015499A  
; Publication No. US20030065142A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan I.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2830PIC42  
; CURRENT APPLICATION NUMBER: US/10/015,499A  
; CURRENT FILING DATE: 2001-12-11  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 477  
; SEQ ID NO 260  
; LENGTH: 802  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-015-499A-260

Query Match 60.3%; Score 44; DB 12; Length 802;  
Best Local Similarity 72.7%; Pred. No. 1.7e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGCRSGEAEAGS 13  
|||||:|  
Db 46 EGCRSGQAAAS 56

## RESULT 17

US-10-176-484-312  
; Sequence 312, Application US/10176484  
; Publication No. US20030059876A9  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3430RIC64  
; CURRENT APPLICATION NUMBER: US/10/176,484  
; CURRENT FILING DATE: 2002-06-20  
; Prior application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 312  
; LENGTH: 802  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-176-484-312

Query Match 60.3%; Score 44; DB 12; Length 802;  
Best Local Similarity 72.7%; Pred. No. 1.7e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGCRSGEAEAGS 13  
|||||:|  
Db 46 EGCRSGQAAAS 56

## RESULT 18

US-10-180-550-312  
; Sequence 312, Application US/10180550  
; Publication No. US20030064440A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3430RIC149  
; CURRENT APPLICATION NUMBER: US/10/180,550  
; CURRENT FILING DATE: 2002-06-25  
; Prior application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 312  
; LENGTH: 802  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-180-550-312

Query Match 60.3%; Score 44; DB 12; Length 802;  
Best Local Similarity 72.7%; Pred. No. 1.7e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGCRSGEAEAGS 13  
|||||:|  
Db 46 EGCRSGQAAAS 56

## RESULT 19

US-10-183-014-312  
; Sequence 312, Application US/10183014  
; Publication No. US20030064441A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3430RIC170

; CURRENT APPLICATION NUMBER: US/10/183,014  
; CURRENT FILING DATE: 2002-06-26  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 312  
; LENGTH: 802  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-183-014-312

Query Match 60.3%; Score 44; DB 12; Length 802;  
Best Local Similarity 72.7%; Pred. No. 1.7e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGCGRSGEAGS 13  
Db 46 EGCGRSGQAAS 56  
|||||:|

RESULT 20  
US-10-187-738-312

; Sequence 312, Application US/10187738  
; Publication No. US20030064442A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430RIC241  
; CURRENT APPLICATION NUMBER: US/10/187,738  
; CURRENT FILING DATE: 2002-07-02  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 312  
; LENGTH: 802  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-187-738-312

Query Match 60.3%; Score 44; DB 12; Length 802;  
Best Local Similarity 72.7%; Pred. No. 1.7e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGCGRSGEAGS 13  
Db 46 EGCGRSGQAAS 56  
|||||:|

RESULT 21  
US-10-187-740-312

; Sequence 312, Application US/10187740  
; Publication No. US20030064443A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430RIC251  
; CURRENT APPLICATION NUMBER: US/10/187,740  
; CURRENT FILING DATE: 2002-07-01  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 312  
; LENGTH: 802  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-187-740-312

Query Match 60.3%; Score 44; DB 12; Length 802;  
Best Local Similarity 72.7%; Pred. No. 1.7e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGCGRSGEAGS 13  
Db 46 EGCGRSGQAAS 56  
|||||:|

RESULT 22  
US-10-187-883-312

; Sequence 312, Application US/10187883  
; Publication No. US20030064444A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430RIC248  
; CURRENT APPLICATION NUMBER: US/10/187,883  
; CURRENT FILING DATE: 2002-07-02  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 312  
; LENGTH: 802  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-187-883-312

Query Match 60.3%; Score 44; DB 12; Length 802;  
Best Local Similarity 72.7%; Pred. No. 1.7e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGCGRSGEAGS 13  
Db 46 EGCGRSGQAAS 56  
|||||:|

RESULT 23  
US-10-194-363-312

; Sequence 312, Application US/10194363  
; Publication No. US20030064445A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria





;; PRIOR APPLICATION NUMBER: 60/082797  
;; PRIOR FILING DATE: 1998-04-22  
;; PRIOR APPLICATION NUMBER: 60/083322  
;; PRIOR FILING DATE: 1998-04-28  
;; PRIOR APPLICATION NUMBER: 60/083495  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083496  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083499  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083559  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/084366  
;; PRIOR FILING DATE: 1998-05-05  
;; PRIOR APPLICATION NUMBER: 60/084414  
;; PRIOR FILING DATE: 1998-05-06  
;; PRIOR APPLICATION NUMBER: 60/084639  
;; PRIOR FILING DATE: 1998-05-07  
;; PRIOR APPLICATION NUMBER: 60/084640  
;; PRIOR FILING DATE: 1998-05-07  
;; PRIOR APPLICATION NUMBER: 60/084643  
;; PRIOR FILING DATE: 1998-05-07  
;; PRIOR APPLICATION NUMBER: 60/085573  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085579  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085580  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085582  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085700  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/086023  
;; PRIOR FILING DATE: 1998-05-18  
;; PRIOR APPLICATION NUMBER: 60/086392  
;; PRIOR FILING DATE: 1998-05-22  
;; PRIOR APPLICATION NUMBER: 60/086486  
;; PRIOR FILING DATE: 1998-05-22  
;; PRIOR APPLICATION NUMBER: 60/087098  
;; PRIOR FILING DATE: 1998-05-28  
;; PRIOR APPLICATION NUMBER: 60/087208  
;; PRIOR FILING DATE: 1998-05-28  
;; PRIOR APPLICATION NUMBER: 60/087609  
;; PRIOR FILING DATE: 1998-06-02  
;; PRIOR APPLICATION NUMBER: 60/087759  
;; PRIOR FILING DATE: 1998-06-02  
;; PRIOR APPLICATION NUMBER: 60/087827  
;; PRIOR FILING DATE: 1998-06-03  
;; PRIOR APPLICATION NUMBER: 60/088025  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088028  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088029  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088033  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088167  
;; PRIOR FILING DATE: 1998-06-05  
;; PRIOR APPLICATION NUMBER: 60/088202  
;; PRIOR FILING DATE: 1998-06-05  
;; PRIOR APPLICATION NUMBER: 60/088212  
;; PRIOR FILING DATE: 1998-06-05  
;; PRIOR APPLICATION NUMBER: 60/088217  
;; PRIOR FILING DATE: 1998-06-05  
;; PRIOR APPLICATION NUMBER: 60/088326  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088655  
;; PRIOR FILING DATE: 1998-06-09  
;; PRIOR APPLICATION NUMBER: 60/088722  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088738  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088740

;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088811  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088824  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088825  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088826  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088861  
;; PRIOR FILING DATE: 1998-06-11  
;; PRIOR APPLICATION NUMBER: 60/088863  
;; PRIOR FILING DATE: 1998-06-11  
;; PRIOR APPLICATION NUMBER: 60/088876  
;; PRIOR FILING DATE: 1998-06-11  
;; PRIOR APPLICATION NUMBER: 60/089090  
;; PRIOR FILING DATE: 1998-06-12  
;; PRIOR APPLICATION NUMBER: 60/089105  
;; PRIOR FILING DATE: 1998-06-12  
;; PRIOR APPLICATION NUMBER: 60/089512  
;; PRIOR FILING DATE: 1998-06-16  
;; PRIOR APPLICATION NUMBER: 60/089514  
;; PRIOR FILING DATE: 1998-06-16  
;; PRIOR APPLICATION NUMBER: 60/089538  
;; PRIOR FILING DATE: 1998-06-17  
;; PRIOR APPLICATION NUMBER: 60/089598  
;; PRIOR FILING DATE: 1998-06-17  
;; PRIOR APPLICATION NUMBER: 60/089653

Query Match 60.3%; Score 44; DB 12; Length 802;  
Best Local Similarity 72.7%; Pred. No. 1.7e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 EGCRSGEAGS 13  
|||||:|  
Db 46 EGCRSGQAAS 56

## RESULT 25

US-10-194-463-312  
; Sequence 312, Application US/10194463  
; Publication No. US20030064447A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430R1C300  
; CURRENT APPLICATION NUMBER: US/10/194,463  
; CURRENT FILING DATE: 2002-07-11  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 312  
; LENGTH: 802  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-194-463-312.

Query Match 60.3%; Score 44; DB 12; Length 802;  
Best Local Similarity 72.7%; Pred. No. 1.7e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 EGCRSGEAGS 13  
|||||:|

Db 46 EGRSGQAAS 56

## RESULT 26

US-10-194-484-312  
; Sequence 312, Application US/10194484  
; Publication No. US2003006448A1

## GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430R1C313

; CURRENT APPLICATION NUMBER: US/10/194,484  
; CURRENT FILING DATE: 2002-07-12

; PRIOR FILING DATE: 2002-01-15  
; PRIOR APPLICATION NUMBER: 60/052586  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059266  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063120  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063121  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063486  
; PRIOR FILING DATE: 1997-10-21  
; PRIOR APPLICATION NUMBER: 60/063540  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063541  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063544  
; PRIOR FILING DATE: 1997-10-28  
; Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 312

; LENGTH: 802

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-194-484-312

Query Match 60.3%; Score 44; DB 12; Length 802;  
Best Local Similarity 72.7%; Pred. No. 1.7e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGRSGQAAS 13

Db 46 EGRSGQAAS 56

## RESULT 27

US-10-195-884-312  
; Sequence 312, Application US/10195884  
; Publication No. US2003006449A1

## GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430R1C335

; CURRENT APPLICATION NUMBER: US/10/195,884  
; CURRENT FILING DATE: 2002-07-15

; PRIOR FILING DATE: 2002-01-15  
; PRIOR APPLICATION NUMBER: 60/052586  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059266  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063120  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063121  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063486  
; PRIOR FILING DATE: 1997-10-21  
; PRIOR APPLICATION NUMBER: 60/063540  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063541  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063544  
; PRIOR FILING DATE: 1997-10-28  
; Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 312

; LENGTH: 802

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-195-884-312

Query Match 60.3%; Score 44; DB 12; Length 802;  
Best Local Similarity 72.7%; Pred. No. 1.7e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGRSGQAAS 13

Db 46 EGRSGQAAS 56

## RESULT 28

US-10-195-896-312  
; Sequence 312, Application US/10195896  
; Publication No. US20030063112A1

## GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430R1C327

; CURRENT APPLICATION NUMBER: US/10/195,896  
; CURRENT FILING DATE: 2002-07-15

; PRIOR FILING DATE: 2002-07-15  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 312

; LENGTH: 802

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-195-896-312

Query Match 60.3%; Score 44; DB 12; Length 802;  
Best Local Similarity 72.7%; Pred. No. 1.7e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGRSGEAGS 13  
DB 46 EGRSGQAAAS 56

RESULT 29

US-10-196-744-312  
; Sequence 312, Application US/10196744  
; Publication No. US20030064450A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430RIC353  
; CURRENT FILING DATE: 2002-07-16

; PRIOR APPLICATION NUMBER: 10/052586  
; PRIOR FILING DATE: 2002-01-15

; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059266  
; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/063120  
; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063121  
; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063486  
; PRIOR FILING DATE: 1997-10-21

; PRIOR APPLICATION NUMBER: 60/063540  
; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063541  
; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063544  
; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 612

SEQ ID NO 312  
LENGTH: 802

TYPE: PRT  
ORGANISM: Homo Sapien

US-10-196-744-312

Query Match 60.3%; Score 44; DB 12; Length 802;  
Best Local Similarity 72.7%; Pred. No. 1.7e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGRSGEAGS 13  
DB 46 EGRSGQAAAS 56

RESULT 30

US-10-196-755-312

; Sequence 312, Application US/10196755  
; Publication No. US20030064451A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430RIC350  
; CURRENT FILING DATE: 2002-07-16

; PRIOR APPLICATION NUMBER: US/10/196,755  
; PRIOR Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612  
SEQ ID NO 312

LENGTH: 802  
TYPE: PRT

ORGANISM: Homo Sapien  
US-10-196-755-312

Query Match 60.3%; Score 44; DB 12; Length 802;

Best Local Similarity 72.7%; Pred. No. 1.7e+02;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGRSGEAGS 13  
DB 46 EGRSGQAAAS 56

RESULT 31

US-10-196-757-312

; Sequence 312, Application US/10196757  
; Publication No. US20030065159A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430RIC345  
; CURRENT FILING DATE: 2002-07-16

; PRIOR APPLICATION NUMBER: US/10/196,757  
; PRIOR Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612  
SEQ ID NO 312

LENGTH: 802  
TYPE: PRT

ORGANISM: Homo Sapien  
US-10-196-757-312

Query Match 60.3%; Score 44; DB 12; Length 802;

Best Local Similarity 72.7%; Pred. No. 1.7e+02;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGRSGEAGS 13  
DB 46 EGRSGQAAAS 56

RESULT 32

US-10-197-704-312  
; Sequence 312, Application US/10197704  
; Publication No. US20030064452A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430RIC364  
; CURRENT APPLICATION NUMBER: US/10/197,704  
; CURRENT FILING DATE: 2002-07-17  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 312  
; LENGTH: 802  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-197-704-312

Query Match 60.3%; Score 44; DB 12; Length 802;  
Best Local Similarity 72.7%; Pred. No. 1.7e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 EGRSGEAGS 13  
Db 46 EGRSGQAAS 56

RESULT 33  
US-10-197-710-312  
; Sequence 312, Application US/10197710  
; Publication No. US20030064453A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430RIC375  
; CURRENT APPLICATION NUMBER: US/10/197,710  
; CURRENT FILING DATE: 2002-07-17  
; Prior Application Number: 10/052586  
; Prior Filing Date: 2002-01-15  
; Prior Application Number: 60/059263  
; Prior Filing Date: 1997-09-18  
; Prior Application Number: 60/059266  
; Prior Filing Date: 1997-09-18  
; Prior Application Number: 60/062250  
; Prior Filing Date: 1997-10-17  
; Prior Application Number: 60/063120  
; Prior Filing Date: 1997-10-24  
; Prior Application Number: 60/063121  
; Prior Filing Date: 1997-10-24  
; Prior Application Number: 60/063486  
; Prior Filing Date: 1997-10-21  
; Prior Application Number: 60/063540

; Prior Filing Date: 1997-10-28  
; Prior Application Number: 60/063541  
; Prior Filing Date: 1997-10-28  
; Prior Application Number: 60/063544  
; Prior Filing Date: 1997-10-28  
; Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 312  
; LENGTH: 802  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-197-710-312

Query Match 60.3%; Score 44; DB 12; Length 802;  
Best Local Similarity 72.7%; Pred. No. 1.7e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 EGRSGEAGS 13  
Db 46 EGRSGQAAS 56

RESULT 34  
US-10-198-758-312  
; Sequence 312, Application US/10198758  
; Publication No. US20030064454A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430RIC383  
; CURRENT APPLICATION NUMBER: US/10/198,758  
; CURRENT FILING DATE: 2002-07-18  
; Prior Application Number: 10/052586  
; Prior Filing Date: 2002-01-15  
; Prior Application Number: 60/059263  
; Prior Filing Date: 1997-09-18  
; Prior Application Number: 60/059266  
; Prior Filing Date: 1997-09-18  
; Prior Application Number: 60/062250  
; Prior Filing Date: 1997-10-17  
; Prior Application Number: 60/063120  
; Prior Filing Date: 1997-10-24  
; Prior Application Number: 60/063121  
; Prior Filing Date: 1997-10-24  
; Prior Application Number: 60/063486  
; Prior Filing Date: 1997-10-21  
; Prior Application Number: 60/063540  
; Prior Filing Date: 1997-10-28  
; Prior Application Number: 60/063541  
; Prior Filing Date: 1997-10-28  
; Prior Application Number: 60/063544  
; Prior Filing Date: 1997-10-28  
; Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 312  
; LENGTH: 802  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-198-758-312

Query Match 60.3%; Score 44; DB 12; Length 802;  
Best Local Similarity 72.7%; Pred. No. 1.7e+02;

Matches	8;	Conservative	1;	Mismatches	2;	Indels	0;	Gaps	0;
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Qy 3 EGCRSGEAGS 13  
Dp 46 EGCRSGOAAAS 56

## RESULT 35

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US-10-198-766-312
/ Sequence 312, Application US/10198766
/ Publication No. US20030064455A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Chen, Jian
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Pan, James
/ APPLICANT: Smith, Victoria
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCES: P3430R1C379
/ CURRENT APPLICATION NUMBER: US/10/198,766
/ CURRENT FILING DATE: 2002-07-18
/ PRIOR APPLICATION NUMBER: 10/052586
/ PRIOR FILING DATE: 2002-01-15
/ PRIOR APPLICATION NUMBER: 60/059263
/ PRIOR FILING DATE: 1997-09-18
/ PRIOR APPLICATION NUMBER: 60/062250
/ PRIOR FILING DATE: 1997-10-17
/ PRIOR APPLICATION NUMBER: 60/063120
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/063121
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/063486
/ PRIOR FILING DATE: 1997-10-21
/ PRIOR APPLICATION NUMBER: 60/063540
/ PRIOR FILING DATE: 1997-10-28
/ PRIOR APPLICATION NUMBER: 60/063541
/ PRIOR FILING DATE: 1997-10-28
/ PRIOR APPLICATION NUMBER: 60/063544
/ PRIOR FILING DATE: 1997-10-28
/ PRIOR Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 612
/ SEQ ID NO 312
/ LENGTH: 802
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-199-304-312

```

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Query Match      60.3%; Score 44; DB 12; Length 802;
Best Local Similarity 72.7%; Pred. No. 1.7e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

Qy 3 EGCRSGEAGS 13  
db 46 EGCRSGOAAAS 56

RESULT 36

RESOL1 36  
US-109-304-312  
; Sequence 312, Application US/10199304  
; Publication No. US20030064456A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnovers, Luc  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3430RIC394  
; CURRENT APPLICATION NUMBER: US/10/199,309  
; CURRENT FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 10/052586  
; PRIOR FILING DATE: 2002-01-15  
; APPLICANT: Zhang, Zemin

; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059266  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063120  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063121  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063486  
; PRIOR FILING DATE: 1997-10-21  
; PRIOR APPLICATION NUMBER: 60/063540  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063541  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063544  
; PRIOR FILING DATE: 1997-10-28  
; Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 312  
; LENGTH: 802  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-199-309-312

Query Match 60.3%; Score 44; DB 12; Length 802;  
Best Local Similarity 72.7%; Pred. No. 1.7e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGCRCGAEAGS 13  
|||||:|  
Db 46 EGCRCGQAAAS 56

RESULT 38  
US-10-199-313-312  
; Sequence 312, Application US/10199313  
; Publication No. US20030064458A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430R1C396  
; CURRENT APPLICATION NUMBER: US/10/199,313  
; CURRENT FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 10/052586  
; PRIOR FILING DATE: 2002-01-15  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059266  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063120  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063121  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063486  
; PRIOR FILING DATE: 1997-10-21  
; PRIOR APPLICATION NUMBER: 60/063540  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063541

; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063544  
; PRIOR FILING DATE: 1997-10-28  
; Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 312  
; LENGTH: 802  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-199-313-312

Query Match 60.3%; Score 44; DB 12; Length 802;  
Best Local Similarity 72.7%; Pred. No. 1.7e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGCRCGAEAGS 13  
|||||:|  
Db 46 EGCRCGQAAAS 56

RESULT 39  
US-10-199-456-312  
; Sequence 312, Application US/10199456  
; Publication No. US20030064459A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430R1C400  
; CURRENT APPLICATION NUMBER: US/10/199,456  
; CURRENT FILING DATE: 2002-07-18  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 312  
; LENGTH: 802  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-199-456-312

Query Match 60.3%; Score 44; DB 12; Length 802;  
Best Local Similarity 72.7%; Pred. No. 1.7e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGCRCGAEAGS 13  
|||||:|  
Db 46 EGCRCGQAAAS 56

RESULT 40  
US-10-201-329-312  
; Sequence 312, Application US/10201329  
; Publication No. US20030064460A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.

```
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C438
; CURRENT APPLICATION NUMBER: US/10/201,329
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 312
; LENGTH: 802
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-201-329-312

Query Match      60.3%; Score 44; DB 12; Length 802;
Best Local Similarity 72.7%; Pred. No. 1.7e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      3 EGCRRGEAEGS 13
DB      46 EGCRRGQAAS 56
      |||||:|
      |||||:|

RESULT 41
US-10-202-412-312
; Sequence 312, Application US/10202412
; Publication No. US2003006461A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C456
; CURRENT APPLICATION NUMBER: US/10/202,412
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 312
; LENGTH: 802
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-201-329-312

Query Match      60.3%; Score 44; DB 12; Length 802;
Best Local Similarity 72.7%; Pred. No. 1.7e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      3 EGCRRGEAEGS 13
DB      46 EGCRRGQAAS 56
      |||||:|
      |||||:|

RESULT 42
US-10-206-919-312
; Sequence 312, Application US/10206919
; Publication No. US2003006462A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C518
; CURRENT APPLICATION NUMBER: US/10/206,919
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 312
; LENGTH: 802
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; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-206-919-312

Query Match 60.3%; Score 44; DB 12; Length 802;  
Best Local Similarity 72.7%; Pred. No. 1.7e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 ECGRSGEAGS 13  
|||||:|  
Db 46 ECGRSGQAAS 56

## RESULT 43

US-10-206-922-312  
; Sequence 312, Application US/10206922  
; Publication No. US20030064463A1

## GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C525  
; CURRENT APPLICATION NUMBER: US/10/206,922

; CURRENT FILING DATE: 2002-07-26  
; PRIOR APPLICATION NUMBER: 10/052586

; PRIOR FILING DATE: 2002-01-15

; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059266

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/063120

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063121

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063486

; PRIOR FILING DATE: 1997-10-21

; PRIOR APPLICATION NUMBER: 60/063540

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063541

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063544

; PRIOR FILING DATE: 1997-10-28

; Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 312

; LENGTH: 802

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-206-922-312

Query Match 60.3%; Score 44; DB 12; Length 802;  
Best Local Similarity 72.7%; Pred. No. 1.7e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 ECGRSGEAGS 13  
|||||:|  
Db 46 ECGRSGQAAS 56

## RESULT 44

US-10-206-924-312

; Sequence 312, Application US/10206924  
; Publication No. US20030064464A1

## GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C512

; CURRENT APPLICATION NUMBER: US/10/206,924

; CURRENT FILING DATE: 2002-07-26

; PRIOR APPLICATION NUMBER: 10/052586

; PRIOR FILING DATE: 2002-01-15

; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059266

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/063120

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063121

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063486

; PRIOR FILING DATE: 1997-10-21

; PRIOR APPLICATION NUMBER: 60/063540

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063541

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063544

; PRIOR FILING DATE: 1997-10-28

; Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 312

; LENGTH: 802

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-206-924-312

Query Match 60.3%; Score 44; DB 12; Length 802;

Best Local Similarity 72.7%; Pred. No. 1.7e+02;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 ECGRSGEAGS 13

|||||:|

Db 46 ECGRSGQAAS 56

## RESULT 45

US-10-206-928-312

; Sequence 312, Application US/10206928

; Publication No. US20030064465A1

## GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC



;; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
;; FILE REFERENCE: P3430RIC490  
;; CURRENT APPLICATION NUMBER: US/10/206,928  
;; CURRENT FILING DATE: 2002-07-25  
;; PRIOR APPLICATION NUMBER: 10/052586  
;; PRIOR FILING DATE: 2002-01-15  
;; PRIOR APPLICATION NUMBER: 60/059263  
;; PRIOR FILING DATE: 1997-09-18  
;; PRIOR APPLICATION NUMBER: 60/059266  
;; PRIOR FILING DATE: 1997-09-18  
;; PRIOR APPLICATION NUMBER: 60/062250  
;; PRIOR FILING DATE: 1997-10-17  
;; PRIOR APPLICATION NUMBER: 60/063120  
;; PRIOR FILING DATE: 1997-10-24  
;; PRIOR APPLICATION NUMBER: 60/063121  
;; PRIOR FILING DATE: 1997-10-24  
;; PRIOR APPLICATION NUMBER: 60/063486  
;; PRIOR FILING DATE: 1997-10-21  
;; PRIOR APPLICATION NUMBER: 60/063540  
;; PRIOR FILING DATE: 1997-10-28  
;; PRIOR APPLICATION NUMBER: 60/063541  
;; PRIOR FILING DATE: 1997-10-28  
;; PRIOR APPLICATION NUMBER: 60/063544  
;; PRIOR FILING DATE: 1997-10-28  
;; Prior Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 612  
;; SEQ ID NO 312  
;; LENGTH: 802  
;; TYPE: PRT  
;; ORGANISM: Homo Sapien  
US-10-206-928-312

Query Match 60.3%; Score 44; DB 12; Length 802;  
Best Local Similarity 72.7%; Pred. No. 1.7e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGRSGEAGS 13  
|||||:|  
DB 46 EGRSGQAAS 56

RESULT 46  
US-10-207-914-312  
;; Sequence 312, Application US/10207914  
;; Publication No. US20030064456A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Baker, Kevin P.  
;; APPLICANT: Chen, Jian  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Pan, James  
;; APPLICANT: Smith, Victoria  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
;; FILE REFERENCE: P3430RIC548  
;; CURRENT APPLICATION NUMBER: US/10/207,914  
;; CURRENT FILING DATE: 2002-07-29  
;; PRIOR APPLICATION NUMBER: 10/052586  
;; PRIOR FILING DATE: 2002-01-15  
;; PRIOR APPLICATION NUMBER: 60/059263  
;; PRIOR FILING DATE: 1997-09-18  
;; PRIOR APPLICATION NUMBER: 60/059266  
;; PRIOR FILING DATE: 1997-09-18  
;; PRIOR APPLICATION NUMBER: 60/062250  
;; PRIOR FILING DATE: 1997-10-17  
;; PRIOR APPLICATION NUMBER: 60/063120  
;; PRIOR FILING DATE: 1997-10-24  
;; PRIOR APPLICATION NUMBER: 60/063121

;; PRIOR FILING DATE: 1997-10-24  
;; PRIOR APPLICATION NUMBER: 60/063486  
;; PRIOR FILING DATE: 1997-10-21  
;; PRIOR APPLICATION NUMBER: 60/063540  
;; PRIOR FILING DATE: 1997-10-28  
;; PRIOR APPLICATION NUMBER: 60/063541  
;; PRIOR FILING DATE: 1997-10-28  
;; PRIOR APPLICATION NUMBER: 60/063544  
;; PRIOR FILING DATE: 1997-10-28  
;; Prior Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 612  
;; SEQ ID NO 312  
;; LENGTH: 802  
;; TYPE: PRT  
;; ORGANISM: Homo Sapien  
US-10-207-914-312

Query Match 60.3%; Score 44; DB 12; Length 802;  
Best Local Similarity 72.7%; Pred. No. 1.7e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGRSGEAGS 13  
|||||:|  
DB 46 EGRSGQAAS 56

RESULT 47  
US-10-207-921-312  
;; Sequence 312, Application US/10207921  
;; Publication No. US20030064467A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Baker, Kevin P.  
;; APPLICANT: Chen, Jian  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Pan, James  
;; APPLICANT: Smith, Victoria  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
;; FILE REFERENCE: P3430RIC546  
;; CURRENT APPLICATION NUMBER: US/10/207,921  
;; CURRENT FILING DATE: 2002-07-29  
;; PRIOR APPLICATION NUMBER: 10/052586  
;; PRIOR FILING DATE: 2002-01-15  
;; PRIOR APPLICATION NUMBER: 60/059263  
;; PRIOR FILING DATE: 1997-09-18  
;; PRIOR APPLICATION NUMBER: 60/059266  
;; PRIOR FILING DATE: 1997-09-18  
;; PRIOR APPLICATION NUMBER: 60/062250  
;; PRIOR FILING DATE: 1997-10-17  
;; PRIOR APPLICATION NUMBER: 60/063120  
;; PRIOR FILING DATE: 1997-10-24  
;; PRIOR APPLICATION NUMBER: 60/063121  
;; PRIOR FILING DATE: 1997-10-24  
;; PRIOR APPLICATION NUMBER: 60/063486  
;; PRIOR FILING DATE: 1997-10-21  
;; PRIOR APPLICATION NUMBER: 60/063540  
;; PRIOR FILING DATE: 1997-10-28  
;; PRIOR APPLICATION NUMBER: 60/063541  
;; PRIOR FILING DATE: 1997-10-28  
;; PRIOR APPLICATION NUMBER: 60/063544  
;; PRIOR FILING DATE: 1997-10-28  
;; Prior Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 612  
;; SEQ ID NO 312  
;; LENGTH: 802  
;; TYPE: PRT  
;; ORGANISM: Homo Sapien

US-10-207-921-312

Query Match 60.3%; Score 44; DB 12; Length 802;  
Best Local Similarity 72.7%; Pred. No. 1.7e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGCRRGEAEGS 13  
|||||:|  
Db 46 EGCRRGQAAS 56

RESULT 48

US-10-207-922-312  
; Sequence 312, Application US/10207922  
; Publication No. US20030064468A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430R1C544  
; CURRENT APPLICATION NUMBER: US/10/208,027  
; PRIOR FILING DATE: 2002-07-29  
; PRIOR APPLICATION NUMBER: 10/052586  
; PRIOR FILING DATE: 2002-01-15  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059266  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063120  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063121  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063486  
; PRIOR FILING DATE: 1997-10-21  
; PRIOR APPLICATION NUMBER: 60/063540  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063541  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063544  
; PRIOR FILING DATE: 1997-10-28  
; Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 312  
; LENGTH: 802  
; TYPE: PRT  
; ORGANISM: Homo Sapien

US-10-207-922-312  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430R1C542  
; CURRENT APPLICATION NUMBER: US/10/207,922

; PRIOR APPLICATION NUMBER: 10/052586  
; PRIOR FILING DATE: 2002-01-15  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059266  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063120  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063121  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063486  
; PRIOR FILING DATE: 1997-10-21  
; PRIOR APPLICATION NUMBER: 60/063540  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063541  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063544  
; PRIOR FILING DATE: 1997-10-28  
; Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 312  
; LENGTH: 802  
; TYPE: PRT  
; ORGANISM: Homo Sapien

US-10-207-922-312  
; ORGANISM: Homo Sapien

Query Match 60.3%; Score 44; DB 12; Length 802;  
Best Local Similarity 72.7%; Pred. No. 1.7e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGCRRGEAEGS 13  
|||||:|  
Db 46 EGCRRGQAAS 56

RESULT 49

US-10-208-027-312  
; Sequence 312, Application US/10208027  
; Publication No. US20030064469A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430R1C544  
; CURRENT APPLICATION NUMBER: US/10/208,027  
; PRIOR FILING DATE: 2002-07-29  
; PRIOR APPLICATION NUMBER: 10/052586  
; PRIOR FILING DATE: 2002-01-15  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059266  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063120  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063121  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063486  
; PRIOR FILING DATE: 1997-10-21  
; PRIOR APPLICATION NUMBER: 60/063540  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063541  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063544  
; PRIOR FILING DATE: 1997-10-28  
; Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 312  
; LENGTH: 802  
; TYPE: PRT  
; ORGANISM: Homo Sapien

US-10-208-027-312

Query Match 60.3%; Score 44; DB 12; Length 802;  
Best Local Similarity 72.7%; Pred. No. 1.7e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGCRRGEAEGS 13  
|||||:|  
Db 46 EGCRRGQAAS 56

RESULT 50

US-10-013-910A-260  
; Sequence 260, Application US/10013910A  
; Publication No. US20030187192A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan I.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.

;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE OF INVENTION: Acids Encoding the Same

;; FILE REFERENCE: P2830PIC33

;; CURRENT APPLICATION NUMBER: US/10/013,910A

;; CURRENT FILING DATE: 2001-12-10

;; PRIOR APPLICATION NUMBER: 60/098716

;; PRIOR FILING DATE: 1998-09-01

;; PRIOR APPLICATION NUMBER: 60/098723

;; PRIOR FILING DATE: 1998-09-01

;; PRIOR APPLICATION NUMBER: 60/098749

;; PRIOR FILING DATE: 1998-09-01

;; PRIOR APPLICATION NUMBER: 60/098750

;; PRIOR FILING DATE: 1998-09-01

;; PRIOR APPLICATION NUMBER: 60/098803

;; PRIOR FILING DATE: 1998-09-02

;; PRIOR APPLICATION NUMBER: 60/098821

;; PRIOR FILING DATE: 1998-09-02

;; PRIOR APPLICATION NUMBER: 60/098843

;; PRIOR FILING DATE: 1998-09-02

;; PRIOR APPLICATION NUMBER: 60/099536

;; PRIOR FILING DATE: 1998-09-09

;; PRIOR APPLICATION NUMBER: 60/099596

;; PRIOR FILING DATE: 1998-09-09

;; PRIOR APPLICATION NUMBER: 60/099598

;; PRIOR FILING DATE: 1998-09-09

;; Remaining Prior Application data removed - See File Wrapper or PALM.

;; NUMBER OF SEQ ID NOS: 477

;; SEQ ID NO 260

;; LENGTH: 802

;; TYPE: PRT

;; ORGANISM: Homo sapiens

;; US-10-013-910A-260

Query Match 60.3%; Score 44; DB 12; Length 802;  
Best Local Similarity 72.7%; Pred. No. 1.7e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGCRCGEAEGS 13

Db 46 EGCRCGQMAAS 56

Search completed: April 19, 2004, 17:46:50  
Job time : 44.4032 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 19, 2004, 17:12:35 ; Search time 13 Seconds  
(without alignments)  
96.192 Million cell updates/sec

Title: US-10-726-692-20

Perfect score: 73

Sequence: 1 GHEGCRSGEAGS 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : PIR 78:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	57.5	186	2 S65723	extracellular hemo
2	42	57.5	261	2 S51678	chitinase (EC 3.2.
3	42	57.5	1429	2 T19422	hypothetical prote
4	41	56.2	1053	2 S34172	sucrose-phosphate
5	40	54.8	152	2 E39225	hypothetical prote
6	40	54.8	164	2 T44280	conserved hypothet
7	40	54.8	626	2 A41284	translation initiat
8	39	53.4	226	1 S37105	phosphoribosylglyc
9	39	53.4	264	2 A84868	probable endochiti
10	39	53.4	292	2 D86438	phosphoribosylglyc
11	39	53.4	716	2 H85089	hypothetical prote
12	39	53.4	1213	2 T51032	hypothetical prote
13	38	52.1	448	2 S41725	integrase - Saccha
14	38	52.1	450	2 A10345	probable heat choc
15	38	52.1	450	2 AB0771	conserved hypothet
16	38	52.1	461	2 T23574	hypothetical prote
17	38	52.1	464	2 T40108	glucan 1,3-beta-gl
18	38	52.1	471	2 F90988	probable heat choc
19	38	52.1	471	2 H85833	probable heat choc
20	38	52.1	471	2 D64973	yegD protein - Esc
21	38	52.1	880	2 P71652	pyruvate,phosphate
22	38	52.1	882	2 G97797	hypothetical prote
23	38	52.1	888	2 T31131	pyruvate, phosphate
24	38	52.1	900	2 G87431	pyruvate, phosphate
25	37	50.7	212	1 W4WLRB	E4 protein - cotto
26	37	50.7	227	2 H82344	rftB protein VC025
27	37	50.7	268	2 T36679	probable morpholog
28	37	50.7	286	2 S16969	O-antigen - Vibrio
29	37	50.7	286	2 A42699	serotype specific

30	37	50.7	286	2 H90066	hypothetical prote
31	37	50.7	350	2 F88804	basic membrane pro
32	37	50.7	415	2 H83067	probable c-type cy
33	37	50.7	416	2 A32947	flaggrin precursor
34	37	50.7	460	2 S34969	outer membrane por
35	37	50.7	610	2 S64126	cell division cont
36	37	50.7	844	2 T00529	hypothetical prote
37	37	50.7	1521	2 T30200	protein-tyrosine k
38	37	50.7	2215	2 T00348	LRIL protein - mou
39	37	50.7	2248	2 A35938	profilaggrin - hum
40	37	50.7	2262	2 T30890	calcium channel al
41	36.5	50.0	646	2 H96665	protein F22C12.10
42	36	49.3	72	2 S39416	metallothionein 10
43	36	49.3	72	2 S39418	metallothionein 10
44	36	49.3	72	2 S39419	metallothionein 10
45	36	49.3	72	2 S39417	metallothionein 10
46	36	49.3	111	2 H97316	hypothetical prote
47	36	49.3	196	2 AB1004	peptidylprolyl iso
48	36	49.3	207	2 D65095	hypothetical prote
49	36	49.3	207	2 A98123	hypothetical prote
50	36	49.3	207	2 H85967	hypothetical prote

ALIGNMENTS

RESULT 1

S65723  
extracellular hemoglobin linker chain L3 - earthworm (Lumbricus terrestris) (fragments)  
C:Species: Lumbricus terrestris (common earthworm)  
C>Date: 06-Dec-1996 #sequence\_revision 13-Mar-1997 #text\_change 02-Sep-2000  
C:Accession: S65723; B46586  
R:Fushitani, K.; Higashiyama, K.; Asao, M.; Hosokawa, K.  
Biochim. Biophys. Acta 1292, 273-280, 1996  
A:Title: Characterization of the constituent polypeptides of the extracellular hemoglobin  
A:Reference number: S65721; MUID:96176855; PMID:8597573  
A:Accession: S65723  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-77;78-102;103-129;130-186 <FUS>  
R:Omby, D.W.; Zhu, H.; Schneider, K.; Beavis, R.C.; Chait, B.T.; Riggs, A.F.  
J. Biol. Chem. 268, 13539-13547, 1993  
A:Title: The extracellular hemoglobin of the earthworm, Lumbricus terrestris. Determina  
A:Reference number: A46586; MUID:93293879; PMID:8514787  
A:Accession: B46586  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-15 <OWN>  
A>Note: sequence extracted from NCBI backbone (NCBIP:134510)  
C:Superfamily: hemoglobin linker chain; LDL receptor ligand-binding repeat homology  
F:60-96/Domain: LDL receptor ligand-binding repeat homology (fragments) <LDL>

Query Match 57.5%; Score 42; DB 2; Length 186;

Best Local Similarity 63.6%; Pred. No. 12; Mismatches 1; Indels 0; Gaps 0;  
Matches 7; Conservative 3; Indels 0; Gaps 0;

QY 1 GHEGCRSGEAG 11

DB 83 GHNDCEGDE 93

RESULT 2

S51678  
chitinase (EC 3.2.1.14) class I - European elder (fragment)  
N:Alternate names: pathogenesis-related protein PR-3 type  
C:Species: Sambucus nigra (European elder)  
C>Date: 07-May-1995 #sequence\_revision 01-Sep-1995 #text\_change 22-Jun-1999  
C:Accession: S51678  
R:Coupe, S.A.; Taylor, J.E.; Roberts, J.A.  
submitted to the EMBL Data Library, December 1994  
A:Description: Characterisation of mRNAs that encode pathogenesis-related proteins that  
A:Reference number: S51645  
A:Accession: S51678

A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-261 <COU>  
A:Cross-references: EMBL:Z46948; NID:G603881; PIDN:CAA87072.1; PID:G603882  
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl  
C:Keywords: glycosidase; hydrolase; polysaccharide degradation  
F:16-51/Domain: hevein chitin-binding domain homology <HCB>  
F:61-561/Domain: plant chitinase homology <PCH>

Query Match 57.5%; Score 42; DB 2; Length 261;  
Best Local Similarity 72.7%; Pred. No. 16;  
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 EGCRCGEARGS 13  
||| ||| ||  
Db 41 EGCRCGFCYGS 51

RESULT 3  
T19422  
hypothetical protein C24F3.5 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 29-Oct-1999  
A:Accession: T19422; T23313; T24960  
R:McMurray, A.  
submitted to the EMBL Data Library, April 1998  
A:Reference number: Z19122  
A:Accession: T19422  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-1429 <WIL>  
A:Cross-references: EMBL:AL022716; PIDN:CAA18775.1; GSPDB:GN00022; CESP:C24F3.5  
A:Experimental source: clone C24F3  
R:Wild, A.  
submitted to the EMBL Data Library, February 1996  
A:Reference number: Z19725  
A:Accession: T23313  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-1429 <W12>  
A:Cross-references: EMBL:Z69664; PIDN:CAA93518.1; GSPDB:GN00022; CESP:C24F3.5  
A:Experimental source: clone K04D7  
R:Ainscough, R.  
submitted to the EMBL Data Library, January 1998  
A:Reference number: Z19961  
A:Accession: T24960  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-1429 <W13>  
A:Cross-references: EMBL:AL021570; PIDN:CAA16510.1; GSPDB:GN00022; CESP:C24F3.5  
A:Experimental source: clone T17B5  
C:Genetics:  
A:Gene: CESP:C24F3.5  
A:Map position: 4  
A:Introns: 23/3; 57/2; 120/3; 150/3; 189/3; 230/1; 466/2; 544/2; 583/2; 642/2; 67

Query Match 57.5%; Score 42; DB 2; Length 1429;  
Best Local Similarity 77.8%; Pred. No. 71;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHEGCRSGE 9  
||| ||| |||  
Db 406 GHHGCGSGE 414

RESULT 4  
S34172  
sucrose-phosphate synthase (EC 2.4.1.14) - potato  
C:Species: Solanum tuberosum (potato)  
C:Date: 22-Nov-1993 #sequence\_revision 03-Aug-1995 #text\_change 18-Jun-1999  
A:Accession: S34172  
R:Sonnemwald, U.; Basner, A.  
submitted to the EMBL Data Library, June 1993

A:Reference number: S34172  
A:Accession: S34172  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1053 <SON>  
A:Cross-references: EMBL:X73477; NID:G313264; PIDN:CAA51872.1; PID:G313265  
C:Function:  
A:Description: catalyzes the formation of sucrose-6-phosphate from UDPglucose and D-fru  
A:Pathway: sucrose biosynthesis  
C:Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homology  
C:Keywords: glycosyltransferase; hexosyltransferase; sucrose biosynthesis  
F:168-651/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>

Query Match 56.2%; Score 41; DB 2; Length 1053;  
Best Local Similarity 66.7%; Pred. No. 79;  
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 HEGCRSGEARGS 13  
||| ||| |||  
Db 439 HEGDMDGTEGS 450

RESULT 5  
E39925  
hypothetical protein 4 - equine arteritis virus  
C:Species: equine arteritis virus  
C:Date: 14-Feb-1992 #sequence\_revision 14-Feb-1992 #text\_change 08-Oct-1999  
A:Accession: E39925  
R:Den Boon, J.A.; Snijder, E.J.; Chirnside, E.D.; De Vries, A.A.F.; Horzinek, M.C.; Spar  
J. Virol. 65, 2910-2920, 1991  
A:Title: Equine arteritis virus is not a togavirus but belongs to the coronaviruslike ex  
A:Reference number: A39925; MUID:91237805; PMID:1851863  
A:Accession: E39925  
A:Status: preliminary  
A:Molecule type: Genomic RNA  
A:Residues: 1-152 <DEN>  
A:Cross-references: EMBL:X53459; NID:G62065; PIDN:CAA37543.1; PID:G62070  
C:Superfamily: equine arteritis virus hypothetical protein 4

Query Match 54.8%; Score 40; DB 2; Length 152;  
Best Local Similarity 85.7%; Pred. No. 22;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHEGCRS 7  
||| ||| |||  
Db 46 GHEGCRN 52

RESULT 6  
T44280  
conserved hypothetical protein [imported] - Azotobacter vinelandii  
C:Species: Azotobacter vinelandii  
C:Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 02-Sep-2000  
A:Accession: T44280  
R:Zheng, L.; Cash, V.L.; Flint, D.H.; Dean, D.R.  
J. Biol. Chem. 273, 13264-13272, 1998  
A:Title: Assembly of iron-sulfur clusters. Identification of an iscSUA-hscBA-fdx gene cl  
A:Reference number: Z22743; MUID:98250785; PMID:9582371  
A:Accession: T44280  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-164 <ZHE>  
A:Cross-references: EMBL:AF010139; NID:G3046315; PIDN:AAC24480.1; PID:G3046321  
A:Experimental source: strain D116  
C:Superfamily: hypothetical protein b2531

Query Match 54.8%; Score 40; DB 2; Length 164;  
Best Local Similarity 77.8%; Pred. No. 23;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHEGCRSGE 9  
||| ||| |||  
Db 94 GDRGCRSGE 102

RESULT 7  
A41284  
translation initiation factor eIF-2 alpha chain kinase (BC 2.7.1.1-) - rabbit  
N:Alternate names: heme-regulated translation initiation factor 2alpha kinase  
C:Species: *Oryctolagus cuniculus* (domestic rabbit)  
C>Date: 03-Apr-1992 #sequence\_revision 03-Apr-1992 #text\_change 31-Mar-2003  
C:Accession: A41284; A39001  
R:Chen, J.J.; Throop, M.S.; Gehrke, L.; Kuo, I.; Pal, J.K.; Brodsky, M.; London, I.M.  
Proc. Natl. Acad. Sci. U.S.A. 88, 7729-7733, 1991  
A:Title: Cloning of the cDNA of the heme-regulated eukaryotic initiation factor 2alpha  
-dependent eIF-2alpha kinase.  
A:Reference number: A41284; MUID:91352063; PMID:1679235  
A:Accession: A41284  
A:Molecule type: mRNA  
A:Residues: 1-626 <CHE>  
A:Cross-references: GB:M69035; NID:gl65002; PIDN:AAA31241.1; PID:gl65003  
R:Chen, J.J.; Pal, J.K.; Petryshyn, R.; Kuo, I.; Yang, J.M.; Throop, M.S.; Gehrke, L.; L  
Proc. Natl. Acad. Sci. U.S.A. 88, 315-319, 1991  
A:Title: Amino acid microsequencing of internal tryptic peptides of heme-regulated eukar  
A:Reference number: A39001; MUID:91110520; PMID:1671169  
A:Accession: A39001  
A:Molecule type: protein  
A:Residues: 166-178; 454-460, 'B', 462-467; 506-525 <CH2>  
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo  
C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; serine/threoni  
F:168-578/Domain: protein kinase homology <KIN>  
F:176-184/Region: protein kinase ATP-binding motif

Query Match 54.8%; Score 40; DB 2; Length 626;  
Best Local Similarity 66.7%; Pred. No. 74;  
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GHEGCRSGEAGEG 12  
| | | | |  
DB 4 GSGATRGGEAGEG 15

RESULT 8  
S37105  
phosphoribosylglycinamide formyltransferase (EC 2.1.2.2) - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 06-Jan-1994 #sequence\_revision 28-Oct-1994 #text\_change 11-Jun-1999  
C:Accession: S37105  
R:Schmorr, K.M.  
submitted to the EMBL Data Library, August 1993  
A:Reference number: S37104  
A:Accession: S37105  
A:Molecule type: mRNA  
A:Residues: 1-226 <SCH>  
A:Cross-references: EMBL:X74767; NID:g398611; PIDN:CAA52779.1; PID:g398612  
C:Genetics:  
A:Gene: PUR3  
C:Superfamily: phosphoribosylglycinamide formyltransferase; phosphoribosylglycinamide fo  
C:Keywords: purine nucleotide biosynthesis; transferase  
F:34-226/Domain: phosphoribosylglycinamide formyltransferase homology <PRGF>

Query Match 53.4%; Score 39; DB 1; Length 226;  
Best Local Similarity 54.5%; Pred. No. 45;  
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 HEGCDSGGEAGEG 12  
| | | | |  
DB 49 HEGCDSGGSVNG 59

RESULT 9  
A84868  
probable endochitinase [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 16-Feb-2001  
C:Accession: A84868

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,  
Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083487; PMID:10617197  
A:Accession: A84868  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-264 <STO>  
A:Cross-references: GB:AE002093; NID:g2281111; PIDN:AAB64047.1; GSPDB:GN00139  
C:Genetics:  
A:Gene: At2g43590  
A:Map position: 2  
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; p  
Query Match 53.4%; Score 39; DB 2; Length 264;  
Best Local Similarity 70.0%; Pred. No. 51;  
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GCRSGEAGEGS 13  
| | | | |  
DB 51 GCRSGPCRGS 60

RESULT 10  
D86438  
phosphoribosylglycinamide formyltransferase - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 02-Nov-2001  
C:Accession: D86438  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Pederspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.,  
anssen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luross, J.S.; Maiti, R.; Marziali  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Accession: D86438  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-292 <STO>  
A:Cross-references: GB:AE005172; NID:g4512619; PIDN:AAD21688.1; GSPDB:GN00141  
C:Genetics:  
A:Map position: 1  
C:Superfamily: phosphoribosylglycinamide formyltransferase; phosphoribosylglycinamide f  
Query Match 53.4%; Score 39; DB 2; Length 292;  
Best Local Similarity 54.5%; Pred. No. 56;  
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 HEGCRSGEAGEG 12  
| | | | |  
DB 95 HEGCDSGGSVNG 105

RESULT 11  
H85089  
hypothetical protein AT4g08920 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 16-Feb-2001  
C:Accession: H85089  
R:Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin  
Nature 402, 769-777, 1999  
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.  
A:Reference number: A85001; MUID:20083488; PMID:10617198  
A:Accession: H85089  
A:Status: preliminary  
A:Molecule type: DNA

A;Residues: 1-716 <STO>  
 A;Cross-references: GB:NC\_001268; NID:G7267534; PIDN:CAB78016.1; GSPDB:GN00140  
 C;Species: Neurospora crassa  
 C;Genetics:  
 A;Gene: A14g08920  
 A;Map position: 4

Query Match 53.4%; Score 39; DB 2; Length 716;  
 Best Local Similarity 75.0%; Pred. No. 1.2e+02;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 HEGCRSGE 9  
 :||| |||  
 Db 696 HKGCSNGE 703

RESULT 12  
 T51032  
 hypothetical protein B15120.20 [imported] - Neurospora crassa  
 C;Species: Neurospora crassa  
 C;Date: 21-Jul-2000 #sequence\_revision 21-Jul-2000 #text\_change 21-Jul-2000  
 C;Accession: T51032  
 R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Partmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, July 2000  
 A;Reference number: Z25286  
 A;Accession: T51032  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-1213 <SCH>  
 A;Cross-references: EMBL:AL389900; GSPDB:GN00116; NCSP:B15120.20  
 A;Experimental source: BAC clone B15120; strain OR74A  
 C;Genetics:  
 A;Gene: NCSP:B15120.20  
 A;Map position: 6  
 A;Introns: 72/3; 958/3; 1055/3

Query Match 53.4%; Score 39; DB 2; Length 1213;  
 Best Local Similarity 54.5%; Pred. No. 1.9e+02;  
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGRSGEAGSGS 13  
 : ||||| :|  
 Db 164 DACRSGEKDG 174

RESULT 13  
 S41725  
 integrase - Saccharopolyspora erythraea  
 C;Species: Saccharopolyspora erythraea  
 C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 22-Oct-1999  
 C;Accession: S41725  
 R;Brown, D.P.; Idler, K.B.; Becker, D.M.; Donadio, S.; Katz, L. Mol. Gen. Genet. 242, 185-193, 1994  
 A;Title: Characterization of the genes and attachment sites for site-specific integration  
 A;Reference number: S41722; MUID:94211208; PMID:8159169  
 A;Accession: S41725  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-448 <BRO>  
 A;Cross-references: EMBL:L11597; NID:g404798; PIDN:AAA26480.1; PID:g404802

Query Match 52.1%; Score 38; DB 2; Length 448;  
 Best Local Similarity 77.8%; Pred. No. 1.2e+02;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCRSGEAGG 12  
 |||||  
 Db 215 GCRQGEALG 223

RESULT 14  
 A10345  
 probable heat shock protein YP02840 [imported] - Yersinia pestis (strain CO92)  
 C;Species: Yersinia pestis

C;Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 02-Nov-2001  
 C;Accession: A10345  
 R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; 11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001  
 A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
 A;Reference number: AB0001; MUID:21470413; PMID:11586360  
 A;Accession: A10345  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-450 <KUR>  
 A;Cross-references: GB:AL590842; PIDN:CAC93072.1; PID:g15980809; GSPDB:GN00175  
 C;Genetics:  
 A;Gene: YP02840

Query Match 52.1%; Score 38; DB 2; Length 450;  
 Best Local Similarity 75.0%; Pred. No. 1.2e+02;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHEGCRSG 8  
 |||||  
 Db 244 GHSGCRVG 251

RESULT 15  
 AB0771  
 conserved hypothetical protein STY2338 [imported] - Salmonella enterica subsp. enterica  
 C;Species: Salmonella enterica subsp. enterica serovar Typhi  
 A;Note: this species has also been called Salmonella typhi  
 C;Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
 C;Accession: AB0771  
 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P. Nature 413, 848-852, 2001  
 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov  
 A;Reference number: AB0502; MUID:21534947; PMID:11677608  
 A;Accession: AB0771  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-450 <PAR>  
 A;Cross-references: GB:AL513382; PIDN:CAD02488.1; PID:g16503352; GSPDB:GN00176  
 C;Genetics:  
 A;Gene: STY2338

Query Match 52.1%; Score 38; DB 2; Length 450;  
 Best Local Similarity 75.0%; Pred. No. 1.2e+02;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHEGCRSG 8  
 |||||  
 Db 244 GHSGCRVG 251

RESULT 16  
 T23574  
 hypothetical protein K10D3.5 - Caenorhabditis elegans  
 C;Species: Caenorhabditis elegans  
 C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C;Accession: T23574  
 R;McMurray, A. submitted to the EMBL Data Library, June 1996  
 A;Reference number: Z19762  
 A;Accession: T23574  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-461 <WIL>  
 A;Cross-references: EMBL:Z75545; PIDN:CAA99887.1; GSPDB:GN00019; CESP:K10D3.5  
 A;Experimental source: clone K10D3  
 C;Genetics:  
 A;Gene: CESP:K10D3.5



A:Map position: 1  
A:Introns: 12/1; 40/1; 124/3; 157/3; 212/3; 345/2; 386/3; 421/2

Query Match 52.1%; Score 38; DB 2; Length 461;  
Best Local Similarity 50.0%; Pred. No. 1.2e+02;  
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 GHEGCRSGAEG 12  
|||:::|  
DB 65 GLSGCQNGSSEG 76

RESULT 17  
T40108  
glucan 1,3-beta-glucosidase SPBC2D10.05 - fission yeast (Schizosaccharomyces pombe)  
C:Species: Schizosaccharomyces pombe  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 07-Dec-1999  
C:Accession: T40108  
R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Taylor, K.; Harris, D.  
submitted to the EMBL Data Library, September 1998  
A:Reference number: Z21906  
A:Accession: T40108  
A:Status: preliminary; translated from GB/EMBL/DD83  
A:Molecule type: DNA  
A:Residues: 1-464 <WOO>  
A:Cross-references: EMBL:AL031788; PIDN:CAA21163.1; GSPDB:GN00067; SPDB:SPBC2D10.05  
A:Experimental source: strain 972h; cosmid c2D10  
C:Genetics:  
A:Gene: SPDB:SPBC2D10.05  
A:Map position: 2  
A:Introns: 230/1

Query Match 52.1%; Score 38; DB 2; Length 464;  
Best Local Similarity 63.6%; Pred. No. 1.2e+02;  
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GHEGCRSGAE 11  
|||:|  
DB 148 GHSGTSSGKAE 158

RESULT 18  
F90988  
probable heat shock protein [imported] - Escherichia coli (strain O157:H7, substrain RIM  
C:Species: Escherichia coli  
C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 18-Jul-2001  
C:Accession: F90988  
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene  
A:Reference number: A99629; MUID:21156231; PMID:11258796  
A:Accession: F90988  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-471 <HAY>  
A:Cross-references: GB:BA000007; PIDN:BA036301.1; PID:G13362347; GSPDB:GN00154  
A:Experimental source: strain O157:H7, substrain RIMD 0509952  
C:Genetics:  
A:Gene: EC92878

Query Match 52.1%; Score 38; DB 2; Length 471;  
Best Local Similarity 75.0%; Pred. No. 1.2e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHEGCRSG 8  
|||  
DB 265 GHSGCCRG 272

RESULT 19  
H85833  
probable heat shock protein yegD [imported] - Escherichia coli (strain O157:H7, substrain

C:Species: Escherichia coli  
C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001  
C:Accession: H85833  
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca  
Natura 409, 529-533, 2001  
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A:Reference number: A85480; MUID:21074935; PMID:11206551  
A:Accession: H85833  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-471 <STO>  
A:Cross-references: GB:AE005174; NID:G12516272; PIDN:AA057132.1; GSPDB:GN00145; UMG:Z3.  
A:Experimental source: strain O157:H7, substrain EDL933  
C:Genetics:  
A:Gene: yegD

Query Match 52.1%; Score 38; DB 2; Length 471;  
Best Local Similarity 75.0%; Pred. No. 1.2e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHEGCRSG 8  
|||  
DB 265 GHSGCCRG 272

RESULT 20  
D64973  
yegD protein - Escherichia coli (strain K-12)  
C:Species: Escherichia coli  
C:Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 01-Mar-2002  
C:Accession: D64973  
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C.  
A.; Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A:Title: The complete genome sequence of Escherichia coli K-12.  
A:Reference number: A64720; MUID:97426617; PMID:9278503  
A:Accession: D64973  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-471 <BLAT>  
A:Cross-references: GB:AE000297; GB:U00096; NID:G1788382; PIDN:AA075130.1; PID:G1788384,  
A:Experimental source: strain K-12, substrain MG1655  
C:Genetics:  
A:Gene: yegD

Query Match 52.1%; Score 38; DB 2; Length 471;  
Best Local Similarity 75.0%; Pred. No. 1.2e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHEGCRSG 8  
|||  
DB 265 GHSGCCRG 272

RESULT 21  
F71652  
pyruvate, phosphate dikinase precursor (ppdk) RP492 - Rickettsia prowazekii  
C:Species: Rickettsia prowazekii  
C:Date: 21-Nov-1998 #sequence\_revision 21-Nov-1998 #text\_change 14-Jul-2003  
C:Accession: F71652  
R:Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, I.  
Nature 396, 133-140, 1998  
A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.  
A:Reference number: A1630; MUID:99039499; PMID:9823893  
A:Accession: F71652  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-880 <AND>  
A:Cross-references: GB:AJ235272; GB:AJ235269; NID:G3861033; PIDN:CAA14944.1; PID:G38610,  
A:Experimental source: strain Madrid E  
C:Genetics:  
A:Gene: ppdk; RP492

C:Superfamily: pyruvate, phosphate dikinase

Query Match 52.1%; Score 38; DB 2; Length 880;  
Best Local Similarity 75.0%; Pred. No. 2.1e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHEGCRSG 8  
||| ||| |  
Db 668 GHRGCRLG 675

RESULT 22

G97797

hypothetical protein ppdk [imported] - Rickettsia conorii (strain Malish 7)

C:Species: Rickettsia conorii

C:Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 14-Jul-2003

C:Accession: G97797

R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; R

Science 293, 2093-2098, 2001

A:Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.

A:Reference number: A97700; MUID:2142074; PMID:11557893

A:Accession: G97797

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-882 <KUR>

A:Cross-references: GB:AE006914; PIDN:AA03321.1; PID:gl5619880; GSPDB:GN00173

C:Genetics:

A:Gene: ppdk

C:Superfamily: pyruvate, phosphate dikinase

Query Match 52.1%; Score 38; DB 2; Length 882;  
Best Local Similarity 75.0%; Pred. No. 2.1e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHEGCRSG 8  
||| ||| |  
Db 671 GHRGCRLG 678

RESULT 23

T31131

pyruvate, phosphate dikinase (EC 2.7.9.1) - Sphingomonas aromaticivorans plasmid pNL1

C:Species: Sphingomonas aromaticivorans

C:Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 14-Jul-2003

C:Accession: T31131

R:Romane, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, S.J.; Sisk, E.C.; Sensen, C.W.; G

submitted to the EMBL Data Library, July 1998

A:Description: Complete sequence of a 184 kb catabolic plasmid from Sphingomonas aromati

A:Reference number: Z20992

A:Accession: T31131

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-888 <ROM>

A:Cross-references: EMBL:AF079317; NID:g3378261; PID:g3378272; PIDN:AA03855.1

C:Genetics:

A:Gene: ppdk

A:Genome: plasmid pNL1

C:Superfamily: pyruvate, phosphate dikinase

C:Keywords: transferase

Query Match 52.1%; Score 38; DB 2; Length 888;  
Best Local Similarity 75.0%; Pred. No. 2.1e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHEGCRSG 8  
||| ||| |  
Db 677 GHRGCRLG 684

RESULT 24

G87431

pyruvate phosphate dikinase [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus

C:Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 14-Jul-2003

C:Accession: G87431

R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.

B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon

n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A:Title: Complete Genome Sequence of Caulobacter crescentus.

A:Reference number: A87249; MUID:21173698; PMID:11259647

A:Accession: G87431

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-900 <STO>

A:Cross-references: GB:AE005673; NID:gl3422841; PIDN:AAK23451.1; GSPDB:GN00148

C:Genetics:

A:Gene: CC1471

C:Superfamily: pyruvate, phosphate dikinase

Query Match 52.1%; Score 38; DB 2; Length 900;  
Best Local Similarity 75.0%; Pred. No. 2.2e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHEGCRSG 8  
||| ||| |  
Db 687 GHRGCRLG 694

RESULT 25

W4WLRB

E4 protein - cottontail rabbit papillomavirus

C:Species: cottontail rabbit papillomavirus

C:Date: 28-Aug-1985 #sequence\_revision 28-Aug-1985 #text\_change 24-Feb-1994

C:Accession: A03674

R:Giri, I.; Danos, O.; Yaniv, M.

Proc. Natl. Acad. Sci. U.S.A. 82, 1580-1584, 1985

A:Title: Genomic structure of the cottontail rabbit (Shope) papillomavirus.

A:Reference number: A94027; MUID:85166175; PMID:2984661

A:Accession: A03674

A:Molecule type: DNA

A:Residues: 1-212 <GIR>

C:Superfamily: rabbit papillomavirus E4 protein

C:Keywords: early protein

Query Match 50.7%; Score 37; DB 1; Length 212;  
Best Local Similarity 62.5%; Pred. No. 90;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHEGCRSG 8  
||| ||| |  
Db 156 GHQGCNEG 163

RESULT 26

H82344

rft protein VC0258 [imported] - Vibrio cholerae (strain N16961 serogroup O1)

C:Species: Vibrio cholerae

C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Feb-2001

C:Accession: H82344

R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.

chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, C.M.

l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A:Reference number: A82035; MUID:20406833; PMID:10952301

A:Accession: H82344

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-227 <HEI>

A:Cross-references: GB:AE004114; GB:AE003852; NID:g9654562; PIDN:AAF93433.1; GSPDB:GN001

A:Experimental source: serogroup O1; strain N16961; biotype El Tor

C:Genetics:

A:Gene: VC0258

A:Map position: 1

A;Status: preliminary  
A:Molecule type: DNA  
A;Residues: 1-286 <STR>  
A;Cross-references: EMBL:X59554; NID:g48381; PIDN:CAA42150.1; PID:g48399  
A;Note: sequence extracted from NCBI backbone (NCBIN:91922, NCBIIP:91924)  
C;Genetics:  
A;Gene: rfbT

Query Match 50.7%; Score 37; DB 2; Length 286;  
Best Local Similarity 63.6%; Pred. No. 1.2e+02;  
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 HECGRSGEAG 12  
Db 134 HFGCAIGENEG 144

RESULT 30  
H90066  
hypothetical protein SA2393 [imported] - Staphylococcus aureus (strain N315)  
C;Species: Staphylococcus aureus  
C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 22-Oct-2001  
C;Accession: H90066  
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogura, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.; Shibata, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.  
Lancet 357, 1225-1240, 2001  
A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.  
A;Reference number: A89758; UID:21311952; PMID:11418146  
A;Accession: H90066  
A;Status: preliminary  
A:Molecule type: DNA  
A;Residues: 1-286 <KUR>  
A;Cross-references: GB:BA000018; PID:g13702557; PIDN:BAB43698.1; GSPDB:GN00149  
A;Experimental source: strain N315  
C;Genetics:  
A;Gene: SA2393

Query Match 50.7%; Score 37; DB 2; Length 286;  
Best Local Similarity 60.0%; Pred. No. 1.2e+02;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 EGCRSGEAG 12  
Db 204 DGCVRQAEG 213

RESULT 31  
F86804  
basic membrane protein A [imported] - Lactococcus lactis subsp. lactis (strain IL1403)  
C;Species: Lactococcus lactis subsp. lactis  
C;Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 03-Aug-2001  
C;Accession: F86804  
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jallou, O.; Malarme, K.; Weissenbach, J.; Ehrlich, Genome Res. 11, 731-753, 2001  
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s  
A;Reference number: A86625; UID:21235186; PMID:11337471  
A;Accession: F86804  
A;Status: preliminary  
A:Molecule type: DNA  
A;Residues: 1-350 <STO>  
A;Cross-references: GB:AE005176; PID:g12724428; PIDN:AAK05536.1; GSPDB:GN00146  
A;Experimental source: strain IL1403  
C;Genetics:  
A;Gene: bmpA.

Query Match 50.7%; Score 37; DB 2; Length 350;  
Best Local Similarity 70.0%; Pred. No. 1.4e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GCRCRGAEGS 13  
Db 21 GCRSHDAAGS 30

```

RESULT 32
H83067
probable c-type cytochrome PA4619 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 21-Jul-2003
C:Accession: H83067
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
Nature 406, 959-964, 2000
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: H83067
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-415 <STO>
A:Cross-references: GB:AE004876; GB:AE004091; NID:g9950869; PIDN:AAG08007.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA4619
C:Superfamily: membrane-bound alcohol dehydrogenase, cytochrome c; cytochrome c6 homolog
C:Keywords: chromoprotein; heme; iron; metalloprotein
F:42/45/Binding site: heme (Cys) (covalent) #status predicted
F:46/Binding site: heme iron (His) (axial ligand) #status predicted
F:188/191/Binding site: heme (Cys) (covalent) #status predicted
F:192/Binding site: heme iron (His) (axial ligand) #status predicted
F:310/313/Binding site: heme (Cys) (covalent) #status predicted
F:314/Binding site: heme iron (His) (axial ligand) #status predicted
Query Match 50.7%; Score 37; DB 2; Length 415;
Best Local Similarity 66.7%; Pred. No. 1.6e+02; Mismatches 3; Indels 0; Gaps 0;
Matches 6; Conservative 0;
QY 4 GCRSGEAE 12
DB 312 GCHGSGEG 320

RESULT 33
A32947
filaggrin precursor - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 20-Dec-1989 #sequence_revision 04-Sep-1992 #text_change 29-Sep-1999
R:McKinley-Grant, L.J.; Idler, W.W.; Bernstein, I.A.; Parry, D.A.D.; Cannizzaro, L.; Cro
Proc. Natl. Acad. Sci. U.S.A. 86, 4848-4852, 1989
A:Title: Characterization of a cDNA clone encoding human filaggrin and localization of t
A:Reference number: A32947; MUID:89296901; PMID:2740331
A:Accession: A32947
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-416 <MCK>
A:Cross-references: GB:M24355; NID:g182604; PIDN:AAAS2454.1; PID:g182605
A:Note: the authors translated the codon CAC for residue 188 as Gln, and AAT for residue
C:Genetics:
A:Gene: GDB:FLG
A:Cross-references: GDB:119912; OMIM:135940
A:Map position: 1q21-q21
C:Superfamily: unassigned calmodulin-related proteins; calmodulin repeat homology
C:Keywords: EF hand; epidermis; polymorphism; tandem repeat
Query Match 50.7%; Score 37; DB 2; Length 416;
Best Local Similarity 53.8%; Pred. No. 1.6e+02;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 1 GHEGCRSGEAGS 13
DB 76 GHRGSSGGRQGS 88

RESULT 34
S34969
outer membrane porin OprE precursor PA0291 [imported] - Pseudomonas aeruginosa (strain F
C:Species: Pseudomonas aeruginosa
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 15-Jun-2001
C:Accession: S34969; E83608
R:Yamano, Y.; Nishikawa, T.; Komatsu, Y.
Mol. Microbiol. 8, 993-1004, 1993
A:Title: Cloning and nucleotide sequence of anaerobically induced porin protein E1 (OprE
A:Reference number: S34969; MUID:93360827; PMID:8394980
A:Accession: S34969
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-460 <YAM>
A:Cross-references: GB:D12711; NID:g433417; PIDN:BAA02207.1; PID:g433418
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
Nature 406, 959-964, 2000
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: E83608
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-460 <STO>
A:Cross-references: GB:AE004467; GB:AE004091; NID:g9946133; PIDN:AAG03680.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: oprE; PA0291
C:Superfamily: Pseudomonas aeruginosa outer membrane porin PA0958
Query Match 50.7%; Score 37; DB 2; Length 460;
Best Local Similarity 58.3%; Pred. No. 1.8e+02;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 GHEGCRSGEAG 12
DB 275 GKNGSRSGRADG 286

RESULT 35
S64126
cell division control protein CDC20 - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein G2939; protein YGL116w
C:Species: Saccharomyces cerevisiae
C:Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 26-May-2000
C:Accession: S64126; S18840; S48507
R:laquin, G.
Submitted to the Protein Sequence Database, May 1996
A:Reference number: S64122
A:Accession: S64126
A:Molecule type: DNA
A:Residues: 1-610 <LAU>
A:Cross-references: EMBL:Z72638; NID:g1322668; PIDN:CAA96824.1; PID:e243344; PID:g132266
A:Experimental source: strain S288C
R:Sethi, N.; Montesquido, M.C.; Koshland, D.; Hogan, E.; Burke, D.J.
Mol. Cell. Biol. 11, 5592-5602, 1991
A:Title: The CDC20 gene product of Saccharomyces cerevisiae, a beta-transducin homology,
A:Reference number: S18840; MUID:92017840; PMID:1922065
A:Accession: S18840
A:Molecule type: DNA
A:Residues: 1-317, 'MA', 320-501, 'ORMQSLFIIMKONS', 514, 'LOK' <SET>
A:Cross-references: EMBL:X59428; NID:g3644; PIDN:CAA42058.1; PID:g3645
A:Note: the authors translated the codon TAT for residue 220 as Gln
R:Doi, A.; Doi, K.
Submitted to the EMBL Data Library, June 1993
A:Description: Correct one of the ORF for the CDC20 gene of Saccharomyces cerevisiae.
A:Reference number: S48507
A:Accession: S48507
A:Molecule type: DNA
A:Residues: 50-610 <DOI>
A:Cross-references: EMBL:D16506; NID:g931938; PIDN:BAA03957.1; PID:d1004473; PID:g416288
C:Comment: This is a G-beta protein.
C:Genetics:

```

A;Gene: SGD: CDC20  
A;Cross-references: SGD: S0003084; MIPS: YGL116w  
A;Map position: 7L  
C;Function:  
A;Description: required for nuclear movements prior to anaphase; required for chromosome  
C;Superfamily: unassigned WD repeat proteins; WD repeat homology  
F: 381-414/Domain: WD repeat homology <WD1>

Query Match 50.7%; Score 37; DB 2; Length 610;  
Best Local Similarity 54.5%; Pred. No. 2.2e+02;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GHEGCRSGEAG 11  
| | | | | : |  
DB 577 GREGCRTNDKE 587

RESULT 36  
T00529  
hypothetical protein At2g19090 [imported] - Arabidopsis thaliana  
N;Alternate names: hypothetical protein T20K24.10  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 01-Feb-1999 #sequence\_revision 01-Feb-1999 #text\_change 16-Feb-2001  
C;Accession: T00529; D84572  
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,  
submitted to the EMBL Data Library, July 1997  
A;Description: Arabidopsis thaliana chromosome II BAC T20K24 genomic sequence.  
A;Reference number: Z14167  
A;Accession: T00529  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-844 <ROU>  
A;Cross-references: EMBL: AC002392; NID: G3176701; PID: G3176711  
A;Experimental source: cultivar Columbia  
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;  
cuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A;Reference number: A84420; MUID: 20083487; PMID: 10617197  
A;Accession: D84572  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-844 <STO>  
A;Cross-references: GB: AE002093; NID: G3176711; PIDN: AAD12027.1; GSPDB: GN00139  
C;Genetics:  
A;Gene: At2g19090; T20K24.10  
A;Map position: 2  
A;Introns: 439/1; 519/3; 594/2  
C;Superfamily: Arabidopsis thaliana hypothetical protein F6G3.160

Query Match 50.7%; Score 37; DB 2; Length 844;  
Best Local Similarity 63.6%; Pred. No. 3e+02; 3; Indels 0; Gaps 0;  
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 EGCRSGEAGS 13  
| | | | | : |  
DB 341 EVRCGGEATGN 351

RESULT 37  
T30200  
protein-tyrosine kinase (EC 2.7.1.112) alk - mouse  
N;Alternate names: anaplastic lymphoma kinase  
C;Species: Mus musculus (house mouse)  
C;Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 21-Jul-2000  
C;Accession: T30200  
R;Iwahara, T.; Fujimoto, J.; Wen, D.; Cupples, R.; Bucay, N.; Arakawa, T.; Mori, S.; Rat  
Oncogene 14, 439-449, 1997  
A;Title: Molecular characterization of ALK, a receptor tyrosine kinase expressed specif  
A;Reference number: Z20774; MUID: 97178863; PMID: 9053841  
A;Accession: T30200  
A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA  
A;Residues: 1-1621 <IWA>  
A;Cross-references: EMBL: D83002; NID: g1864006; PIDN: BAA11673.1; PID: g1864007  
A;Experimental source: brain and testis  
C;Genetics:  
A;Gene: alk  
C;Function:  
A;Description: may play an important role in development of the brain  
C;Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase

Query Match 50.7%; Score 37; DB 2; Length 1621;  
Best Local Similarity 54.5%; Pred. No. 5.2e+02;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 HEGCRSGEAG 12  
| | | | | : |  
DB 462 HQDCAQGEDEG 472

RESULT 38  
T00348  
LR11 protein - mouse  
N;Alternate names: gp250 precursor  
C;Species: Mus musculus (house mouse)  
C;Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 23-Sep-2002  
C;Accession: T00348; T09123  
R;Kanaki, T.; Bujo, H.; Hirayama, S.; Tanaka, K.; Yamazaki, H.; Seimiya, K.; Morisaki,  
DNA Cell Biol. 17, 647-657, 1998  
A;Title: Developmental regulation of LR11 expression in murine brain.  
A;Reference number: Z14140; MUID: 98392848; PMID: 9726247  
A;Accession: T00348  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-2215 <KAN>  
A;Cross-references: EMBL: AB015790; NID: G3273351; PIDN: BAA31219.1; PID: G3273352  
A;Experimental source: brain  
R;Hermann-Borgmeyer, I.; Hampe, W.; Schinke, B.; Methner, A.; Nykjaer, A.; Susens, U.;  
Mech. Dev. 70, 65-76, 1998  
A;Title: Unique expression pattern of a novel mosaic receptor in the developing cerebra  
A;Reference number: Z16574; MUID: 98168844; PMID: 9510025  
A;Accession: T09123  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 183-705; F, 707-767, F', 769-784, S', 786-795, G', 797-952, R', 954-1267, EQ', 1  
A;Cross-references: EMBL: AF031816; NID: G2654024; PIDN: AAC16739.1; PID: G2654025  
A;Experimental source: tissue type brain; cell line neuroblastoma x glioma cell line NH  
C;Genetics:  
A;Gene: LR11; sorLA  
C;Superfamily: LR11 protein; laminin-type EGF-like homology; LDL receptor ligand-binding  
C;Keywords: receptor; transmembrane protein  
F: 1078-1112/Domain: LDL receptor ligand-binding repeat homology <LDL1>  
F: 1117-1153/Domain: LDL receptor ligand-binding repeat homology <LDL2>  
F: 1158-1192/Domain: LDL receptor ligand-binding repeat homology <LDL4>  
F: 1199-1235/Domain: LDL receptor ligand-binding repeat homology <LDL5>  
F: 1239-1271/Domain: LDL receptor ligand-binding repeat homology <LDL6>  
F: 1275-1315/Domain: LDL receptor ligand-binding repeat homology <LDL7>  
F: 1325-1359/Domain: LDL receptor ligand-binding repeat homology <LDL8>  
F: 1368-1403/Domain: LDL receptor ligand-binding repeat homology <LDL9>  
F: 1419-1453/Domain: LDL receptor ligand-binding repeat homology <LDL10>  
F: 1471-1506/Domain: LDL receptor ligand-binding repeat homology <LDL11>  
F: 1514-1549/Domain: LDL receptor ligand-binding repeat homology <LDL12>

Query Match 50.7%; Score 37; DB 2; Length 2215;  
Best Local Similarity 38.5%; Pred. No. 6.9e+02;  
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 GHEGCRSGEAGS 13  
| | | | | : |  
DB 1493 GHQDCQDQGDAN 1505

RESULT 39  
A35938

profilaggrin - human (fragments)  
 C:Species: Homo sapiens (man)  
 C:Date: 14-Dec-1990 #sequence\_revision 02-Jul-1996 #text\_change 29-Sep-1999  
 C:Accession: A35938  
 R:Gan, S.O.; McBride, O.W.; Idler, W.W.; Markova, N.; Steinert, P.M.  
 Biochemistry 29, 9432-9440, 1990  
 A:Title: Organization, structure, and polymorphisms of the human profilaggrin gene.  
 A:Reference number: A35938; MUID:91064347; PMID:2248957  
 A:Accession: A35938  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 1-2248 <GAN>  
 A:Cross-references: GB:J02929  
 C:Genetics:  
 A:Gene: GDB:PLG  
 A:Cross-references: GDB:119912; OMIM:135940  
 A:Map position: 1q21-1q21  
 C:Superfamily: unassigned calmodulin-related proteins; calmodulin repeat homology  
 C:Keywords: Ef hand; epidermis; polymorphism; tandem repeat  
 F:246-569/Region: filaggrin repeat  
 F:570-893/Region: filaggrin repeat  
 F:1074-1397/Region: filaggrin repeat  
 F:1573-1896/Region: filaggrin repeat

Query Match 50.7%; Score 37; DB 2; Length 2248;  
 Best Local Similarity 53.8%; Pred. No. 7e+02; Mismatches 5; Indels 0; Gaps 0;  
 Matches 7; Conservative 1;

QY 1 GHEGCRSGEAE 13  
 ||||| :||  
 Db 1947 GHGSGRGRGQGS 1959

RESULT 40  
 T30890  
 calcium channel alpha-chain - sea squirt (Halocynthia roretzi)  
 N:Alternate names: ascidian calcium channel alpha-subunit  
 C:Species: Halocynthia roretzi  
 C:Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 20-Jun-2000  
 C:Accession: T30890  
 R:Okamura, Y.; Okagaki, R.  
 submitted to the EMBL Data Library, May 1998  
 A:Description: TuCa1, ascidian calcium channel alpha-subunit.  
 A:Reference number: Z20924  
 A:Accession: T30890  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-2262 <OKA>  
 A:Cross-references: EMBL:AB013604; PIDN:BAA34927.1  
 A:Experimental source: young tadpole larvae  
 C:Genetics:  
 A:Gene: TuCa1  
 C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain  
 C:Keywords: calcium binding; calcium channel

Query Match 50.7%; Score 37; DB 2; Length 2262;  
 Best Local Similarity 61.5%; Pred. No. 7e+02; Mismatches 1; Indels 2; Gaps 1;  
 Matches 8; Conservative 1;

QY 1 GHEGCRSGEAE 11  
 ||||| :||  
 Db 2239 GHEGCIERDEAD 2251

RESULT 41  
 H96665  
 protein F22C12.10 [imported] - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
 C:Accession: H96665  
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, T.H.; Dewar, K.;  
 ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000  
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,  
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
 A:Reference number: A86141; MUID:21016719; PMID:11130712  
 A:Accession: H96665  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-646 <STO>  
 A:Cross-references: GB:AE005173; NID:G6692098; PIDN:AAF24563.1; GSPDB:GN00141  
 C:Genetics:  
 A:Gene: F22C12.10  
 A:Map position: 1

Query Match 50.0%; Score 36.5; DB 2; Length 646;  
 Best Local Similarity 66.7%; Pred. No. 2.9e+02;  
 Matches 8; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 2 HEGCRSGEAE 13  
 ||||| :||  
 Db 411 HSGCTKG-AEGS 421

RESULT 42  
 S39416  
 metallothionein 10-I - blue mussel  
 C:Species: Mytilus edulis (blue mussel)  
 C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 17-Mar-1999  
 C:Accession: S39416  
 R:Mackay, E.A.; Overnell, J.; Dunbar, B.; Davidson, I.; Hunziker, P.E.; Kaegi, J.H.R.;  
 Eur. J. Biochem. 218, 183-194, 1993  
 A:Title: Complete amino acid sequences of five dimeric and four monomeric forms of meta-  
 A:Reference number: S39416; MUID:94062828; PMID:8243463  
 A:Accession: S39416  
 A:Molecule type: protein  
 A:Residues: 1-72 <MAC>  
 C:Superfamily: metallothionein  
 C:Keywords: metal binding

Query Match 49.3%; Score 36; DB 2; Length 72;  
 Best Local Similarity 75.0%; Pred. No. 52;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 EGCRSGEA 10  
 ||||| :||  
 Db 21 EGCRGCGDA 28

RESULT 43  
 S39418  
 metallothionein 10-III - blue mussel  
 C:Species: Mytilus edulis (blue mussel)  
 C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 17-Mar-1999  
 C:Accession: S39418  
 R:Mackay, E.A.; Overnell, J.; Dunbar, B.; Davidson, I.; Hunziker, P.E.; Kaegi, J.H.R.;  
 Eur. J. Biochem. 218, 183-194, 1993  
 A:Title: Complete amino acid sequences of five dimeric and four monomeric forms of meta-  
 A:Reference number: S39416; MUID:94062828; PMID:8243463  
 A:Accession: S39418  
 A:Molecule type: protein  
 A:Residues: 1-72 <MAC>  
 C:Superfamily: metallothionein  
 C:Keywords: metal binding

Query Match 49.3%; Score 36; DB 2; Length 72;  
 Best Local Similarity 75.0%; Pred. No. 52;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 EGCRSGEA 10  
 ||||| :||

```
Db      21  EGCRCGDA 28

RESULT 44
S39419
metallothionein 10-IV - blue mussel
C:Species: Mytilus edulis (blue mussel)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-1999
C:Accession: S39419
R:MacKay, E.A.; Overnell, J.; Dunbar, B.; Davidson, I.; Hunziker, P.E.; Kaegi, J.H.R.; F
Eur. J. Biochem. 218, 183-194, 1993
A:Title: Complete amino acid sequences of five dimeric and four monomeric forms of metal
A:Reference number: S39416; MUID:94062828; PMID:8243463
A:Accession: S39419
A:Molecule type: protein
A:Residues: 1-72 <MAC>
C:Superfamily: metallothionein
C:Keywords: metal binding

Query Match      49.3%; Score 36; DB 2; Length 72;
Best Local Similarity 75.0%; Pred. No. 52;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3  EGCRCGEA 10
      ||||| |
Db      21  EGCRCGDA 28

RESULT 45
S39417
metallothionein 10-II - blue mussel
C:Species: Mytilus edulis (blue mussel)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-1999
C:Accession: S39417
R:MacKay, E.A.; Overnell, J.; Dunbar, B.; Davidson, I.; Hunziker, P.E.; Kaegi, J.H.R.; F
Eur. J. Biochem. 218, 183-194, 1993
A:Title: Complete amino acid sequences of five dimeric and four monomeric forms of metal
A:Reference number: S39416; MUID:94062828; PMID:8243463
A:Accession: S39417
A:Molecule type: protein
A:Residues: 1-72 <MAC>
C:Superfamily: metallothionein
C:Keywords: metal binding

Query Match      49.3%; Score 36; DB 2; Length 72;
Best Local Similarity 75.0%; Pred. No. 52;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3  EGCRCGEA 10
      ||||| |
Db      21  EGCRCGDA 28

RESULT 46
H97316
hypothetical protein CAC3393 [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C:Accession: H97316
R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: H97316
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-111 <KUR>
A:Cross-references: GB:AE001437; PIDN:AAK81323.1; PID:g15026479; GSPDB:GNO0168
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC3393

Db      21  EGCRCGDA 28

Query Match      49.3%; Score 36; DB 2; Length 111;
Best Local Similarity 55.6%; Pred. No. 75;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      2  HEGCRSGEA 10
      |.|||.||
Db      56  HKGCKAAEA 64

RESULT 47
AB1004
peptidylprolyl isomerase (EC 5.2.1.8) - Salmonella enterica subsp. enterica serovar Typhi
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AB1004
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher
th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AB1004
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-196 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD08158.1; PID:g16505134; GSPDB:GNO0176
C:Genetics:
A:Gene: glyD
C:Keywords: cis-trans-isomerase

Query Match      49.3%; Score 36; DB 2; Length 196;
Best Local Similarity 53.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY      1  GHEGCRSGEAGS 13
      ||||| |
Db      180  GGGCGCGGGGKGS 192

RESULT 48
D65095
hypothetical protein b3071 - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C:Accession: D65095
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: D65095
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-207 <BLAT>
A:Cross-references: GB:AE000389; GB:U00096; NID:g1789451; PIDN:AACT6106.1; PID:g1789452.
A:Experimental source: strain K-12, substrain MG1655

Query Match      49.3%; Score 36; DB 2; Length 207;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2  HEGCRSGE 9
      ||||| |
Db      17  HEGCKCKGE 24

RESULT 49
A98123
hypothetical protein ECs3953 [imported] - Escherichia coli (strain O157:H7, substrain R
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
```

C/Accession: A98123  
 R:Havashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
 Gnaawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
 DNA Res. 8, 11-22, 2001  
 A>Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen  
 A/Reference number: A99629; MUID:21156231; PMID:11258796

A/Accession: A98123  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A/Residues: 1-207 <HAY>  
 A/Cross-references: GB:BA000007; PIDN:BA837376.1; PID:gi33363426; GSPDB:GN00154  
 A/Experimental source: strain O157:H7, substrain RIMD 0509952  
 C/Genetics:  
 A/Gene: ECs3953

Query Match 49.3%; Score 36; DB 2; Length 207;  
 Best Local Similarity 75.0%; Pred. No. 1.3e+02;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 HEGCRSGE 9  
 |||||  
 Db 17 HEGCCKGE 24

## RESULT 50

H85967  
 hypothetical protein yqjI [imported] - Escherichia coli (strain O157:H7, substrain EDL93  
 C/Species: Escherichia coli  
 C/Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001  
 C/Accession: H85967  
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
 iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,  
 Nature 409, 529-533, 2001  
 A>Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
 A/Reference number: A85480; MUID:21074935; PMID:11206551  
 A/Accession: H85967  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A/Residues: 1-207 <STO>  
 A/Cross-references: GB:AE005174; NID:gl2517652; PIDN:AG58204.1; GSPDB:GN00145; UWGP:244  
 A/Experimental source: strain O157:H7, substrain EDL933  
 C/Genetics:  
 A/Gene: yqjI

Query Match 49.3%; Score 36; DB 2; Length 207;  
 Best Local Similarity 75.0%; Pred. No. 1.3e+02;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 HEGCRSGE 9  
 |||||  
 Db 17 HEGCCKGE 24

Search completed: April 19, 2004, 17:23:17  
 Job time : 15 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 19, 2004, 17:13:16 ; Search time 17.1935 Seconds  
(without alignments)  
39.034 Million cell updates/sec

Title: US-10-726-692-22

Perfect score: 71

Sequence: 1 SHEGCRSAGEAGS 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/prodata/2/iaa/5A COMB.pep:\*\*
- 2: /cgn2\_6/prodata/2/iaa/5B COMB.pep:\*\*
- 3: /cgn2\_6/prodata/2/iaa/6A COMB.pep:\*\*
- 4: /cgn2\_6/prodata/2/iaa/6B COMB.pep:\*\*
- 5: /cgn2\_6/prodata/2/iaa/PCTUS COMB.pep:\*\*
- 6: /cgn2\_6/prodata/2/iaa/backfiles1.pcp:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	59.2	187	4	US-09-252-991A-26696
2	41	57.7	711	4	US-09-252-991A-32397
3	41	57.7	846	1	US-08-356-354-2
4	41	57.7	846	2	US-08-778-656-2
5	41	57.7	908	1	US-08-356-354-6
6	41	57.7	908	2	US-08-778-656-6
7	41	57.7	1053	4	US-09-394-272-6
8	41	57.7	1054	1	US-08-356-354-4
9	41	57.7	1054	2	US-08-778-656-4
10	40	56.3	469	4	US-09-347-650-16
11	40	56.3	489	4	US-09-252-991A-16940
12	39	54.9	193	4	US-09-252-991A-24586
13	39	54.9	268	4	US-09-461-325-346
14	39	54.9	268	4	US-10-012-542-346
15	38	53.5	142	4	US-09-252-991A-23673
16	38	53.5	184	4	US-09-252-991A-26628
17	38	53.5	458	4	US-09-252-991A-30327
18	37	52.1	223	4	US-09-252-991A-27694
19	37	52.1	372	4	US-09-252-991A-31788
20	37	52.1	593	4	US-09-252-991A-30673
21	37	52.1	875	4	US-09-252-991A-30056
22	36	50.7	115	4	US-09-800-729-126
23	36	50.7	128	4	US-09-071-035-434
24	36	50.7	135	4	US-09-134-000C-6310
25	36	50.7	151	4	US-09-252-991A-25250
26	36	50.7	176	4	US-09-252-991A-18408
27	36	50.7	201	4	US-09-252-991A-27995

28	36	50.7	250	4	US-09-252-991A-27781	Sequence 27781, A
29	36	50.7	258	4	US-09-252-991A-23894	Sequence 23894, A
30	36	50.7	392	4	US-09-252-991A-20001	Sequence 20001, A
31	36	50.7	434	4	US-09-252-991A-25043	Sequence 25043, A
32	36	50.7	466	4	US-09-724-864-44	Sequence 44, Appl
33	36	50.7	553	4	US-09-252-991A-32621	Sequence 32621, A
34	36	50.7	626	1	US-07-938-782A-2	Sequence 2, Appli
35	36	50.7	626	1	US-08-630-524-2	Sequence 2, Appli
36	36	50.7	626	4	US-09-578-441-5	Sequence 5, Appli
37	36	50.7	626	5	PCT-US93-08131-2	Sequence 2, Appli
38	36	50.7	685	4	US-09-252-991A-32382	Sequence 32382, A
39	36	50.7	1073	4	US-09-252-991A-27341	Sequence 27341, A
40	36	50.7	1197	4	US-09-618-425-2	Sequence 2, Appli
41	35	49.3	68	2	US-08-117-952-772	Sequence 772, App
42	35	49.3	151	4	US-09-252-991A-27007	Sequence 27007, A
43	35	49.3	154	4	US-09-252-991A-32846	Sequence 32846, A
44	35	49.3	178	4	US-09-252-991A-22153	Sequence 22153, A
45	35	49.3	188	4	US-09-252-991A-28878	Sequence 28878, A
46	35	49.3	282	3	US-09-120-365-79	Sequence 79, Appl
47	35	49.3	282	3	US-09-515-039-79	Sequence 79, Appl
48	35	49.3	301	4	US-09-252-991A-25370	Sequence 25370, A
49	35	49.3	341	4	US-09-252-991A-27327	Sequence 27327, A
50	35	49.3	348	4	US-09-252-991A-21706	Sequence 21706, A

#### ALIGNMENTS

RESULT 1  
US-09-252-991A-26696  
; Sequence 26696, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 26696  
; LENGTH: 187  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-26696  
Query Match 59.2%; Score 42; DB 4; Length 187;  
Best Local Similarity 77.8%; Pred. No. 13;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 4 GCRSAGEAG 12  
DB 1 GCRSAGEAG 9  
RESULT 2  
US-09-252-991A-32397  
; Sequence 32397, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190

;  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 32397  
; LENGTH: 711  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-32397

Query Match 57.7%; Score 41; DB 4; Length 711;  
Best Local Similarity 50.0%; Pred. No. 71;  
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 HEGCRSGEAEGS 13  
| | | | | :  
Db 251 HPGCRHGDRGT 262

RESULT 3  
US-08-356-354-2  
; Sequence 2, Application US/08356354  
; Patent No. 5767365  
; GENERAL INFORMATION:  
; APPLICANT: SONNEWALD, Uwe  
; TITLE OF INVENTION: DNA SEQUENCES AND PLASMIDS FOR THE  
; PREPARATION OF PLANTS WITH CHANGED SUCROSE CONCENTRATION  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen  
; STREET: 1180 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: US  
; ZIP: 10036-8403  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/356,354  
; FILING DATE: 20-DEC-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US PCT/EP93/01605  
; FILING DATE: 22-JUN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meilman, Edward A.  
; REGISTRATION NUMBER: 24,735  
; REFERENCE/DOCKET NUMBER: P/951-105  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 382-0700  
; TELEFAX: (212) 382-0888  
; TELEX: 236925  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 846 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-356-354-2

Query Match 57.7%; Score 41; DB 1; Length 846;  
Best Local Similarity 66.7%; Pred. No. 84;  
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 HEGCRSGEAEGS 13  
| | | | | :  
Db 232 HEGMDGETEGS 243

RESULT 4  
US-08-778-656-2  
; Sequence 2, Application US/08778656  
; Patent No. 5976869  
; GENERAL INFORMATION:  
; APPLICANT: SONNEWALD, Uwe  
; TITLE OF INVENTION: DNA SEQUENCES AND PLASMIDS FOR THE  
; PREPARATION OF PLANTS WITH CHANGED SUCROSE CONCENTRATION  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen  
; STREET: 1180 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: US  
; ZIP: 10036-8403  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/778,656  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/356,354  
; FILING DATE: 20-DEC-1994  
; APPLICATION NUMBER: US PCT/EP93/01605  
; FILING DATE: 22-JUN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE P42 20 758.4  
; FILING DATE: 24-JUN-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meilman, Edward A.  
; REGISTRATION NUMBER: 24,735  
; REFERENCE/DOCKET NUMBER: P/951-105  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 382-0700  
; TELEFAX: (212) 382-0888  
; TELEX: 236925  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 846 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-778-656-2

Query Match 57.7%; Score 41; DB 2; Length 846;  
Best Local Similarity 66.7%; Pred. No. 84;  
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 HEGCRSGEAEGS 13  
| | | | | :  
Db 232 HEGMDGETEGS 243

RESULT 5  
US-08-356-354-6  
; Sequence 6, Application US/08356354  
; Patent No. 5767365  
; GENERAL INFORMATION:  
; APPLICANT: SONNEWALD, Uwe  
; TITLE OF INVENTION: DNA SEQUENCES AND PLASMIDS FOR THE  
; PREPARATION OF PLANTS WITH CHANGED SUCROSE CONCENTRATION  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen  
; STREET: 1180 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: US

ZIP: 10036-8403  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/356,354  
FILING DATE: 20-DEC-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US PCT/EP93/01605  
FILING DATE: 22-JUN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P42 20 758.4  
FILING DATE: 24-JUN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Meilman, Edward A.  
REGISTRATION NUMBER: 24,735  
REFERENCE/DOCKET NUMBER: P/951-105  
TELEPHONE: (212) 382-0700  
TELEFAX: (212) 382-0888  
TELEX: 236925  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 908 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-356-354-6

Query Match 57.7%; Score 41; DB 1; Length 908;  
Best Local Similarity 66.7%; Pred. No. 90;  
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 HEGCRSGEAECS 13  
||| |||  
Db 294 HEGDMDGETEGS 305

RESULT 6  
US-08-778-656-6  
Sequence 6, Application US/08778656  
Patent No. 5976869  
GENERAL INFORMATION:  
APPLICANT: SONNEWALD, Uwe  
TITLE OF INVENTION: DNA SEQUENCES AND PLASMIDS FOR THE PREPARATION OF PLANTS WITH CHANGED SUCROSE CONCENTRATION  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen  
STREET: 1180 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: US  
ZIP: 10036-8403  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/778,656  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/356,354  
FILING DATE: 20-DEC-1994  
APPLICATION NUMBER: US PCT/EP93/01605  
FILING DATE: 22-JUN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P42 20 758.4

FILING DATE: 24-JUN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Meilman, Edward A.  
REGISTRATION NUMBER: 24,735  
REFERENCE/DOCKET NUMBER: P/951-105  
TELEPHONE: (212) 382-0700  
TELEFAX: (212) 382-0888  
TELEX: 236925  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 908 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-778-656-6

Query Match 57.7%; Score 41; DB 2; Length 908;  
Best Local Similarity 66.7%; Pred. No. 90;  
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 HEGCRSGEAECS 13  
||| |||  
Db 294 HEGDMDGETEGS 305

RESULT 7  
US-09-394-272-6  
Sequence 6, Application US/09394272  
Patent No. 6472588  
GENERAL INFORMATION:  
APPLICANT: Haigler, Candace H.  
APPLICANT: Holaday, A. Scott  
TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED  
TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE  
FILE REFERENCE: 201304/1000  
CURRENT APPLICATION NUMBER: US/09/394,272  
CURRENT FILING DATE: 1999-09-10  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 6  
LENGTH: 1053  
TYPE: PRT  
ORGANISM: Solanum tuberosum  
US-09-394-272-6

Query Match 57.7%; Score 41; DB 4; Length 1053;  
Best Local Similarity 66.7%; Pred. No. 14+02; 4; Indels 0; Gaps 0;  
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 HEGCRSGEAECS 13  
||| |||  
Db 439 HEGDMDGETEGS 450

RESULT 8  
US-08-356-354-4  
Sequence 4, Application US/08356354  
Patent No. 5767365  
GENERAL INFORMATION:  
APPLICANT: SONNEWALD, Uwe  
TITLE OF INVENTION: DNA SEQUENCES AND PLASMIDS FOR THE  
TITLE OF INVENTION: PREPARATION OF PLANTS WITH CHANGED SUCROSE CONCENTRATION  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen  
STREET: 1180 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: US  
ZIP: 10036-8403  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/356,354  
FILING DATE: 20-DEC-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US PCT/EP93/01605  
FILING DATE: 22-JUN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P42 20 758.4  
FILING DATE: 24-JUN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Meilman, Edward A.  
REGISTRATION NUMBER: 24,735  
REFERENCE/DOCKET NUMBER: P/951-105  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 382-0700  
TELEFAX: (212) 382-0888  
TELEX: 236925  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1054 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-356-354-4

Query Match 57.7%; Score 41; DB 1; Length 1054;  
Best Local Similarity 66.7%; Pred. No. 1e+02;  
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 2 HEGCRSGEAEGS 13  
||| |||  
DB 440 HEGDMDGETEGS 451

RESULT 9  
US-08-778-656-4  
Sequence 4, Application US/08778656  
Patent No. 5976869  
GENERAL INFORMATION:  
APPLICANT: SONNEWALD, Uwe  
TITLE OF INVENTION: DNA SEQUENCES AND PLASMIDS FOR THE  
PREPARATION OF PLANTS WITH CHANGED SUCROSE CONCENTRATION  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen  
STREET: 1180 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: US  
ZIP: 10036-8403  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/778,656  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/356,354  
FILING DATE: 20-DEC-1994  
APPLICATION NUMBER: US PCT/EP93/01605  
FILING DATE: 22-JUN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P42 20 758.4  
FILING DATE: 24-JUN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Meilman, Edward A.

REGISTRATION NUMBER: 24,735  
REFERENCE/DOCKET NUMBER: P/951-105  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 382-0700  
TELEFAX: (212) 382-0888  
TELEX: 236925  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1054 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-778-656-4

Query Match 57.7%; Score 41; DB 2; Length 1054;  
Best Local Similarity 66.7%; Pred. No. 1e+02;  
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 2 HEGCRSGEAEGS 13  
||| |||  
DB 440 HEGDMDGETEGS 451

RESULT 10  
US-09-347-650-16  
Sequence 16, Application US/09347650  
Patent No. 6576814  
GENERAL INFORMATION:  
APPLICANT: Briggs, Steven  
TITLE OF INVENTION: Manipulation of Mlo Genes to Enhance Disease Resistance  
FILE REFERENCE: 5718-42035718/158714  
CURRENT APPLICATION NUMBER: US/09/347,650  
CURRENT FILING DATE: 1999-07-06  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 16  
LENGTH: 469  
TYPE: PRT  
ORGANISM: Zea mays  
FEATURE:  
OTHER INFORMATION: Mlo9  
US-09-347-650-16

Query Match 56.3%; Score 40; DB 4; Length 469;  
Best Local Similarity 75.0%; Pred. No. 68;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SHEGCRSG 8  
:|||||  
DB 13 NHEGCRG 20

RESULT 11  
US-09-252-991A-16940  
Sequence 16940, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 16940  
LENGTH: 489  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-16940

Query Match 56.3%; Score 40; DB 4; Length 489;  
Best Local Similarity 77.8%; Pred. No. 71;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCRSGEAG 12  
|||:|||||

Db 354 GCRAGEAG 362

RESULT 12

US-09-252-991A-24586  
; Sequence 24586, Application US/09252991A

; Patent No. 6551795  
; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 24586

; LENGTH: 193

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

; FEATURES:

; NAME/KEY: UNSURE

; LOCATION: (56)

; OTHER INFORMATION: Identity of amino acid at the above locations are unknown.

US-09-252-991A-24586

Query Match 54.9%; Score 39; DB 4; Length 193;

Best Local Similarity 53.8%; Pred. No. 41;

Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 SHEGCRSGEAGS 13

|||:|||||

Db 15 SHAACRSQGQGA 27

RESULT 13

US-09-461-325-346

; Sequence 346, Application US/09461325A

; Patent No. 6475753

; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: 94 Human Secreted Proteins

; FILE REFERENCE: PZ029P1

; CURRENT APPLICATION NUMBER: US/09/461,325A

; CURRENT FILING DATE: 1999-12-14

; EARLIER APPLICATION NUMBER: PCT/US99/13418

; EARLIER FILING DATE: 1999-06-15

; EARLIER APPLICATION NUMBER: 60/089,507

; EARLIER FILING DATE: 1998-06-16

; EARLIER APPLICATION NUMBER: 60/089,508

; EARLIER FILING DATE: 1998-06-16

; EARLIER APPLICATION NUMBER: 60/089,509

; EARLIER FILING DATE: 1998-06-16

; EARLIER APPLICATION NUMBER: 60/089,510

; EARLIER FILING DATE: 1998-06-16

; EARLIER APPLICATION NUMBER: 60/090,112

; EARLIER FILING DATE: 1998-06-22

; EARLIER APPLICATION NUMBER: 60/090,113

; EARLIER FILING DATE: 1998-06-22

; NUMBER OF SEQ ID NOS: 532

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 346

; LENGTH: 268

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SITE

; LOCATION: (83)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; FEATURE:

; NAME/KEY: SITE

; LOCATION: (137)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; FEATURE:

; NAME/KEY: SITE

; LOCATION: (141)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-461-325-346

Query Match 54.9%; Score 39; DB 4; Length 268;

Best Local Similarity 63.6%; Pred. No. 57;

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SHEGCRSGEAE 11

|||||

Db 225 SHEGCAQPEAQ 235

RESULT 14

US-10-012-542-346

; Sequence 346, Application US/10012542

; Patent No. 6627741

; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: 94 Human Secreted Proteins

; FILE REFERENCE: PZ029P1

; CURRENT APPLICATION NUMBER: US/10/012,542

; CURRENT FILING DATE: 2001-12-12

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/461,325

; PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-14

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,507

; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,508

; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,509

; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,510

; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,112

; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,113

; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22

; NUMBER OF SEQ ID NOS: 532

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 346

; LENGTH: 268

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SITE

; LOCATION: (83)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (137)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (141)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-10-012-542-346

Query Match 54.9%; Score 39; DB 4; Length 268;

Best Local Similarity 63.6%; Pred. No. 57;

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SHEGCRSGEAE 11

```
Db      225 SHEGCAPOEAQ 235
||||| ||:
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30327
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30327

Query Match      53.5%; Score 38; DB 4; Length 458;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      3 EGCRSGEAG 12
       :||::||
Db      27 QCCQAGDGE 36

RESULT 18
US-09-252-991A-27694
; Sequence 27694, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27694
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27694

Query Match      52.1%; Score 37; DB 4; Length 223;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 HEGCRSGEA 10
       :|||:|
Db      66 HRCRQGPA 74

RESULT 19
US-09-252-991A-31788
; Sequence 31788, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31788
; LENGTH: 372

Db      225 SHEGCAPOEAQ 235
||||| ||:
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09252991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23673
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23673

Query Match      53.5%; Score 38; DB 4; Length 142;
Best Local Similarity 60.0%; Pred. No. 44;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      4 GCRSGEAGS 13
       :|||:|
Db      129 GCRSGSSRA 138

RESULT 16
US-09-252-991A-26628
; Sequence 26628, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26628
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26628

Query Match      53.5%; Score 38; DB 4; Length 184;
Best Local Similarity 66.7%; Pred. No. 57;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      4 GCRSGEAG 12
       :|||:|
Db      1 GCRTGSAGK 9

RESULT 17
US-09-252-991A-30327
; Sequence 30327, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
```

; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-31788

Query Match 52.1%; Score 37; DB 4; Length 372;  
Best Local Similarity 66.7%; Pred. No. 1.7e+02;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GCRSGEAG 12  
|||  
DB 50 GCHGGEAG 58

## RESULT 20

US-09-252-991A-30673  
; Sequence 30673, Application US/09252991A  
; Patent No. 6551795

## GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 30673  
; LENGTH: 593  
; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-30673

Query Match 52.1%; Score 37; DB 4; Length 593;  
Best Local Similarity 66.7%; Pred. No. 2.6e+02;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GCRSGEAG 12  
|||  
DB 490 GCHGGEAG 498

## RESULT 21

US-09-252-991A-30056  
; Sequence 30056, Application US/09252991A  
; Patent No. 6551795

## GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 30056  
; LENGTH: 875  
; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-30056

Query Match 52.1%; Score 37; DB 4; Length 875;  
Best Local Similarity 71.4%; Pred. No. 3.9e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 HEGCRSG 8  
|:|:|:|  
DB 158 HQGCRAG 164

## RESULT 22

US-09-800-729-126  
; Sequence 126, Application US/09800729  
; Patent No. 6605592

## GENERAL INFORMATION:

; APPLICANT: Ni et al.  
; TITLE OF INVENTION: 32 Human secreted proteins  
; FILE REFERENCE: P2044P1  
; CURRENT APPLICATION NUMBER: US/09/800,729  
; CURRENT FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: PCT/US00/26013  
; PRIOR FILING DATE: 2000-09-22  
; PRIOR APPLICATION NUMBER: 60/155,709  
; PRIOR FILING DATE: 1999-09-24  
; NUMBER OF SEQ ID NOS: 217  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 126  
; LENGTH: 115  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (101)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (106)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-800-729-126

Query Match 50.7%; Score 36; DB 4; Length 115;  
Best Local Similarity 54.5%; Pred. No. 75;  
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 SHEGCRSGEAE 11  
|:|:|:|:|  
DB 87 SKGCGACGAD 97

## RESULT 23

US-09-071-035-434  
; Sequence 434, Application US/09071035  
; Patent No. 6448043

## GENERAL INFORMATION:

; APPLICANT: Gil H. Choi  
; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides  
; NUMBER OF SEQUENCES: 496  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/071.035  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: A. Anders Brookes  
; REGISTRATION NUMBER: 36,373  
; REFERENCE/DOCKET NUMBER: PB369P2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 309-8504

```
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 434:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 128 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-09-071-035-434

Query Match      50.7%; Score 36; DB 4; Length 128;
Best Local Similarity 75.0%; Pred. No. 84;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      4 GCRSGEAE 11
Db      16 GCKSGEKE 23

RESULT 24
US-09-134-000C-6310
; Sequence 6310, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6310
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-6310

Query Match      50.7%; Score 36; DB 4; Length 135;
Best Local Similarity 75.0%; Pred. No. 88;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      4 GCRSGEAE 11
Db      23 GCKSGEKE 30

RESULT 25
US-09-252-991A-25250
; Sequence 25250, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25250
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25250

Query Match      50.7%; Score 36; DB 4; Length 151;
Best Local Similarity 66.7%; Pred. No. 98;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      4 GCRSGEAE 12
Db      26 GCRSGQHNG 34

RESULT 26
US-09-252-991A-18408
; Sequence 18408, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18408
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18408

Query Match      50.7%; Score 36; DB 4; Length 176;
Best Local Similarity 77.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5 CRSGEAECS 13
Db      18 CRSGAAGPS 26

RESULT 27
US-09-252-991A-27995
; Sequence 27995, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27995
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27995

Query Match      50.7%; Score 36; DB 4; Length 201;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      3 EGRSGEAE 12
Db      38 ETCRNGSAQ 47

RESULT 28
US-09-252-991A-27781
; Sequence 27781, Application US/09252991A
; Patent No. 6551795
```



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; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27781
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27781

Query Match          50.7%; Score 36; DB 4; Length 250;
Best Local Similarity 77.8%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5 CRSGEAGS 13
Db      39 CRSGYARGS 47

RESULT 29
US-09-252-991A-23894
; Sequence 23894, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23894
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23894

Query Match          50.7%; Score 36; DB 4; Length 258;
Best Local Similarity 61.5%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1 SHEGCRSGEAGS 13
Db      208 SHIGCSGGCASDS 220

RESULT 30
US-09-252-991A-20001
; Sequence 20001, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
```

```
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20001
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (47)
; OTHER INFORMATION: Identity of amino acid at the above locations are unknown.
US-09-252-991A-20001

Query Match          50.7%; Score 36; DB 4; Length 392;
Best Local Similarity 66.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      5 CRSGEAGS 13
Db      49 CRGGHADGS 57

RESULT 31
US-09-252-991A-25043
; Sequence 25043, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25043
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25043

Query Match          50.7%; Score 36; DB 4; Length 434;
Best Local Similarity 63.6%; Pred. No. 2.8e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2 HEGCRSGEAG 12
Db      66 HRGVVGGEAG 76

RESULT 32
US-09-724-864-44
; Sequence 44, Application US/09724864
; Patent No. 6380362
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Murison, James G.
; TITLE OF INVENTION: Polynucleotides, polypeptides expressed
; FILE REFERENCE: 11000.1050U1
; CURRENT APPLICATION NUMBER: US/09/724,864
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Mouse
US-09-724-864-44
```

```
Query Match          50.7%; Score 36; DB 4; Length 466;
Best Local Similarity 45.5%; Pred. No. 3e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 EGRSGEAEAGS 13
DB 267 QGCRGRLDGA 277

RESULT 33
US-09-252-991A-32621
; Sequence 32621, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 32621
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32621

Query Match          50.7%; Score 36; DB 4; Length 553;
Best Local Similarity 63.6%; Pred. No. 3.6e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SHEGCRSGEAE 11
DB 419 SHGTGAGAE 429

RESULT 34
US-07-938-782A-2
; Sequence 2, Application US/07938782A
; Patent No. 5525513
; GENERAL INFORMATION:
; APPLICANT: Chen, Jane J.
; TITLE OF INVENTION: DNA Encoding the Heme-Regulated
; TITLE OF INVENTION: Burkaryotic Initiation Factor 2 alpha kinase
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: US
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/938,782A
; FILING DATE: 31-AUG-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: WU101CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)873-8794
```

```
TELEFAX: (404)873-8795
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 626 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Rabbit
; CELL TYPE: Reticulocytes
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 166..170
; OTHER INFORMATION: /label= P-56
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 454..459
; OTHER INFORMATION: /label= P-52
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 506..510
; OTHER INFORMATION: /label= P-74
US-07-938-782A-2

Query Match          50.7%; Score 36; DB 1; Length 626;
Best Local Similarity 77.8%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCRSGEAEAG 12
DB 7 GTRGGEAG 15

RESULT 35
US-08-630-524-2
; Sequence 2, Application US/08630524
; Patent No. 5690930
; GENERAL INFORMATION:
; APPLICANT: Chen, Jane J.
; TITLE OF INVENTION: DNA Encoding the Heme-Regulated
; TITLE OF INVENTION: Burkaryotic Initiation Factor 2 alpha kinase
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: US
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,524
; FILING DATE: 10-APR-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938,782
; FILING DATE: 31-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: WU101CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)873-8794
```

TELEFAX: (404)873-8795  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 626 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Rabbit  
CELL TYPE: Reticulocytes  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 454..459  
OTHER INFORMATION: /label= P-52  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 506..510  
OTHER INFORMATION: /label= P-74  
US-08-630-524-2

Query Match 50.7%; Score 36; DB 1; Length 626;  
Best Local Similarity 77.8%; Pred. No. 4.1e+02;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCRSGEAG 12  
| | | | |  
DB 7 GTRGGEAG 15

RESULT 36  
US-09-578-441-5  
Sequence 5, Application US/09578441  
Patent No. 6562571  
GENERAL INFORMATION:  
APPLICANT: Wu, J.H. David  
APPLICANT: Omasa, Takeshi  
APPLICANT: Mantalaris, Athanasios  
APPLICANT: Chen, Yi-Guang  
APPLICANT: Tsai, Ying-Chueh  
TITLE OF INVENTION: HUMAN HEME-REGULATED INITIATION FACTOR 2.ALPHA KINASE  
FILE REFERENCE: 176/60571  
CURRENT APPLICATION NUMBER: US/09/578,441  
CURRENT FILING DATE: 2000-05-25  
PRIOR APPLICATION NUMBER: 60/135,713  
PRIOR FILING DATE: 1999-05-25  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 5  
LENGTH: 626  
TYPE: PRT  
ORGANISM: Oryctolagus cuniculus  
US-09-578-441-5

Query Match 50.7%; Score 36; DB 4; Length 626;  
Best Local Similarity 77.8%; Pred. No. 4.1e+02;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCRSGEAG 12  
| | | | |  
DB 7 GTRGGEAG 15

RESULT 37  
PCT-US93-08131-2  
Sequence 2, Application PC/TUS9308131

GENERAL INFORMATION:  
APPLICANT: Massachusetts Institute Of Technology  
TITLE OF INVENTION: DNA Encoding the Heme-Regulated  
TITLE OF INVENTION: Eukaryotic Initiation Factor 2 alpha Kinase  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kilpatrick & Cody  
STREET: 1100 Peachtree Street  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: US  
ZIP: 30309  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/08131  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: MIT 5807  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404-815-6508  
TELEFAX: 404-815-6555  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 626 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Rabbit  
CELL TYPE: Reticulocytes  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 166..170  
OTHER INFORMATION: /label= P-56  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 454..459  
OTHER INFORMATION: /label= P-52  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 506..510  
OTHER INFORMATION: /label= P-74  
PCT-US93-08131-2

Query Match 50.7%; Score 36; DB 5; Length 626;  
Best Local Similarity 77.8%; Pred. No. 4.1e+02;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCRSGEAG 12  
| | | | |  
DB 7 GTRGGEAG 15

RESULT 38  
US-09-252-991A-32382  
Sequence 32382, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 32382  
; LENGTH: 685  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-32382

Query Match 50.7%; Score 36; DB 4; Length 685;  
Best Local Similarity 46.2%; Pred. No. 4.4e+02;  
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 SHEGCRSGEAGS 13  
: ||| : |||  
Db 306 AHRGCRAREERS 318

## RESULT 39

US-09-252-991A-27341  
; Sequence 27341, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 27341  
; LENGTH: 1073  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: (803)  
; OTHER INFORMATION: Identity of amino acid at the above locations are unknown.  
US-09-252-991A-27341

Query Match 50.7%; Score 36; DB 4; Length 1073;  
Best Local Similarity 45.5%; Pred. No. 7e+02;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 HEGCRSGEAG 12  
: ||| : |||  
Db 891 HQPCRGSGQG 901

## RESULT 40

US-09-618-425-2  
; Sequence 2, Application US/09618425  
; Patent No. 6475744  
; GENERAL INFORMATION:  
; APPLICANT: Reppert, Steven M.  
; APPLICANT: Weaver, David R.  
; APPLICANT: Zylka, Mark  
; APPLICANT: Jin, Xiaowei  
; APPLICANT: Kume, Kazuhiko  
; APPLICANT: Sirram, Sathyanarayanan  
; APPLICANT: Shearman, Lauren  
; TITLE OF INVENTION: METHODS FOR IDENTIFYING COMPOUNDS WHICH  
; FILE REFERENCE: 00786-428001  
; CURRENT APPLICATION NUMBER: US/09/618,425

; CURRENT FILING DATE: 2000-07-18  
; PRIOR APPLICATION NUMBER: 60/203,005  
; PRIOR FILING DATE: 2000-05-10  
; PRIOR APPLICATION NUMBER: 60/145,363  
; PRIOR FILING DATE: 1999-07-22  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 1197  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-618-425-2

Query Match 50.7%; Score 36; DB 4; Length 1197;  
Best Local Similarity 53.8%; Pred. No. 7.8e+02;  
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 SHEGCRSGEAGS 13  
: ||| : |||  
Db 983 SEGLPSGGGGS 995

## RESULT 41

US-08-117-952-772  
; Sequence 772, Application US/08117952  
; Patent No. 5851760  
; GENERAL INFORMATION:  
; APPLICANT: Evans, Glen A.  
; APPLICANT: Smith, Michael W.  
; TITLE OF INVENTION: METHOD FOR GENERATION OF SEQUENCE  
; TITLE OF INVENTION: SAMPLED MAPS OF COMPLEX GENOMES  
; NUMBER OF SEQUENCES: 797  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
; STREET: 444 South Flower Street, Suite 2000  
; CITY: Los Angeles  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/117,952  
; FILING DATE: 07-SEP-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/078,471  
; FILING DATE: 15-JUN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Reiter, Stephen E.  
; REGISTRATION NUMBER: 31,192  
; REFERENCE/DOCKET NUMBER: P41 9423  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-546-4737  
; TELEFAX: 619-546-9392  
; INFORMATION FOR SEQ ID NO: 772:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 68 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
US-08-117-952-772

Query Match 49.3%; Score 35; DB 2; Length 68;  
Best Local Similarity 45.5%; Pred. No. 65;  
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 EGCRSGEAGS 13  
: ||| : |||

```
Db      13  ECGTTCGSGA 23

RESULT 42
US-09-252-991A-27007
; Sequence 27007, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27007
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27007

Query Match      49.3%; Score 35; DB 4; Length 151;
Best Local Similarity 46.2%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      1  SHEGCRSGEAGS 13
      : ||| : |||
Db      111 AHGCPAGRHAGS 123

RESULT 43
US-09-252-991A-32846
; Sequence 32846, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 32846
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32846

Query Match      49.3%; Score 35; DB 4; Length 154;
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 6; Gaps 1;

QY      2  HEGC-----RGSEAE 11
      : |||
      : |||
Db      115 HTGCRSGSERSGDAE 130

RESULT 44
US-09-252-991A-22153
; Sequence 22153, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 22153
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22153

Query Match      49.3%; Score 35; DB 4; Length 178;
Best Local Similarity 60.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      4  GCRSGEAGS 13
      : ||| : |||
Db      99 GCRSGRGYGT 108
```

```
FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 22153
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22153

Query Match      49.3%; Score 35; DB 4; Length 178;
Best Local Similarity 60.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      4  GCRSGEAGS 13
      : ||| : |||
Db      99 GCRSGRGYGT 108

RESULT 45
US-09-252-991A-28878
; Sequence 28878, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28878
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28878

Query Match      49.3%; Score 35; DB 4; Length 188;
Best Local Similarity 58.3%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1  SHEGCRSGEAG 12
      : ||| : |||
Db      31 SAPGCRPGRAG 42

RESULT 46
US-09-120-365-79
; Sequence 79, Application US/09120365
; Patent No. 6103514
; GENERAL INFORMATION:
; APPLICANT: Natori, Shunji
; TITLE OF INVENTION: NEW PROTEASE
; FILE REFERENCE: 32290-144749
; CURRENT APPLICATION NUMBER: US/09/120,365
; CURRENT FILING DATE: 1998-07-22
; EARLIER APPLICATION NUMBER: JP 9-333 474
; EARLIER FILING DATE: 1997-11-18
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 79
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Homo sapien cathepsin B
US-09-120-365-79
```

```
Query Match          49.3%; Score 35; DB 3; Length 282;
Best Local Similarity 63.6%; Pred. No. 2.7e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 SHEGCRSGEAE 11
      |||||
Db      175 SHVGCRPYSAE 185

RESULT 47
US-09-515-039-79
; Sequence 79, Application US/09515039
; Patent No. 6214599
; GENERAL INFORMATION:
; APPLICANT: Natori, Shunji
; TITLE OF INVENTION: NEW PROTEASE
; FILE REFERENCE: 32290-144749
; CURRENT APPLICATION NUMBER: US/09/515,039
; CURRENT FILING DATE: 2000-03-06
; EARLIER APPLICATION NUMBER: JP 9-333 474
; EARLIER FILING DATE: 1997-11-18
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 79
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Homo sapien cathepsin B
US-09-515-039-79

Query Match          49.3%; Score 35; DB 3; Length 282;
Best Local Similarity 63.6%; Pred. No. 2.7e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 SHEGCRSGEAE 11
      |||||
Db      175 SHVGCRPYSAE 185

RESULT 48
US-09-252-991A-25370
; Sequence 25370, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25370
; LENGTH: 301
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25370

Query Match          49.3%; Score 35; DB 4; Length 301;
Best Local Similarity 60.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2 HEGCRSGEAE 11
      |||||
Db      130 HPGCRGPLE 139

RESULT 49
US-09-252-991A-27327
; Sequence 27327, Application US/09252991A
```

```
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27327
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27327

Query Match          49.3%; Score 35; DB 4; Length 341;
Best Local Similarity 63.6%; Pred. No. 3.2e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 SHEGCRSGEAE 11
      |||||
Db      97 SARGCRGAEE 107

RESULT 50
US-09-252-991A-21706
; Sequence 21706, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21706
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21706

Query Match          49.3%; Score 35; DB 4; Length 348;
Best Local Similarity 70.0%; Pred. No. 3.3e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      3 EGCRSGEAE 12
      |||||
Db      94 EGREAGEAE 103

Search completed: April 19, 2004, 17:24:48
Job time : 18.1935 secs
```

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 19, 2004, 17:11:35 ; Search time 38.5806 Seconds  
(without alignments)  
106.316 Million cell updates/sec

Title: US-10-726-692-22

Perfect score: 71

Sequence: 1 SHEGCRSGEAGS 13

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 50 summaries

Database :

SPTREMBL\_25.\*  
1: sp\_arched.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_rvirus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	ID	Description
1	46	64.8	Q9Y2J5	Q9Y2J5 homo sapien
2	46	64.8	Q86X52	Q86X52 homo sapien
3	43	60.6	118	Q7XP56 oryza sativ
4	42	59.2	261	Q43150 sambucus ni
5	42	59.2	453	Q9LU91
6	42	59.2	453	Q9LU91 arabidopsis
7	42	59.2	466	Q8L720
8	42	59.2	491	Q88Q52 pseudomonas
9	42	59.2	997	Q9UL35 leishmania
10	41	57.7	519	Q74242 cryptococcu
11	41	57.7	11	Q8CCP5
12	41	57.7	1905	Q9BL30 caenorhabdi
13	40	56.3	111	Q8VI56 mus musculu
14	40	56.3	209	Q7RDS9 clostridium
15	40	56.3	224	Q7URS4 rhodospirill
16	40	56.3	286	Q8S0H3 oryza sativ
				Q7WNK5 bordetella

17	40	56.3	292	2	Q8GFC1	Q8GFC1 photorhabdu
18	40	56.3	379	2	Q9EYU5	Q9EYU5 rhizobium 1
19	40	56.3	379	16	Q98AW1	Q98AW1 rhizobium 1
20	40	56.3	384	16	Q9AMS5	Q9AMS5 bradyrhizob
21	40	56.3	469	10	Q94CG6	Q94CG6 zea mays (m
22	40	56.3	1017	5	Q8SQJ6	Q8SQJ6 encephalito
23	39	54.9	136	10	Q8S6A7	Q8S6A7 oryza sativ
24	39	54.9	255	4	Q9HIN5	Q9HIN5 homo sapien
25	39	54.9	261	10	Q94LD2	Q94LD2 oryza sativ
26	39	54.9	264	10	Q246S8	Q246S8 arabidopsis
27	39	54.9	355	16	Q8PGD8	Q8PGD8 xanthomonas
28	39	54.9	355	16	Q8P4R8	Q8P4R8 xanthomonas
29	39	54.9	491	10	Q8LJ60	Q8LJ60 oryza sativ
30	39	54.9	942	11	Q8VB16	Q8VB16 mus musculu
31	39	54.9	1213	3	Q9P3K9	Q9P3K9 neurospora
32	39	54.9	1607	5	Q94599	Q94599 leishmania
33	38.5	54.2	1234	4	Q8TES6	Q8TES6 homo sapien
34	38.5	54.2	1304	5	Q8WT63	Q8WT63 plasmodium
35	38.5	54.2	1311	4	Q86K83	Q86K83 homo sapien
36	38.5	54.2	1311	4	Q8IX10	Q8IX10 homo sapien
37	38.5	54.2	1311	11	Q8CIQ2	Q8CIQ2 mus musculu
38	38.5	54.2	1311	11	Q8VDS6	Q8VDS6 mus musculu
39	38.5	54.2	1347	4	Q8IYZ2	Q8IYZ2 homo sapien
40	38.5	54.2	1421	10	Q9FIH7	Q9FIH7 arabidopsis
41	38	53.5	105	11	Q8BLK5	Q8BLK5 mus musculu
42	38	53.5	127	10	Q04321	Q04321 arabidopsis
43	38	53.5	133	10	Q9LU15	Q9LU15 arabidopsis
44	38	53.5	135	2	Q93M31	Q93M31 gamma-prote
45	38	53.5	135	2	Q93M32	Q93M32 gamma-prote
46	38	53.5	170	8	Q8SWE6	Q8SWE6 uncultured
47	38	53.5	185	13	Q8UWK4	Q8UWK4 ictalurus p
48	38	53.5	206	13	Q8UWG3	Q8UWG3 ictalurus p
49	38	53.5	206	13	Q8UWK5	Q8UWK5 ictalurus p
50	38	53.5	230	10	Q8SB58	Q8SB58 oryza sativ

## ALIGNMENTS

### RESULT 1

Q9Y2J5 PRELIMINARY; PRT; 802 AA.  
AC Q9Y2J5; DT 01-NOV-1999 (TREMREL. 12, Created)  
DT 01-NOV-1999 (TREMREL. 12, Last sequence update)  
DT 01-OCT-2003 (TREMREL. 25, Last annotation update)  
DE Hypothetical protein KIAA0990 (Chondroitin synthase).  
GN KIAA0990 OR CHSY.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=93246063; PubMed=10231032;  
RA Nagase T., Ishikawa K., Suyama M., Kikuno R., Hirose M.,  
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;  
RT "Prediction of the coding sequences of unidentified human genes. XIII.  
RT The complete sequences of 100 new cDNA clones from brain which code  
RT for large proteins in vitro.";  
RN [2]  
RX DNA Res. 6:63-70(1999).  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21486534; PubMed=11514575;  
RA Kitagawa H., Uyama T., Sugahara K.;  
RT "Molecular Cloning and Expression of a Human Chondroitin Synthase.";  
RL J. Biol. Chem. 276:38721-38726(2001).  
DR EMBL; AB023207; BAA76834.1; -;  
DR EMBL; AB071402; BAB64936.1; -;  
DR InterPro; IPR008428; CHGN.  
DR Pfam; PF05679; CHGN; 1.  
KW Hypothetical protein.

```

SQ SEQUENCE 802 AA; 91729 MW; 9115C204FAF298D7 CRC64;
Query Match 64.8%; Score 46; DB 4; Length 802;
Best Local Similarity 69.2%; Pred. No. 9.9;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SHEGCRSGEAGS 13
| | | | | | | |
Db 44 SPEGCRSGQAAS 56

RESULT 2
Q86X52 PRELIMINARY; PRT; 802 AA.
AC Q86X52;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Carbohydrate (Chondroitin) synthase 1.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC046247; AAH46247.1; -.
SQ SEQUENCE 802 AA; 91784 MW; 5B4C02670332FA0E CRC64;

Query Match 64.8%; Score 46; DB 4; Length 802;
Best Local Similarity 69.2%; Pred. No. 9.9;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SHEGCRSGEAGS 13
| | | | | | | |
Db 44 SPEGCRSGQAAS 56

RESULT 3
Q7XP56 PRELIMINARY; PRT; 118 AA.
AC Q7XP56;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE OSJNBA0013K16.11 protein.
GN OSJNBA0013K16.11
OS Oryza sativa (Rice)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartioideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Han B., Feng Q., Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X.,
RA Liu Y.L., Mu J., Yu Z., Chen L., Fan D.L., Weng Q.J., Zhang L.,
RA Lu Y.Q., Yu S.L., Liu X.H., Lu T.T., Zhang Y.J., Lu Y., Li C., Li T.,
RA Zhang Y., Hu H., Jia P.X., Qian Y.M., Ying K., Zhou B., Chen Z.H.,
RA Hao P., Zhang L., Wu M., Zhang R.O., Guan J.P., Fu G., Wang S.Y.,
RA Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F., Jia J., Yin H.F.,
RA Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y., Shao C.Y., Sun Y.,
RA Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W., Sheng H.H.,
RA Gu J.L., Chen S.T., Ni L., Zhu F.H., Hong G.F.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL662957; CAE03762.1; -.
SQ SEQUENCE 118 AA; 12527 MW; A6A9FA5B83270D33 CRC64;

Query Match 60.6%; Score 43; DB 10; Length 118;
Best Local Similarity 72.7%; Pred. No. 5;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 2 HEGCRSGEAG 12
| | | | | | | |
Db 97 HGGCRSBEEG 107

RESULT 4
Q43150 PRELIMINARY; PRT; 261 AA.
AC Q43150;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Pathogenesis-related protein PR-3 type (EC 3.2.1.14) (Fragment).
GN CHITINASE, CLASS I.
OS Sambucus nigra (European elder).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Campanulids; Dipsacales; Adoxaceae; Sambucus.
OX NCBI_TaxID=4202;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=common elder; TISSUE=Abscission zone;
RA Coupe S.A., Taylor J.E., Roberts J.A.;
RT "Temporal and spatial expression of mRNAs encoding pathogenesis-
RT related proteins during ethylene-promoted leaflet abscission in
RT Sambucus nigra";
RN [1]
RL Plant Cell Environ. 20:1517-1524 (1997).
DR EMBL; Z46948; CAA87072.1; -.
DR PIR; S51678; S51678.
DR HSSP; P27275; 1MWC.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0008843; F:endochitinase activity; IEA.
DR GO; GO:0016799; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0016998; P:cell wall catabolism; IEA.
DR GO; GO:0006032; P:chitin catabolism; IEA.
DR GO; GO:0009613; P:response to pest/pathogen/parasite; IEA.
DR InterPro; IPR001002; Chitin binding_1.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00187; Chitin bind_1; 1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRINTS; PR00451; CHITINBINDING.
DR ProDom; PD00609; Chitin binding_1; 1.
DR ProDom; PD354900; Glyco_hydro_19; 1.
DR SMART; SM00270; ChtBD1; 1.
DR PROSITE; PS00773; CHITINASE 19 1; 1.
DR PROSITE; PS00774; CHITINASE 19 2; 1.
DR PROSITE; PS00026; CHITIN BINDING; 1.
KW Chitin-binding; Glycosidase; Hydrolase.
FT NON TER 1
SQ SEQUENCE 261 AA; 27954 MW; E22A26D718BE662B CRC64;

Query Match 59.2%; Score 42; DB 10; Length 261;
Best Local Similarity 72.7%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 EGCGRSGEAGS 13
| | | | | | | |
Db 41 EGCGRSGPCYGS 51

RESULT 5
Q9LU91 PRELIMINARY; PRT; 453 AA.
AC Q9LU91;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Gb|AADI2709.1 (Ar3g26000/MPe11.15).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

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Qy	1	SHGCRSGEAGS	13	
Db	175	SHENARNGEVGS	187	
RESULT 7				
Q88Q52		PRELIMINARY;	PRT;	466 AA.
ID	Q88Q52			
AC	Q88Q52;			
DT	01-JUN-2003 (TEMBLrel. 24, Created)			
DT	01-JUN-2003 (TEMBLrel. 24, Last sequence update)			
DT	01-JUN-2003 (TEMBLrel. 24, Last annotation update)			
DE	Hypothetical protein.			
GN	PP0646.			
OS	Pseudomonas putida (strain KT2440).			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;			
OC	Pseudomonadaceae; Pseudomonas.			
OX	NCBI_TaxID=160488;			
RN	[1]			
RX	SEQUENCE FROM N.A.			
RY	MEDLINE=22423060; PubMed=12534463;			
RA	Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,			
RA	Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,			
RA	Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,			
RA	Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,			
RA	Chris Lee P., Holtzaple E., Scanlan D., Tran K., Moazzez A.,			
RA	Uterback T., Rizzo M., Lee K., Kosack D., Mostl D., Wedler H.,			
RA	Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,			
RA	Kiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuemmler B.,			
RA	Fraser C.M.;			
RT	"Complete genome sequence and comparative analysis of the			
RT	metabolically versatile Pseudomonas putida KT2440."			
RL	Environ. Microbiol. 4:799-808(2002).			
DR	ENBL; AE016776; AAN66271.1; -			
DR	TIGR; PP0646; -			
KW	Hypothetical protein; Complete proteome.			
SQ	SEQUENCE 466 AA; 48738 MW; FF7C1BAA4B2B706B CRC64;			
Query Match	59.2%;	Score 42;	DB 16;	Length 466;
Best Local Similarity	70.0%;	Pred. No. 30;		
Matches	7;	Conservative	1;	Mismatches 2; Indels 0; Gaps
Qy	3	EGCRSGEAG	12	
Db	375	EACRAGETEG	384	
RESULT 8				
Q9U135		PRELIMINARY;	PRT;	491 AA.
ID	Q9U135			
AC	Q9U135;			
DT	01-MAY-2000 (TEMBLrel. 13, Created)			
DT	01-MAY-2000 (TEMBLrel. 13, Last sequence update)			
DT	01-OCT-2003 (TEMBLrel. 25, Last annotation update)			
DE	Hypothetical protein.			
GN	L4520.08.			
OS	Leishmania major.			
OC	Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.			
OX	NCBI_TaxID=5664;			
RN	[1]			
RY	SEQUENCE FROM N.A.			
RC	STRAIN=Frledlin;			
RA	Hilbert H., Wedler H., Duesterhoeft A., Ivens A.C.,			
RA	Lawson D., Quall M., Rajandream M.A., Barrell B.G.;			
RL	Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.			
RZ	[2]			
RN	SEQUENCE FROM N.A.			
RC	STRAIN=Frledlin;			
RY	MEDLINE=98146435; Pubmed=9477341;			
RA	Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,			
RA	Smith D.F.;			
RT	"A physical map of the Leishmania major Friedlin genome."			

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RL Genome Res. 8:135-145(1998).
DR EMBL; AL117268; CAB5511.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR004776; Auxin_eff.
DR Pfam; PF03547; Auxin_eff; 1.
KW Hypothetical protein.
SQ SEQUENCE 491 AA; 53473 MW; C4CB0C840B08582C CRC64;

Query Match 59.2%; Score 42; DB 5; Length 491;
Best Local Similarity 66.7%; Pred. No. 32;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SHEGCRSGEAG 12
| : ||| |||||
DB 188 SMDGVDGEAG 199

RESULT 9
O74242 PRELIMINARY; PRT; 997 AA.
AC O74242;
DT 01-NOV-1998 (TRENBLrel. 08, Created)
DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Plasma membrane H(+)-ATPase 1 (EC 3.6.1.35).
GN PMA1
OS Cryptococcus neoformans (Filobasidiella neoformans).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX NCBI_TaxID=5207;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B-3501;
RX MEDLINE=20568793; PubMed=11118522;
RA Gorgojo B., Portillo F., Martinez-Suarez J.V.;
RT "Sequencing and heterologous expression in Saccharomyces cerevisiae of
RT a Cryptococcus neoformans cDNA encoding a plasma membrane H(+)-
RT ATPase.";
RL Biochim. Biophys. Acta 1509:1103-110(2000).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2
CC ATPASES).
DR EMBL; AF077766; AAC27788.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0015662; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:0016887; F:ATPase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR GO; GO:0015992; P:proton transport; IEA.
DR InterPro; IPR006534; ATPase-IIIA_H.
DR InterPro; IPR001757; ATPase_E1-E2.
DR InterPro; IPR004014; Cation_ATPase_N.
DR InterPro; IPR008250; E1-E2_ATPase_reg.
DR InterPro; IPR005834; Hydrolase.
DR InterPro; IPR000695; H_ATPase.
DR Pfam; PF00690; Cation_ATPase_N; 1.
DR Pfam; PF00122; E1-E2_ATPase; 1.
DR Pfam; PF00702; Hydrolase; 1.
DR PRINTS; PR00119; CATATPASE.
DR PRINTS; PR00120; HATPASE.
DR TIGRPFams; TIGR01647; ATPase-IIIA_H; 1.
DR TIGRPFams; TIGR01494; ATPase_P-type; 4.
DR PROSITE; PS00154; ATPase_E1_E2; 1.
KW ATP-binding; Hydrolase; Phosphorylation; Transmembrane.
SQ SEQUENCE 997 AA; 108693 MW; ECAEB09A66F7A744 CRC64;

Query Match 59.2%; Score 42; DB 3; Length 997;
Best Local Similarity 47.4%; Pred. No. 65;
Matches 9; Conservative 1; Mismatches 1; Indels 8; Gaps 1;

QY 2 HEG-----CRSGEAG 12
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Db 257 HEGDCFSGSGTCKQGEAG 275

RESULT 10
Q8CCP5 PRELIMINARY; PRT; 519 AA.
AC Q8CCP5;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Hypothetical Low density lipoprotein.
GN 6430526J12RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK032360; BAC27835.1; -.
DR PIR; PT0645; PT0645.
DR MGD; MGI:2442252; 6430526J12RIK.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_s.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR002172; LDL_receptor_A.
DR InterPro; IPR000033; Ldl_receptor_rep.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00057; ldl_recept_a; 8.
DR Pfam; PF00058; ldl_recept_b; 1.
DR PRINTS; PR00261; LDLRECEPTOR.
DR SMART; SM00181; EGF; 3.
DR SMART; SM00179; EGF_CA; 2.
DR SMART; SM00192; LDLa; 8.
DR SMART; SM00135; LY; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS01209; LDLRA_1; 8.
DR PROSITE; PS00068; LDLRA_2; 8.
KW Hypothetical protein.
SQ SEQUENCE 519 AA; 57606 MW; CD4061FE220C389A CRC64;

Query Match 57.7%; Score 41; DB 11; Length 519;
Best Local Similarity 77.8%; Pred. No. 51;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SHEGCRSGE 9
||| : |||||
DB 227 SHQPCRSGE 235

RESULT 11
Q9BLJ30 PRELIMINARY; PRT; 716 AA.
AC Q9BLJ30;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN Y7IH2AW.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
SQ
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OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Leonard S.;
RT "The sequence of C. elegans cosmid Y1H2AM.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC024859; AAK29976.1; -.
DR HSSP; O60911; 1FH0.
DR WormPep; Y71H2AM.3; CE26272.
DR GO; GO:0004182; F:carboxypeptidase A activity; IEA.
DR GO; GO:0008234; F:cysteine-type peptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000668; Peptidase C1.
DR InterPro; IPR000834; Peptidase M14.
DR Pfam; PF00112; Peptidase_C1; 1.
DR PRODOM; PD000158; Peptidase_C1; 1.
DR SMART; SM00645; Pept C1; 1.
DR PROSITE; PS00133; CARBOXYPEPT_ZN_2; 1.
DR KW Hypothetical protein.
SQ SEQUENCE 716 AA; 80007 MW; A7595D3F01F82740 CRC64;

Query Match 57.7%; Score 41; DB 5; Length 716;
Best Local Similarity 81.8%; Pred. NO. 71;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 EGCSEAEAGS 13
Db 628 EGLRSEAEAGS 638

RESULT 12
Q8VI56 PRELIMINARY; PRT; 1905 AA.
AC Q8VI56;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE LDLR dan.
GN 6430526J12RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Simon-Chazottes D.C., Tutois S., Bourgade F., Evans M., Kuehn M.,
RA Guenet J.-L.;
RT "Characterization of an insertional mutation responsible for abnormal
RT limb development.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF247637; AAL36970.1; -.
DR MGD; MGI:2442252; 6430526J12RIK.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR000152; ASX hydroxyl S.
DR InterPro; IPR001881; EGF Ca.
DR InterPro; IPR006209; EGF_like.

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DR InterPro; IPR002172; LDL_receptor_A.
DR InterPro; IPR000033; Ldl_receptor_rep.
DR Pfam; PF00008; EGF; 5.
DR Pfam; PF00057; ldl_recept_a; 8.
DR Pfam; PF00058; ldl_recept_b; 19.
DR PRINTS; PR00261; LDLRECEPTOR.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00192; LDLA; 8.
DR SMART; SM00135; LY; 20.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS01209; LDLRA_1; 8.
DR PROSITE; PS00068; LDLRA_2; 8.
DR KW EGF-like domain.
SQ SEQUENCE 1905 AA; 212035 MW; D771E135FA3814C1 CRC64;

Query Match 57.7%; Score 41; DB 11; Length 1905;
Best Local Similarity 77.8%; Pred. NO. 1.9e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SHEGCRSGE 9
Db 227 SHQPCRSGE 235

RESULT 13
Q97DS9 PRELIMINARY; PRT; 111 AA.
AC Q97DS9;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein CAC3393.
GN CAC3393.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA Bennett G.N., Koonin E.V., Smith D.R.;
RT "Genome sequence and comparative analysis of the solvent-producing
RT bacterium Clostridium acetobutylicum.";
RL J. Bacteriol. 183:4823-4838(2001).
DR EMBL; AB007837; AAK81323.1; -.
DR PIR; H97316; H97316.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 111 AA; 12368 MW; 8793CB8F4B42DA69 CRC64;

Query Match 56.3%; Score 40; DB 16; Length 111;
Best Local Similarity 60.0%; Pred. NO. 17;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SHEGCRSGEA 10
Db 55 SHKGCCKAAEA 64

RESULT 14
Q7URS4 PRELIMINARY; PRT; 209 AA.
AC Q7URS4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Probable two component system response regulator.

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GN RB5477.
OS Rhodopirellula baltica.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxID=117;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416;
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
RA Schlesner H., Amann R., Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete Pirellula sp.
RT strain 1.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
DR EMBL; EX294142; CND74264.1; -.
KW Complete proteome.
SQ SEQUENCE 209 AA; 23562 MW; BDBD2D3290341A50 CRC64;

Query Match 56.3%; Score 40; DB 16; Length 209;
Best Local Similarity 60.0%; Pred. No. 31;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 HEGCRSGEAE 11
Db 196 HQGCSAETE 205
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|:|:|:|

RESULT 15
Q8S0H3 PRELIMINARY; PRT; 224 AA.
AC Q8S0H3;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE B1142C05.27 protein.
GN B1142C05.27.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, BAC
RT clone:B1142C05.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF003410; BAB89127.1; -.
DR Granene; Q8S0H3; -.
SQ SEQUENCE 224 AA; 23355 MW; 86985008FE9D9024 CRC64;

Query Match 56.3%; Score 40; DB 10; Length 224;
Best Local Similarity 77.8%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCRSGEAG 12
Db 120 GCRSGRAG 128
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|:|:|:|

RESULT 16
Q7WNK5 PRELIMINARY; PRT; 286 AA.
AC Q7WNK5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN BB1032.
OS Bordetella bronchiseptica (Alcaligenes bronchisepticus).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;

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OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=518;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RB50 / ATCC BAA-598;
RX MEDLINE=22827954; PubMed=12910271;
RA Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdono-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feitwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moulle S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640440; CAE31531.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 286 AA; 28672 MW; 598C61B98C6306F5 CRC64;

Query Match 56.3%; Score 40; DB 16; Length 286;
Best Local Similarity 63.6%; Pred. No. 43;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SHEGCRSGEAE 11
Db 90 SHASCRIGDAE 100
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|:|:|:|

RESULT 17
Q8GFC1 PRELIMINARY; PRT; 292 AA.
AC Q8GFC1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hpad.
GN HPAD.
OS Photorhabdus luminescens (Xenorhabdus luminescens).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=29488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=W14;
RX MEDLINE=21185117; PubMed=11286884;
RA Waterfield N.R., Bowen D.J., Fetherston J.D., Perry R.D.,
RA ffrench-Constant R.H.;
RT "The tc genes of Photorhabdus: a growing family.";
RL Trends Microbiol. 9:185-191(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=W14;
RA Waterfield N.R., ffrench-Constant R.H.;
RT "Pathogenicity islands in Photorhabdus luminescens strain W14.";
RL Trends Microbiol. 0:0-0(2002).
DR EMBL; AF346500; AA017180.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016491; E:oxidoreductase activity; IEA.
DR GO; GO:0006725; P:aromatic compound metabolism; IEA.
DR GO; GO:0001584; P:rhodopsin-like receptor activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR004183; LigB_.
DR Pfam; PF02900; LigB_1
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
SQ SEQUENCE 292 AA; 33043 MW; A6D7474EB4BCC084 CRC64;

Query Match 56.3%; Score 40; DB 2; Length 292;

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Best Local Similarity 54.5%; Pred. No. 44;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 HEGCRSGRAEG 12
DB 25 HHGCRQGAIDG 35

RESULT 18
Q9EYU5
ID Q9EYU5 PRELIMINARY; PRT; 379 AA.
AC Q9EYU5;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE BioF (?-keto-8-amino-pelargonic acid synthetase protein).
GN BioF.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R7A;
RX MEDLINE=21220762; PubMed=11320134;
RA Sullivan J.T., Brown S.D., Yocum R.R., Ronson C.W.;
RT "The bio operon on the acquired symbiosis island of Mesorhizobium sp. strain R7A includes a novel gene involved in pimeloyl-CoA synthesis.";
RL Microbiology 147:1315-1322(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=R7A;
RX MEDLINE=21999272; PubMed=12003951;
RA Sullivan J.T., Trzebiatowski J.R., Cruickshank R.W., Gouzy J., Brown S.D., Elliot R.M., Fleetwood D.J., McCallum N.G., Rossbach U., Stuart G.S., Weaver J.E., Webby R.J., de Bruijn F.J., Ronson C.W.;
RT "Comparative sequence analysis of the symbiosis island of Mesorhizobium loti strain R7A.";
RL J. Bacteriol. 184:3086-3095(2002).
DR EMBL; AF311738; AAG47792.1; -.
DR EMBL; AL672114; CAD31400.1; -.
DR HSSP; P12998; 1BS0.
DR GO; GO:0008483; F:transaminase activity; IEA.
DR GO; GO:0009058; P:biosynthesis; IEA.
DR InterPro; IPR004839; Aminotrans_I/II.
DR Pfam; PF00155; aminotran_1_2; 1.
SQ SEQUENCE 379 AA; 40399 MW; 3B02D5848CF700F9 CRC64;

Query Match 56.3%; Score 40; DB 2; Length 379;
Best Local Similarity 70.0%; Pred. No. 57;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 HEGCRSGRAE 11
DB 127 HEGARAGRAE 136

RESULT 19
Q98AW1
ID Q98AW1 PRELIMINARY; PRT; 379 AA.
AC Q98AW1;
DT 01-OCT-2001 (TReMBLrel. 18, Created)
DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE 8-amino-7-oxononanoate synthase, KAPA synthase.
GN MLL5830.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;

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RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Ideasa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR EMBL; AP003007; BAB52211.1; -.
DR GO; GO:0008483; F:transaminase activity; IEA.
DR GO; GO:0009058; P:biosynthesis; IEA.
DR InterPro; IPR004839; Aminotrans_I/II.
DR Pfam; PF00155; aminotran_1_2; 1.
KW Complete proteome.
SQ SEQUENCE 379 AA; 40271 MW; 67859C2B5D9541E1 CRC64;

Query Match 56.3%; Score 40; DB 16; Length 379;
Best Local Similarity 70.0%; Pred. No. 57;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 HEGCRSGRAE 11
DB 127 HEGARAGRAE 136

RESULT 20
Q9AMS5
ID Q9AMS5 PRELIMINARY; PRT; 384 AA.
AC Q9AMS5;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE ID901 (8-amino-7-oxononanoate synthase).
GN ID901 OR B10F OR BLR2097.
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1108PC4;
RX MEDLINE=21101824; PubMed=11157954;
RA Gottfert M., Rothlisberger S., Kundig C., Beck C., Marty R., Hennecke H.;
RT "Potential symbiosis-specific genes uncovered by sequencing a 410-kb DNA region of the Bradyrhizobium japonicum chromosome.";
RL J. Bacteriol. 183:1405-1412(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA 110;
RX MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T., Sasamoto S., Watanabe A., Ideasa K., Iriguchi M., Kawashima K., Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M., Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
RL DNA Res. 9:189-197(2002).
DR EMBL; AF322013; AAG61072.1; -.
DR EMBL; AP005942; BAC47362.1; -.
DR HSSP; P12998; 1BS0.
DR GO; GO:0008483; F:transaminase activity; IEA.
DR GO; GO:0009058; P:biosynthesis; IEA.
DR InterPro; IPR004839; Aminotrans_I/II.
DR Pfam; PF00155; aminotran_1_2; 1.
KW Complete proteome.
SQ SEQUENCE 384 AA; 41376 MW; DC40495CCC4A7698 CRC64;

Query Match 56.3%; Score 40; DB 16; Length 384;
Best Local Similarity 70.0%; Pred. No. 58;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY      2 HEGCRSGRAE 11
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Db      130 HEGARAGRAE 139

RESULT 21
Q94CG6 PRELIMINARY; PRT; 469 AA.
AC Q94CG6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Seven transmembrane protein Mlo9 (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. B73;
RA Briggs S.P., Simmons C.R.;
RT "Manipulation of mlo genes to enhance disease resistance in plants.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. B73;
RA Devoto A., Hartmann A., Piffanelli P., Elliott C., Simmons C.R.,
RA Tarantino G., Goh C.-S., Cohen F.E., Schulze-Lefert P., Panstruga R.;
RT "Molecular phylogeny and domain-specific co-evolution of the plant-
RT specific seven transmembrane Mlo family.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY029320; AAK38345.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008219; P:cell death; IEA.
DR InterPro; IPR004326; Mlo.
DR Pfam; PF03094; Mlo; 1.
KW Transmembrane.
FT NON_TER 1
SQ SEQUENCE 469 AA; 53623 MW; 64440FB706643F0A CRC64;

Query Match 56.3%; Score 40; DB 10; Length 469;
Best Local Similarity 75.0%; Pred. No. 70;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 SHEGCRSG 8
      :|||||
Db      13 NHEGCREG 20

RESULT 22
Q8SQJ6 PRELIMINARY; PRT; 1017 AA.
AC Q8SQJ6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Chromosome segregation protein of the SMC family.
GN ECU09 1910.
OS Encephalitozoon cuniculi.
OC Eukaryota; Fungi; Microsporidia; Unikaryonidae; Encephalitozoon.
OX NCBI_TaxID=6035;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GB-M1;
RA Genoscope;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=GB-M1;
RX MEDLINE=21576510; PubMed11719806;
RA Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F.,
RA Prensier G., Barbe V., Peyretallade E., Brottier P., Wincker P.,

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RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
RA Weissbach J., Vivares C.P.;
RT "Genome sequence and gene compaction of the eukaryote parasite
RT Encephalitozoon cuniculi.";
RL Nature 414:450-453(2001).
DR EMBL; AL590451; CAD27164.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. .; IEA.
DR GO; GO:0007059; P:chromosome segregation; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003439; ABC transporter.
DR InterPro; IPR003405; SMC_C.
DR InterPro; IPR003395; SMC_N.
DR Pfam; PF02483; SMC_C; 1.
DR Pfam; PF02463; SMC_N; 1.
DR PROSITE; PS00211; ABC TRANSPORTER 1; 1.
SQ SEQUENCE 1017 AA; 117312 MW; 12194088BE5CC3C7 CRC64;

Query Match 56.3%; Score 40; DB 5; Length 1017;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2 HEGCRSGRAEGS 13
      |||||
Db      63 HEGSRAMEEGS 74

RESULT 23
Q8S6A7 PRELIMINARY; PRT; 136 AA.
AC Q8S6A7;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN OJ1004_D04.17.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,
RA Overton II L.L., Bera J.J., Tsitrin T., Krol M.I., Jarrahi B.B.,
RA Jin S.S., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S.,
RA Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B.,
RA Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
RT "Oryza sativa chromosome 3 BAC OJ1004_D04 genomic sequence.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC093180; AAL93074.1; -.
DR Gramene; O8S6A7; -.
KW Hypothetical protein.
SQ SEQUENCE 136 AA; 15196 MW; 6EB971784C98BED3 CRC64;

Query Match 54.9%; Score 39; DB 10; Length 136;
Best Local Similarity 64.3%; Pred. No. 31;
Matches 9; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY      1 SHEGCR--SGEABG 12
      |||||
Db      10 SERGCRNSGETEG 23

RESULT 24
Q9HINS PRELIMINARY; PRT; 255 AA.
AC Q9HINS;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

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DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE BA486022.3 (Similar to RPS3A (Ribosomal protein S3A)).
GN BA486022.3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Theria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilson S.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL356115; CAC17682.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; F:ribosomal constituent of ribosome; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR001593; Ribosomal_S3AE.
DR Pfam; PF01015; Ribosomal_S3AE; 1.
DR ProDom; PD003035; Ribosomal_S3AE; 1.
KW Ribosomal protein.
SQ SEQUENCE 255 AA; 28485 MW; B1FC541B5F903449 CRC64;

Query Match 54.9%; Score 39; DB 4; Length 255;
Best Local Similarity 70.0%; Pred. No. 58;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGCSSGEARG 12
Db 225 EGCSSGKATG 234

RESULT 25
Q94LD2
ID Q94LD2 PRELIMINARY; PRT; 261 AA.
AC Q94LD2
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Gansberger K.,
RA Brenner M., Burgess S., Hance M., Shvartsbeyn M., Tsitrin T.,
RA Riggs F., Hsiao J., Zismann V., Blunt S., Pai G., Vanaken S.B.,
RA Utterback T.R., Feldblyum T.V., Quackenbush J., Salzberg S.L.,
RA White O., Fraser C.M.;
RA "Oryza sativa chromosome 3 BAC OSJNBa002A15 genomic sequence.";
RT Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AC084404; AAK50593.1; -.
DR Gramene; Q94LD2; -.
DR Hypothetical protein.
KW SEQUENCE 261 AA; 27090 MW; 4FCFB97E2910A498 CRC64;

Query Match 54.9%; Score 39; DB 10; Length 261;
Best Local Similarity 81.8%; Pred. No. 59;
Matches 9; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 4 GCR--SGEARG 12
Db 57 GCRNRSGEARG 67

RESULT 26
Q24658
ID Q24658 PRELIMINARY; PRT; 264 AA.
AC Q24658
DT 01-JAN-1998 (TrEMBLrel. 05, Created)

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DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
GN Putative endochitinase (At2g43590).
AT AT2G43590.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroside II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=cnv. Columbia;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., Vanaken S.E., Umavayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrara A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhagen G.P., Preuss D., Niernan W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana.";
RN [2]
RL Nature 402:761-768(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=cnv. Columbia;
RC STRAIN=cnv. Columbia;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA STRAIN=cnv. Columbia;
RC Rounsley S.D., Techudy M.M., Lin X., Ketchum K.A., Crosby M.L.,
RA Brandon R.C., Spriggs T.A., Mason T.M., Kerlavage A.R., Adams M.D.,
RA Somerville C.R., Venter J.C.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA STRAIN=cnv. Columbia;
RC Town C.D., Kaul S.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Shinn P., Bowser L., Carninci P.,
RA Dale J.M., Hayashizaki Y., Ishida J., Jones T., Kamiya A.,
RA Karlin-Neumann G., Kawai J., Lam B., Lin J., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
RA Seki M., Southwick A., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G.,
RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Arabidopsis ORF clones.";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC002333; AAB64047.1; -.
DR EMBL; AC002335; AAM14810.1; -.
DR EMBL; BT009726; AAP88360.1; -.
DR PIR; A84868; A84868.
DR HSP; P27275; IMMC.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:004568; F:chitinase activity; IEA.
DR GO; GO:0016998; P:cell wall catabolism; IEA.
DR GO; GO:0006032; P:chitin catabolism; IEA.
DR GO; GO:0009613; P:response to pest/pathogen/parasite; IEA.
DR InterPro; IPR001002; Chitin binding_1.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00187; Chitin_bind_1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRINTS; PRO0451; CHITINBINDING.
DR ProDom; PD000609; Chitin binding_1; 1.
DR ProDom; PD354900; Glyco_hydro_19; 1.
DR SMART; SM00270; ChtBD1; 1.
DR PROSITE; PS00773; CHITINASE_19; 1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR PROSITE; PS00026; CHITIN_BINDING; 1.
KW Chitin-binding.
SQ SEQUENCE 264 AA; 28353 MW; DBBD0F3FA82D19E5 CRC64;

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Query Match          54.9%; Score 39; DB 10; Length 264;
Best Local Similarity 70.0%; Pred. No. 60;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GCRSGEARGS 13
    |||||
    |||||
Db 51 GCRSGPCRGS 60

RESULT 27
Q8PGD8
ID Q8PGD8 PRELIMINARY; PRT; 355 AA.
AC Q8PGD8;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Ribosomal RNA small subunit methyltransferase C.
GN RSMC OR XAC3679.
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=22022145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RL Nature 417:459-463(2002).
DR EMBL; AE012018; M12018.1; -.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0008170; F:N-methyltransferase activity; IEA.
DR GO; GO:0008757; F:S-adenosylmethionine-dependent methyltransf. . .; IEA.
DR GO; GO:0006306; P:DNA methylation; IEA.
DR InterPro; IPR007848; MTS.
DR InterPro; IPR001005; Myb DNA binding.
DR InterPro; IPR002052; N6_Mtase.
DR InterPro; IPR000051; SAM_bind.
DR Pfam; PF05175; MTS; 1.
DR PROSITE; PS00037; MYB_1; 1.
DR PROSITE; PS00092; N6_Mtase; 1.
DR Transferase; Methyltransferase; Complete proteome.
SQ SEQUENCE 355 AA; 38847 MW; 8C320F48409C2E56 CRC64;

Query Match          54.9%; Score 39; DB 16; Length 355;
Best Local Similarity 63.6%; Pred. No. 81;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SHEGCRSGEAE 11
    :|||
    :|||
Db 118 NNEGARGSEAD 128

RESULT 28
Q8P4R8
ID Q8P4R8 PRELIMINARY; PRT; 355 AA.
AC Q8P4R8;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Ribosomal RNA small subunit methyltransferase C.
GN RSMC OR XAC3639.
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=340;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33913 / NCPPB 528;
RX MEDLINE=22022145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RL Nature 417:459-463(2002).
DR EMBL; AE012485; AAM42909.1; -.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0008170; F:N-methyltransferase activity; IEA.
DR GO; GO:0008757; F:S-adenosylmethionine-dependent methyltransf. . .; IEA.
DR GO; GO:0016740; P:transferase activity; IEA.
DR GO; GO:0006306; P:DNA methylation; IEA.
DR InterPro; IPR001601; Methyltransf.
DR InterPro; IPR007848; MTS.
DR InterPro; IPR002052; N6_Mtase.
DR InterPro; IPR000051; SAM_bind.
DR Pfam; PF05175; MTS; 1.
DR PROSITE; PS00092; N6_Mtase; 1.
DR Transferase; Methyltransferase; Complete proteome.
SQ SEQUENCE 355 AA; 38648 MW; 8E30A7BF2E2F6057 CRC64;

Query Match          54.9%; Score 39; DB 16; Length 355;
Best Local Similarity 63.6%; Pred. No. 81;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SHEGCRSGEAE 11
    :|||
    :|||
Db 118 NNEGARGSEAD 128

RESULT 29
Q8LJ60
ID Q8LJ60 PRELIMINARY; PRT; 491 AA.
AC Q8LJ60;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE OSJNB0024F06.4 protein.
GN OSJNB0024F06.4.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, BAC
  clone:OSJNB0024F06.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP003341; BAC01227.1; -.
DR Granene; QBLJ60; -.
DR InterPro; IPR001810; F-box.
DR InterPro; IPR008945; Skp1_Skp2.
DR Pfam; PF00646; F-box; 1.
SQ SEQUENCE 491 AA; 54971 MW; C68A3855621ED5EB CRC64;

Query Match          54.9%; Score 39; DB 10; Length 491;
Best Local Similarity 60.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCRSGEAGS 13
DB 214 GCRAGRGEGA 223

RESULT 30
QVBT6 PRELIMINARY; PRT; 942 AA.
AC QVBT6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Apolipoprotein B48 receptor.
GN APOB48.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RA Gianturco S.H., Bradley W.A., Yui K., Brown M.L.;
RT "Murine ApoB48 Receptor gene.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RA Gianturco S.H., Bradley W.A., Yui K., Brown M.L.;
RT "Murine ApoB48 Receptor.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF141336; AAL54863.1; -.
DR EMBL; AF141335; AAL54862.1; -.
DR EMBL; BC030718; AAH30718.1; -.
DR MGD; MGI:2176230; Apob48r.
DR GO; GO:0030226; F:apolipoprotein receptor activity; IDA.
DR InterPro; IPR002048; EF-hand.
DR PROSITE; PS00018; EF HAND; 1.
KW Lipoprotein; Receptor.
SQ SEQUENCE 942 AA; 102705 MW; D88B379D1928C6AF CRC64;

Query Match          54.9%; Score 39; DB 11; Length 942;
Best Local Similarity 70.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 ECRSGEAGS 12
DB 65 EGLRSGQSEG 74

RESULT 31
Q9P3K9 PRELIMINARY; PRT; 1213 AA.
AC Q9P3K9;

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DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Conserved hypothetical protein.
GN B15120.20.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OC NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RA Schulte U., Alim V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
RA Nyakatura G., Mewes H.W., Mannhaupt G.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA German Neurospora genome project;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL389900; CAB97456.1; -.
DR PIR; T51032; T51032.
DR InterPro; IPR007213; LCM.
DR InterPro; IPR003347; TF_JmjC.
DR Pfam; PF04072; LCM; 1.
DR SMART; SM00558; JmjC; 1.
KW Hypothetical protein.
SQ SEQUENCE 1213 AA; 132708 MW; 492FD9E2E53CECCA CRC64;

Query Match          54.9%; Score 39; DB 3; Length 1213;
Best Local Similarity 54.5%; Pred. No. 2.8e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 ECRSGEAGS 13
DB 164 DACRSGEKDGA 174

RESULT 32
Q94599 PRELIMINARY; PRT; 1607 AA.
AC Q94599;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE LCFACAS5.
GN LCFACAS5.
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OC NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Friedlin;
RX MEDLINE=99178987; PubMed=10077609;
RA Myler P.J., Audleman L., devos T., Hixson G., Kiser P., Lemley C.,
RA Magness C., Rickel E., Sisk E., Sunkin S., Swartzell S., Westlake T.,
RA Bastien P., Fu G., Ivens A., Stuart K.;
RT "Leishmania major Friedlin chromosome 1 has an unusual distribution of
  protein-coding genes.";
RT Proc. Natl. Acad. Sci. U.S.A. 96:2902-2906(1999).
RL EMBL; AE001274; AAC24660.1; -.
DR PIR; A81461; T02837.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR000873; AMP-bind.
DR Pfam; PF00501; AMP-binding; 3.
SQ SEQUENCE 1607 AA; 168973 MW; 989C2EFE12B373A3 CRC64;

Query Match          54.9%; Score 39; DB 5; Length 1607;
Best Local Similarity 70.0%; Pred. No. 3.7e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 SHEGCRSGEA 10
DB 714 SHSACASGEA 723

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RESULT 33
Q8TES6 PRELIMINARY; PRT; 1234 AA.
ID Q8TES6;
AC Q8TES6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE FLJ00107 protein (Fragment).
GN FLJ00107.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Chara O., Nagase T., Kikuno R., Okumura K.;
RT "The nucleotide sequence of a long cDNA clone isolated from human
RT spleen."
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK074046; BAB84872.1; -.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF00096; zf-C2H2; 27.
DR SMART; SM00355; Znf_C2H2; 29.
DR PROSITE; PS00190; CYTOCHROME C; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 27.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 22.
KW Metal-binding; Zinc; Zinc-finger.
FT NON_TER 1
SQ SEQUENCE 1234 AA; 139147 MW; 1CB4705331C1E47A CRC64;

Query Match 54.2%; Score 38.5; DB 4; Length 1234;
Best Local Similarity 69.2%; Pred. No. 3.5e+02;
Matches 9; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 SH-EGCRSGEARG 12
DB 23 SHGEGCDFGEERG 35

RESULT 34
Q8WT63 PRELIMINARY; PRT; 1304 AA.
AC Q8WT63;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Multidomain scavenger receptor protein PDSR precursor.
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
RN [1]
RP SEQUENCE FROM N.A.
RA Claudianos C., Dessens J.T., Trueman H.E., Mendoza J., Arai M.,
RA Butcher G.A., Crompton T., Sinden R.E.;
RT "A malaria scavenger receptor-like protein essential for parasite
RT development."
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY034780; AAK64185.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005044; F:scavenger receptor activity; IEA.
DR InterPro; IPR008985; ConA_like_lec_gl.
DR InterPro; IPR004043; LCCL_dom.
DR InterPro; IPR001024; Lipoxxygenase_LH2.
DR InterPro; IPR008976; PLAT_LH2.
DR InterPro; IPR001190; Srcr_receptor.
DR Pfam; PF03815; LCCL; 3.

Query Match 54.2%; Score 38.5; DB 4; Length 1311;
Best Local Similarity 69.2%; Pred. No. 3.7e+02;
Matches 9; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 SH-EGCRSGEARG 12
DB 100 SHGEGCDFGEERG 112

RESULT 36
Q8IX10 PRELIMINARY; PRT; 1311 AA.
ID Q8IX10;
AC Q8IX10;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Early hematopoietic zinc finger.
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DR Pfam; PF01477; PLAT; 1.
DR Pfam; PF00530; SRCR; 2.
DR SMART; SM00202; SR; 2.
DR PROSITE; PS50820; ICCL; 3.
DR PROSITE; PS50095; PLAT; 1.
DR PROSITE; PS50287; SRCR_2; 2.
KW Signal; Receptor.
FT SIGNAL 1 22 POTENTIAL.
SQ SEQUENCE 1304 AA; 148247 MW; F936CC94E7B19F1C CRC64;

Query Match 54.2%; Score 38.5; DB 5; Length 1304;
Best Local Similarity 50.0%; Pred. No. 3.7e+02;
Matches 9; Conservative 1; Mismatches 3; Indels 5; Gaps 1;

QY 1 SHE-----GCRSGEARG 13
DB 638 SHEEDIIIGCASAEEN 655

RESULT 35
Q96K83 PRELIMINARY; PRT; 1311 AA.
ID Q96K83
AC Q96K83;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ14448.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Wagatsuma M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuno Y.,
RA Ninomiya K., Iwayanagi T.;
RT "NEDO human cDNA sequencing project."
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK027354; BAB55056.1; -.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR007087; Znf_C2H2.
DR InterPro; IPR00096; zf-C2H2; 28.
DR Pfam; PF00096; zf-C2H2; 28.
DR SMART; SM00355; Znf_C2H2; 30.
DR PROSITE; PS00190; CYTOCHROME C; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 27.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 22.
KW Hypothetical protein; Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 1311 AA; 147865 MW; C52DCC71C2B16C8F CRC64;

Query Match 54.2%; Score 38.5; DB 4; Length 1311;
Best Local Similarity 69.2%; Pred. No. 3.7e+02;
Matches 9; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 SH-EGCRSGEARG 12
DB 100 SHGEGCDFGEERG 112

RESULT 36
Q8IX10 PRELIMINARY; PRT; 1311 AA.
ID Q8IX10;
AC Q8IX10;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Early hematopoietic zinc finger.
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GN EHZF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bond H.M., Mesuraca M., Carbone E., Di Nicola M., Gianni A.M.,
RA Barberi T., Agosti V., Moore M.A.S., Grieco M., Morrone G., Venuta S.;
RT "EHZF, an early hematopoietic zinc finger transcription factor is
RT expressed in CD34+ cells and is involved in BMP signalling.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RE EMBL: AJ518106; CAD57322.1; -.
DR GO; GO:0005489; P.electron transporter activity; IEA.
DR GO; GO:0006118; P.electron transport; IEA.
DR InterPro; IPR000345; Znf_FINGER_C2H2_1; 27.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF00096; zf-C2H2; 28.
DR SMART; SM00355; Znf_C2H2; 30.
DR PROSITE; PS00190; CYTOCHROME_C; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 27.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 22.
SQ SEQUENCE 1311 AA; 147820 MW; 14583828AE0B31A4 CRC64;

Query Match 54.2%; Score 38.5; DB 4; Length 1311;
Best Local Similarity 69.2%; Pred. No. 3.7e+02;
Matches 9; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 SH-EGCRSGEAG 12
||| ||| |||
Db 100 SHGEGCDFGEERG 112

RESULT 37
OBC1Q2 PRELIMINARY; PRT; 1311 AA.
AC Q8C1Q2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Ecotropic viral integration site 3.
GN EVI3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Warming S., Liu P., Suzuki T., Akagi K., Lindtner S., Pavlakis G.N.,
RA Jenkins N.A., Copeland N.G.;
RT "Evi3, a common retroviral integration site in murine B-cell lymphoma,
RT encodes an EBFAZ-related kruppel-like zinc finger protein.";
RL Blood 0:0-0(2002).
DR EMBL; AX147406; AAN39839.1; -.
DR PIR; PT0558; PT0677.
DR MGD; MGI:95459; Evi3.
DR GO; GO:0005489; P.electron transporter activity; IEA.
DR GO; GO:0006118; P.electron transport; IEA.
DR InterPro; IPR000345; Znf_FINGER_C2H2_1; 27.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF00096; zf-C2H2; 28.
DR SMART; SM00355; Znf_C2H2; 30.
DR PROSITE; PS00190; CYTOCHROME_C; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 27.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 22.
SQ SEQUENCE 1311 AA; 147623 MW; 5B810EC6345C3D07 CRC64;

Query Match 54.2%; Score 38.5; DB 11; Length 1311;
Best Local Similarity 69.2%; Pred. No. 3.7e+02;
Matches 9; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 SH-EGCRSGEAG 12
||| ||| |||
Db 100 SHGEGCDFGEERG 112

RESULT 38
O8VDS6 PRELIMINARY; PRT; 1311 AA.
AC Q8VDS6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN EVI3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC021376; AAH21376.1; -.
DR MGD; MGI:95459; Evi3.
DR GO; GO:0005489; P.electron transporter activity; IEA.
DR GO; GO:0006118; P.electron transport; IEA.
DR InterPro; IPR000345; Znf_FINGER_C2H2_1; 27.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF00096; zf-C2H2; 28.
DR SMART; SM00355; Znf_C2H2; 30.
DR PROSITE; PS00190; CYTOCHROME_C; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 27.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 22.
KW Hypothetical protein; Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 1311 AA; 147665 MW; C8D922B535C099A CRC64;

Query Match 54.2%; Score 38.5; DB 11; Length 1311;
Best Local Similarity 69.2%; Pred. No. 3.7e+02;
Matches 9; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 SH-EGCRSGEAG 12
||| ||| |||
Db 100 SHGEGCDFGEERG 112

RESULT 39
O8IY22 PRELIMINARY; PRT; 1347 AA.
AC Q8IY22;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to early B-cell factor associated zinc finger protein, early
DE B-cell factor associated zinc finger transcription factor
DE (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC032869; AAH32869.1; -.
DR GO; GO:0005489; P.electron transporter activity; IEA.
DR GO; GO:0006118; P.electron transport; IEA.
DR InterPro; IPR000345; Znf_FINGER_C2H2_1; 27.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF00096; zf-C2H2; 27.
DR SMART; SM00355; Znf_C2H2; 30.
DR PROSITE; PS00190; CYTOCHROME_C; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 27.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 22.

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```
FT NON TER 1 1
SQ SEQUENCE 1347 AA; 151912 MW; 2EF77A23CBE2F505 CRC64;

Query Match 54.2%; Score 38.5; DB 4; Length 1347;
Best Local Similarity 69.2%; Pred. No. 3.8e+02;
Matches 9; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 SH-EGCRSGEAG 12
||| ||| ||| |||
Db 136 SHGEGCDFGEEG 148

RESULT 40
Q9FIH7 PRELIMINARY; PRT; 1421 AA.
AC Q9FIH7
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similarity to SET-domain transcriptional regulator.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroside II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RX MEDLINE=99156233; PubMed=10048488;
RA Asamizu E., Sato S., Kaneko T., Nakamura Y., Kotani H., Miyajima N.,
RA Tabata S.
RT "Structural analysis of Arabidopsis thaliana chromosome 5. VIII.
RT Sequence features of the regions of 1,081,958 bp covered by seventeen
RT physically assigned PI and TAC clones."
RL DNA Res. 5:379-391(1998).
CC -!- SIMILARITY: CONTAINS 1 SET DOMAIN.
DE EMBL; AB016888; BAB10481.1; -.
DR InterPro; IPR003169; GYF.
DR InterPro; IPR001214; SET.
DR Pfam; PF00856; SET; 1.
DR SMART; SM00317; SET; 1.
DR PROSITE; PS50829; GYF; 1.
DR PROSITE; PS50280; SET; 1.
SQ SEQUENCE 1421 AA; 158388 MW; 9406F4AEA394D215 CRC64;

Query Match 54.2%; Score 38.5; DB 10; Length 1421;
Best Local Similarity 64.3%; Pred. No. 4e+02;
Matches 9; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 SHGCRSG-EAGS 13
||| ||| ||| |||
Db 87 SNEDCRAGQEAGS 100

RESULT 41
Q8BLK5 PRELIMINARY; PRT; 105 AA.
AC Q8BLK5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical phosphatidylinositol-specific phospholipase C.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of

RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK044842; BAC32115.1; -.
DR GO; GO:0004435; P:phosphoinositide phospholipase C activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006629; P:lipid metabolism; IEA.
DR InterPro; IPR001192; PI_PLC.
DR InterPro; IPR000909; PI_PLC_Xdom.
DR Pfam; PF00388; PI-PLC-X; 1.
DR PRINTS; PR00390; PHEPLIPASEC.
DR SMART; SM00148; PLCX; 1.
DR PROSITE; PS50007; PIPLC_X_DOMAIN; 1.
KW Hypothetical protein.
SQ SEQUENCE 105 AA; 11961 MW; 6F774EB1B8C44D2F CRC64;

Query Match 53.5%; Score 38; DB 11; Length 105;
Best Local Similarity 60.0%; Pred. No. 36;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCRSGEAGS 13
||||| :|
Db 85 GCRSGNQDN 94

RESULT 42
O04321 PRELIMINARY; PRT; 127 AA.
AC O04321
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein (HPT PHOSPHOTRANSMITTER).
GN T02004.15 OR AHP4.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroside II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Rounsley S.D., Lin X., Ketchum K.A., Phillips C.A., Brandon R.C.,
RA Fuhrmann J.L., White O., Kerlavage A.R., Adams M.D., Somerville C.R.,
RA Venter J.C.;
RA Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
RL [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Suzuki T., Sakurai K., Imamura A., Nakamura A., Ueguchi C., Mizuno T.;
RT "Compilation and characterization of histidine-containing (HPT)
RT phosphotransmitters implicated in His-to-Asp phosphorylay: AHP signal
RT transducers of Arabidopsis thaliana."
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC001645; AAB63642.1; -.
DR EMBL; AB041766; BAA94763.1; -.
DR InterPro; IPR008207; HPT.
DR PROSITE; PS50894; HPT; 1.
SQ SEQUENCE 127 AA; 14669 MW; D03C095E55DF05B5 CRC64;

Query Match 53.5%; Score 38; DB 10; Length 127;
Best Local Similarity 70.0%; Pred. No. 44;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGCRSGEAG 12
||| ||| |||
Db 91 EYCRAGNAG 100

RESULT 43
Q9LU15 PRELIMINARY; PRT; 133 AA.
ID Q9LU15
AC Q9LU15;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
```

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Histidine-containing phosphotransfer protein-like.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Columbia;  
 RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Columbia;  
 RX MEDLINE=20277480; PubMed=10819329;  
 RA Nakamura Y.;  
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence  
 RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC  
 RT clones.";  
 RL DNA Res. 7:131-135(2000).  
 DR EMBL; AB023046; BAB01275.1; -;  
 DR InterPro; IPR008207; Hpt.  
 DR PROSITE; PS50894; HPT; 1.  
 SQ SEQUENCE 133 AA; 15449 MW; 298F8CD12AB0E113 CRC64;  
 Query Match 53.5%; Score 38; DB 10; Length 133;  
 Best Local Similarity 70.0%; Pred. No. 46;  
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 3 EGRSGEARG 12  
 Db | | | | |  
 Db 97 EYCRAGNARG 106  
 RESULT 44  
 Q93M31 ID Q93M31 PRELIMINARY; PRT; 135 AA.  
 AC Q93M31;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DE Naphthalene dioxygenase (Fragment).  
 OS Gamma-proteobacterium Hot 75m4.  
 OC Bacteria; environmental samples.  
 OX NCBI\_TaxID=77133;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Stach J.E.M., Burns R.G.;  
 RT "Real-time diversity of cnda, nahAc and phnAc naphthalene dioxygenase  
 RT mRNA in soil assessed by RT-PCR-single-strand conformation  
 RT polymorphism.";  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY032945; AAK85526.1; -;  
 DR GO; GO:0005506; F:iron ion binding; IEA.  
 DR GO; GO:0016702; F:oxidoreductase activity, acting on single d. . .; IEA.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO; GO:0006725; P:aromatic compound metabolism; IEA.  
 DR GO; GO:0006118; P:electron transport; IEA.  
 DR InterPro; IPR005806; Rieske dom.  
 DR InterPro; IPR001663; Ring\_hydroxyl\_A.  
 DR PRINTS; PR00355; Rieske; 1.  
 DR PROSITE; PS00570; RING\_HYDROXYL\_ALPHA; 1.  
 KW Dioxygenase.  
 FT NON\_TER 1 1  
 FT NON\_TER 135 135  
 SQ SEQUENCE 135 AA; 15058 MW; 955CACF2299AEA03 CRC64;  
 Query Match 53.5%; Score 38; DB 2; Length 135;  
 Best Local Similarity 46.2%; Pred. No. 46;  
 Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 SHEGCRSGEARG 13  
 Db | | | | |  
 Db 122 SRQGDQGLEGT 134  
 RESULT 46  
 Q85WE6 ID Q85WE6 PRELIMINARY; PRT; 170 AA.  
 AC Q85WE6;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DE Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit  
 DE (Fragment).  
 GN RBCl.  
 OS uncultured marine eukaryote.  
 OG Chloroplast.  
 OC Eukaryota; environmental samples.  
 OX NCBI\_TaxID=203449;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Wawrik B., Paul J.H.;  
 RT "Picophytoplankton succession associated with a coastal plume event in  
 RT the Gulf of Mexico.";  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY157428; AAO61029.1; -;  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 DR GO; GO:0009573; C:ribulose biphosphate carboxylase complex; IEA.  
 DR GO; GO:0016984; F:ribulose-bisphosphate carboxylase activity; IEA.

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DR GO: 0015977; P: carbon utilization by fixation of carbon di. . .; IEA.
DR InterPro: IPR000685; RuBisCO large.
DR Pfam: PF00016; RuBisCO_large; 1.
KW Chloroplast.
FT NON TER 1
FT NON TER 170 170
SQ SEQUENCE 170 AA; 19227 MW; DD9CE5571495BF22 CRC64;

Query Match 53.5%; Score 38; DB 8; Length 170;
Best Local Similarity 50.0%; Pred. No. 58;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 SHEGCRSGRAEG 12
Db 17 NHAACMSGEVKG 28

RESULT 47
Q8UWK4 PRELIMINARY; PRT; 185 AA.
AC Q8UWK4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Novel immune-type receptor 11.
GN NITR11.
OS Ictalurus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Ictaluridae; Ictalurus.
OX NCBI_TaxID=7998;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21574523; PubMed=11698645;
RA Hawke N.A., Yoder J.A., Haire R.N., Mueller M.G., Litman R.T.,
RA Miracle A.L., Stuge T., Shen L., Miller N., Litman G.W.;
RT "Extraordinary variation in a diversified family of immune-type
RT receptor genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:13832-13837(2001).
DR EMBL; AF397464; AAL35552.1; -.
DR GO: 0004872; F:receptor activity; IEA.
DR InterPro: IPR003599; Ig.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Receptor.
SQ SEQUENCE 185 AA; 20987 MW; 8F2B09C98842BA37 CRC64;

Query Match 53.5%; Score 38; DB 13; Length 185;
Best Local Similarity 53.8%; Pred. No. 64;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 SHEGCRSGRAEGS 13
Db 134 SNEGKSSDGEKS 146

RESULT 48
Q8UWG3 PRELIMINARY; PRT; 206 AA.
AC Q8UWG3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Immune-type receptor 10.
OS Ictalurus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Ictaluridae; Ictalurus.
OX NCBI_TaxID=7998;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21574523; PubMed=11698645;

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RA Hawke N.A., Yoder J.A., Haire R.N., Mueller M.G., Litman R.T.,
RA Miracle A.L., Stuge T., Shen L., Miller N., Litman G.W.;
RT "Extraordinary variation in a diversified family of immune-type
RT receptor genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:13832-13837(2001).
DR EMBL; AY046076; AAL01590.1; -.
DR GO: 0004872; F:receptor activity; IEA.
DR InterPro: IPR003599; Ig.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Receptor.
SQ SEQUENCE 206 AA; 23083 MW; AEB49F98EA93075A CRC64;

Query Match 53.5%; Score 38; DB 13; Length 206;
Best Local Similarity 53.8%; Pred. No. 71;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 SHEGCRSGRAEGS 13
Db 155 SNEGKSSDGEKS 167

RESULT 49
Q8UWK5 PRELIMINARY; PRT; 206 AA.
AC Q8UWK5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Novel immune-type receptor 10.
GN NITR10.
OS Ictalurus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Ictaluridae; Ictalurus.
OX NCBI_TaxID=7998;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21574523; PubMed=11698645;
RA Hawke N.A., Yoder J.A., Haire R.N., Mueller M.G., Litman R.T.,
RA Miracle A.L., Stuge T., Shen L., Miller N., Litman G.W.;
RT "Extraordinary variation in a diversified family of immune-type
RT receptor genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:13832-13837(2001).
DR EMBL; AF397463; AAL35551.1; -.
DR GO: 0004872; F:receptor activity; IEA.
DR InterPro: IPR003599; Ig.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Receptor.
SQ SEQUENCE 206 AA; 23158 MW; EEC136B8C9D9F15E CRC64;

Query Match 53.5%; Score 38; DB 13; Length 206;
Best Local Similarity 53.8%; Pred. No. 71;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 SHEGCRSGRAEGS 13
Db 155 SNEGKSSDGEKS 167

RESULT 50
Q8SB58 PRELIMINARY; PRT; 230 AA.
AC Q8SB58;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN OSJNB0091009.1 OR OSJNAA0019N10.21.
OS Oryza sativa (Rice), and

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OS Oryza sativa (japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzaceae; Oryza.  
 OX NCBI\_TaxID=4530, 39947;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=O.sativa;  
 RA Wing R.A., Yu Y., Soderlund C., Chen M., Kim H.-R., Rambo T.,  
 RA Saski C., Henry D., Oates R., Simmons J.;  
 RT "Rice Genomic Sequence."  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=O.sativa (japonica cultivar-group); STRAIN=cv. Nipponbare;  
 RA McCombie W.R., de la Bastide M., Spiegel L., Preston R., Ferraro K.,  
 RA Kuit K., Nascimeto L., Zutavern T., Balijs V., Bell M., Baker J.,  
 RA Miller B., Katzenberger F., Muller S., King L., Sullivan P., Yang C.,  
 RA Dike S., O'Shaughnessy A., Palmer L., Dedhia N.;  
 RT "Genomic sequence for Oryza sativa, Nipponbare strain, clone  
 RT OSJNaa0019N10, from chromosome 10, complete sequence."  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=O.sativa (japonica cultivar-group); STRAIN=cv. Nipponbare;  
 RA The Rice Chromosome 10 Sequencing Consortium;  
 RT "In-depth view of structure, activity, and evolution of 'rice  
 RT chromosome 10."  
 RL Science 300:1566-1569(2003).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=O.sativa (japonica cultivar-group); STRAIN=cv. Nipponbare;  
 RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;  
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AC091732; AAL77150.1; -;  
 DR EMBL; AC124213; AAM74463.1; -;  
 DR EMBL; AE017087; AAP53488.1; -;  
 DR Gramene; Q8SB58; -;  
 KW Hypothetical protein.  
 SQ SEQUENCE 230 AA; 24713 MW; DF6BD62DAC8FE4A1 CRC64;

Query Match 53.5%; Score 38; DB 10; Length 230;  
 Best Local Similarity 46.2%; Pred. No. 79;  
 Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 SHEGCRSGRAEGS 13  
 DB 111 SHRGCMHEESDGN 123

Search completed: April 19, 2004, 17:22:08  
 Job time : 40.5806 secs

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OM protein - protein search, using sw model

Run on: April 19, 2004, 17:08:15 ; Search time 7.33871 Seconds  
(without alignments)  
92.239 Million cell updates/sec

Title: US-10-726-692-22

Perfect score: 71

Sequence: 1 SHEGCRSGEAGS 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	57.7	1053	1 SPS SOLTU	Q43845 solanum tub
2	39	54.9	292	1 PUR3 ARATH	P52422 arabidopsis
3	38	53.5	72	1 MT13 MYTED	P80248 mytilus edu
4	38	53.5	72	1 MT14 MYTED	P80249 mytilus edu
5	38	53.5	72	1 MT1A MYTED	P80246 mytilus edu
6	38	53.5	72	1 MT1B MYTED	O62554 mytilus edu
7	38	53.5	73	1 MT PERVI	Q9u568 perna virid
8	38	53.5	501	1 YB06 YEAST	P38081 saccharomyc
9	37	52.1	278	1 AS13 HUMAN	Q8wxk3 homo sapien
10	37	52.1	627	1 RRN3 YEAST	P36070 saccharomyc
11	37	52.1	796	1 STR3 MOUSE	Q9erg2 mus musculu
12	37	52.1	797	1 STR3 HUMAN	P13033 homo sapien
13	37	52.1	1621	1 ALK MOUSE	P97793 mus musculu
14	36	50.7	207	1 YQJ1 ECOLI	Q46872 escherichia
15	36	50.7	263	1 DAP1 LISIN	Q92aa1 listeria in
16	36	50.7	451	1 NFS1 MOUSE	Q921j3 mus musculu
17	36	50.7	451	1 NFS1 RAT	Q9p3p9 rattus norv
18	36	50.7	457	1 NFS1 HUMAN	Q9v597 homo sapien
19	36	50.7	594	1 Y410 ARATH	P16128 arabidopsis
20	36	50.7	626	1 E2K1 RABIT	P33279 o eukaryoti
21	36	50.7	704	1 FBL1 CHICK	O73775 gallus gall
22	36	50.7	1687	1 MT12 HUMAN	P52746 homo sapien
23	35	49.3	72	1 MT12 MYTED	P80247 mytilus edu
24	35	49.3	89	1 TUBE MYCTU	P02944 mycobacteri
25	35	49.3	164	1 YOR2 AZOVI	O69219 azotobacter
26	35	49.3	184	1 BGB DROME	Q24040 drosophila
27	35	49.3	228	1 Y429 TREPA	O83992 treponema p
28	35	49.3	382	1 P2IN LACLA	Q9ci63 lactococcus
29	35	49.3	475	1 DBDR RAT	P52115 rattus norv
30	35	49.3	487	1 OPT DROME	Q95fw8 drosophila
31	35	49.3	495	1 WD21 HUMAN	Q8wv16 homo sapien
32	35	49.3	562	1 TPPI MOUSE	O89023 mus musculu
33	35	49.3	563	1 TPPI RAT	Q9eqv6 rattus norv

34	35	49.3	588	1 TAN ASPOR	P78581 aspergillus
35	35	49.3	606	1 PO23 POPJA	Q05118 popillia ja
36	35	49.3	622	1 ACHA CHICK	P09482 gallus gall
37	35	49.3	667	1 TS11 GIALA	Q03185 giardia lam
38	35	49.3	719	1 PRH1 SCHPO	Q03319 schizosacch
39	35	49.3	782	1 SP4 MOUSE	Q62445 mus musculu
40	35	49.3	784	1 SP4 HUMAN	Q02446 homo sapien
41	35	49.3	933	1 PRGR HUMAN	P06401 homo sapien
42	35	49.3	950	1 URB1 USTMA	P40349 ustilago ma
43	35	49.3	1083	1 KCH3 HUMAN	Q9uid8 homo sapien
44	35	49.3	1130	1 REPT MOUSE	P97347 mus musculu
45	35	49.3	1182	1 HAIR MOUSE	Q61645 mus musculu
46	35	49.3	3415	1 POLG POWVL	Q04538 t genome po
47	34.5	48.6	2717	1 ZEB1 HUMAN	P15822 homo sapien
48	34	47.9	152	1 YOR4 EAV	P28994 equine arte
49	34	47.9	164	1 YFDN ECOLI	P76510 escherichia
50	34	47.9	171	1 Y334 RALSO	Q8y2k1 ralstonia s

ALIGNMENTS

RESULT 1

ID	SPS_SOLTU	STANDARD	PRT	1053 AA
AC	Q43845			
DT	15-DEC-1998 (Rel. 37, Created)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DT	15-DEC-1998 (Rel. 37, Last annotation update)			
DE	Sucrose-phosphate synthase (EC 2.4.1.14) (UDP-glucose-fructose-phosphate glucosyltransferase).			
DE	SPS.			
GN	Solanum tuberosum (Potato).			
OS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;			
OC	Lamiids; Solanales; Solanaceae; Solanum.			
OX	NCBI_TaxID=4113;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Desiree; TISSUE=Leaf;			
RX	MEDLINE=95201832; PubMed=7894514;			
RA	Zrenner R., Salanoubat M., Willmitzer L., Sonnewald U.;			
RT	"Evidence of the crucial role of sucrose synthase for sink strength			
RL	using transgenic potato plants (Solanum tuberosum L.).";			
RL	Plant J. 7:97-107(1995).			
CC	FUNCTION: Involved in the regulation of carbon partitioning in the			
CC	leaves of plants. May regulate the synthesis of sucrose and			
CC	therefore play a major role as a limiting factor in the export of			
CC	photoassimilates out of the leaf.			
CC	PHOTOASSIMILATES OUT OF THE LEAF.			
CC	CATALYTIC ACTIVITY: UDP-glucose + D-fructose 6-phosphate = UDP +			
CC	sucrose 6-phosphate.			
CC	ENZYMATIC REGULATION: Activity regulated by phosphorylation and			
CC	moderated by concentration of metabolites and light.			
CC	PATHWAY: Sucrose synthesis.			
CC	SUBUNIT: Homodimer or homotetramer (By similarity).			
CC	PTM: Phosphorylated. However, phosphorylation is not essential for			
CC	enzyme function (By similarity).			
CC	SIMILARITY: Belongs to the glucosyltransferase family 1.			

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EMBL: X73477; CAA51872.1; -  
PIR: S34172; S34172.  
InterPro: IPR001296; Glyco\_transf\_1.  
Pfam: PF00534; Glycosyltransferase; Phosphorylation.  
Transferase; Glycosyltransferase; Phosphorylation.  
SEQUENCE 1053 AA; 118292 MW; D6C933798567B20A CRC64;

Query Match 57.7%; Score 41; DB 1; Length 1053;  
 Best Local Similarity 66.7%; Pred. No. 23;  
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 HEGCRSGEAGS 13  
 DB 439 HEGDMDGETEGS 450

RESULT 2  
 ID PUR3 ARATH STANDARD; PRT; 292 AA.  
 AC P52422;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Phosphoribosylglycinamide transferase, chloroplast precursor  
 DE (EC 2.1.2.2) (GART) (GAR transformylase) (5'-phosphoribosylglycinamide  
 DE transformylase)  
 GN PUR3 OR ATIG31220 OR F28K20.18.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=95004650; PubMed=7920700;  
 RA Schnorr K.M., Nygaard P., Laloue M.;  
 RT "Molecular characterization of Arabidopsis thaliana cDNAs encoding  
 RT three purine biosynthetic enzymes.";  
 RL Plant J. 6:113-121(1994).  
 RN [2]  
 RP REVISIONS.  
 RA Schnorr K.M.;  
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=21016719; PubMed=11130712;  
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,  
 RA White O., Alonso J., Altai H., Araujo R., Bowman C.L., Brooks S.Y.,  
 RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,  
 RA Dunn M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,  
 RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,  
 RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,  
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,  
 RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,  
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,  
 RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marzilli A.,  
 RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,  
 RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,  
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,  
 RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,  
 RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,  
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;  
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis  
 RT thaliana.";  
 RL Nature 408:816-820(2000).  
 CC -!- CATALYTIC ACTIVITY: 10-formyltetrahydrofolate + N(1)-(5-phospho-D-  
 CC ribosyl)glycinamide = tetrahydrofolate + N(2)-formyl-N(1)-(5-  
 CC phospho-D-ribosyl)glycinamide.  
 CC -!- PATHWAY: De novo purine biosynthesis; third step.  
 CC -!- SUBCELLULAR LOCATION: Chloroplast.  
 CC -!- SIMILARITY: TO OTHER GART FROM BACTERIA AND EUKARYOTES.  
 CC  
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 CC  
 CC EMBL; AJ005454; CAA06551.1; -.  
 CC PIR; S39418; S39418.  
 CC InterPro; IPR003019; Metallthion\_2.  
 CC InterPro; IPR001008; Metallthion\_2.

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 CC  
 CC EMBL; X74767; CAA52779.2; -.  
 CC EMBL; AC004793; AAD21688.1; -.  
 CC PIR; D86438; D86438.  
 CC HSP; P08179; IGRC.  
 CC InterPro; IPR002376; formyl transf.  
 CC InterPro; IPR001555; GART\_AS.  
 CC Pfam; PF00553; formyl transf; 1.  
 CC PROSITE; PS00373; GART; 1.  
 CC Purine biosynthesis; Transferase; Chloroplast; Transit peptide.  
 FT TRANSIT 1 ?  
 FT CHAIN ? 292  
 FT PHOSPHORIBOSYLGLYCINAMIDE  
 FT FORMYLTRANSFERASE.  
 FT BY SIMILARITY.  
 FT ACT SITE 227 227  
 FT SEQUENCE 292 AA; 32170 MW; 880DBE443C7B493C CRC64;  
 SQ  
 Query Match 54.9%; Score 39; DB 1; Length 292;  
 Best Local Similarity 54.5%; Pred. No. 13;  
 Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 HEGCRSGEAGS 12  
 DB 95 HEGCSDGSVNG 105

RESULT 3  
 ID MT13 MYTED STANDARD; PRT; 72 AA.  
 AC P80248;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Metallothionein 10-III (MT-10-III).  
 OS Mytilus edulis (Blue mussel).  
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;  
 OC Mytiloidea; Mytilidae; Mytilus.  
 OX NCBI\_TaxID=6550;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=94062828; PubMed=8243463;  
 RA Mackay E.A., Overnell J., Dunbar B., Davidson I., Hunziker P.E.,  
 RA Kaegi J.H.R., Forcberg J.E.;  
 RT "Complete amino acid sequences of five dimeric and four monomeric  
 RT forms of metallothionein from the edible mussel Mytilus edulis.";  
 RL Eur. J. Biochem. 218:183-194(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Digestive gland;  
 RX MEDLINE=93206055; PubMed=10190057;  
 RA Barsyte D., White K.N., Lovejoy D.A.;  
 RT "Cloning and characterization of metallothionein cDNAs in the mussel  
 RT Mytilus edulis L. digestive gland.";  
 RL Comp. Biochem. Physiol. 122C:287-296(1999).  
 CC -!- FUNCTION: The metallothioneins are involved in the cellular  
 CC sequestration of toxic metal ions.  
 CC -!- SUBUNIT: Monomer.  
 CC -!- INDUCTION: By cadmium.  
 CC -!- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 2.  
 CC  
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 CC  
 CC EMBL; AJ005454; CAA06551.1; -.  
 CC PIR; S39418; S39418.  
 CC InterPro; IPR003019; Metallthion\_2.  
 CC InterPro; IPR001008; Metallthion\_2.



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RESULT 6
MT1B_MYTED STANDARD; PRT; 72 AA.
ID MT1B_MYTED
AC O62554;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Metallothionein 10-1b (MT-10-1b).
OS Mytilus edulis (Blue mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
OC Mytiloidea; Mytilidae; Mytilus.
OX NCBI_TaxID=6550;
RN [1]_TaxID=6550;
RP SEQUENCE FROM N.A.
RC TISSUE=Digestive gland;
RA MEDLINE=99206055; PubMed=10190057;
RX Barsyte D., White K.N., Lovejoy D.A.;
RT "Cloning and characterization of metallothionein cDNAs in the mussel
RT Mytilus edulis L. digestive gland";
RL Comp. Biochem. Physiol. 122C:287-296(1999).
CC -!- FUNCTION: The metallothioneins are involved in the cellular
CC sequestration of toxic metal ions.
CC -!- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 2.
-----
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-----
DR EMBL; AF092971; AAF22486.1; -
DR EMBL; AF092972; AAF22487.1; -
DR EMBL; AF036904; AAD02054.1; -
DR HSSP; P05106; 1DV2.
DR InterPro; IPR003019; Metallothion_
DR InterPro; IPR001008; Metallothion_2.
DR Pfam; PF00131; metalthio; 1.
DR PRINTS; PR00875; MTWOLLUSC.
KW Metal-binding; Metal-thiolate cluster; Cadmium.
FT CONFLICT 38 38 C -> CGC (IN REF. 1; AAD02054).
SQ SEQUENCE 73 AA; 7254 MW; 42293A9547DF5CA8 CRC64;
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Query Match 53.5%; Score 38; DB 1; Length 73;
Best Local Similarity 70.0%; Pred. No. 4.7; Mismatches 1; Indels 0; Gaps 0;
Matches 7; Conservative 1;

QY 1 SHEGCRSGEA 10
Db | ||||| |
20 SGEGRCCGDA 29

RESULT 8
YBQ6 YEAST STANDARD; PRT; 501 AA.
ID YBQ6 YEAST
AC P38081;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 57.8 kDa protein in PRP6-MUM2 intergenic region.
GN YBR056W OR YBR0510.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]_TaxID=4932;
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=95321020; PubMed=7597852;
RA Aljinovic G., Pohl T.M.;
RT "Sequence and analysis of 24 kb on chromosome II of Saccharomyces
RT cerevisiae.";
RL Yeast 11:475-479(1995).
CC -!- SIMILARITY: Belongs to cellulase family A (family 5 of glycosyl
CC hydrolases).
-----
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-----
DR EMBL; Z35925; CAA84999.1; -
DR EMBL; Z46260; CAA86399.1; -
DR FIR; S45914; S45914.
DR Germonline; 138599; -.
SGD; S0000260; YBR056W.
DR InterPro; IPR001547; Glyco_hydro_5.
DR PROSITE; PS00659; GLYCOSYL_HYDROL_F5; FALSE NEG.
KW Hypothetical protein; Hydrolase; Glycosidase.

```

```

FT ACT_SITE 236 236 PROTON DONOR (BY SIMILARITY).
FT ACT_SITE 333 333 NUCLEOPHILE (BY SIMILARITY).
SQ SEQUENCE 501 AA; 57822 MW; 5133A161736ADD3 CRC64;

Query Match 53.5%; Score 38; DB 1; Length 501;
Best Local Similarity 70.0%; Pred. No. 35;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SHEGCRSGEA 10
Db 188 SHSGSKSGEA 197

RESULT 9
AS13 HUMAN
ID AS13 HUMAN STANDARD; PRT; 278 AA.
AC Q8WXK3; Q96EP7; Q9H8Z1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ankyrin repeat and SOCS box containing protein 13 (ASB-13).
GN ASB13.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Kile B.T., Nicola N.A.;
RT "SOCS box proteins";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Isoqai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Wagatsuma M., Hoesiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saiko K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA Ninomiya K., Iwayanagi T.;
RT "NEO human cDNA sequencing project.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny B., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Hellton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- ALTERNATIVE PRODUCTS:
CC Name=1;
CC IsoId=Q8WXK3-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q8WXK3-2; Sequence=VSP 000272, VSP 000273;
CC Note=No experimental confirmation available;

```

us-10-726-692-22.rsp

Page 5

CC -!- SIMILARITY: Contains 6 ANK repeats.  
CC -!- SIMILARITY: Contains 1 SOCS box domain.  
CC -!- CAUTION: Ref.1 sequence differs from that shown due to a  
frame shift in position 14.  
CC -----  
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CC -----  
CC EMBL; AF403031; AAL57350.1; ALT\_FRAME.  
CC EMBL; AK023196; BAB14456.1; -.  
CC EMBL; BC012056; AAI12056.1; -.  
CC Genew; HGNC:19765; ASB13.  
CC InterPro; IPR002110; ANK.  
CC InterPro; IPR001496; SOCS\_C.  
CC Pfam; PF00023; ank; 6.  
CC PRINTS; PR01415; ANKYRIN.  
CC SMART; SM00248; ANK; 6.  
CC PROSITE; PS50088; ANK\_REPEAT; 6.  
CC PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
CC PROSITE; PS50225; SOCS; 1.  
CC ANK repeat; Repeat; Alternative splicing.  
CC REPEAT 18 47 ANK 1.  
CC REPEAT 51 80 ANK 2.  
CC REPEAT 84 113 ANK 3.  
CC REPEAT 116 145 ANK 4.  
CC REPEAT 149 178 ANK 5.  
CC REPEAT 181 210 ANK 6.  
CC DOMAIN 229 278 SOCS BOX.  
CC VARSPLIC 173 173 G -> A (in isoform 2).  
CC VARSPLIC 174 278 /FTID=VSP 000272.  
CC VARSPLIC 104 104 Missing (in isoform 2).  
CC CONFLICT 104 104 /FTID=VSP 000273.  
CC CONFLICT 129 129 L -> S (IN REF. 2).  
CC CONFLICT 129 129 S -> D (IN REF. 1).  
CC SEQUENCE 278 AA; 30007 MW; 6E54725A70AB32EF CRC64;  
Query Match 52.1%; Score 37; DB 1; Length 278;  
Best Local Similarity 60.0%; Pred. No. 29;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 2 HEGCRSGEAE 11  
Db 122 HEACMSGSE 131  
RESULT 10  
ID RN3 YEAST STANDARD; PRT; 627 AA.  
AC P36070;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE RNA polymerase I specific transcription initiation factor RN3.  
GN RN3 OR YKL125W.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
RX MEDLINE=96324404; PubMed=8670901;  
RA Yamamoto R.T., Nogi Y., Dodd J.A., Nomura M.;  
RT "RN3 gene of Saccharomyces cerevisiae encodes an essential RNA  
polymerase I transcription factor which interacts with the polymerase  
independently of DNA template.";  
RL EMBL J. 15:3964-3973 (1996).  
RN [2]  
RP SEQUENCE FROM N.A.

RA Rad M.R., Xu G., Kirchrath L., Fritz C., Keuchel H., Hollenberg C.P.;  
 RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Required for efficient transcription initiation by RNA  
 CC polymerase I. Interacts with Pol I in the absence of template DNA  
 CC and stimulates recruitment of Pol I, but does not remain as part  
 CC of stable pre-initiation complex.  
 CC -!- SUBUNIT: Monomer (Probable).  
 CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).  
 CC -!- SIMILARITY: TO S.POMBE SPAC1866.11C AND C.ELEGANS C36E8.1.  
 CC  
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 CC  
 CC EMBL; 271927; CAA96470.1; -.  
 CC EMBL; 281125; CA81966.1; -.  
 CC PIR; S37954; S37954.  
 CC Germonline; 139881; -.  
 CC TRANSFAC; T03565; -.  
 CC SGD; S0001608; RRM3.  
 CC InterPro; IPR007991; RNApoli\_tif\_RRM3.  
 CC Pfam; PF05327; RRM3; 1.  
 CC Transcription regulation; Nuclear protein.  
 CC DOMAIN 252 259 POLY-ASP.  
 CC FT REPEAT 267 274 POLY-ASP.  
 CC FT DOMAIN 277 280 POLY-ASP.  
 CC FT DOMAIN 546 549 POLY-ASN.  
 CC SEQUENCE 627 AA; 72387 MW; A31E7386A9873FDB CRC64;  
 SQ  
 Query Match 52.1%; Score 37; DB 1; Length 627;  
 Best Local Similarity 61.5%; Pred. No. 67;  
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 SHEGCRSGEAGS 13  
 Db 286 SNEELRSGAAGS 298  
 ||:| ||| |||  
 RESULT 11  
 STR3 MOUSE  
 ID STR3\_MOUSE STANDARD; PRT; 796 AA.  
 AC Q9ERG2;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Striatin 3 (Cell-cycle autoantigen SG2NA) (S/G2 antigen).  
 GN STRN3 OR SG2NA OR GS2NA.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Castets F., Rakitina T.;  
 RT "Expression analysis of SG2NA isoform.";  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP TISSUE SPECIFICITY.  
 RX MEDLINE=20347911; PubMed=10748158;  
 RA Castets F., Rakitina T., Gaillard S., Moqrigh A., Mattei M.-G.,  
 RA Monneron A.;  
 RT "Zinedin, SG2NA, and striatin are calmodulin-binding, WD repeat  
 RT proteins principally expressed in the brain.";  
 RL J. Biol. Chem. 275:19970-19977(2000).  
 CC -!- FUNCTION: Binds calmodulin in a calcium dependent manner. May  
 CC function as scaffolding or signaling protein (By similarity).  
 CC -!- SUBUNIT: INTERACTS WITH PROTEIN PHOSPHATASE 2A (PP2A) (POTENTIAL).  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic and membrane-bound.  
 CC -!- TISSUE SPECIFICITY: MAINLY EXPRESSED IN THE BRAIN AND MUSCLES BUT

CC IS ALSO DETECTED AT LOW LEVELS IN VARIOUS TISSUES SUCH AS KIDNEY,  
 CC SPLEEN AND LUNG.  
 CC -!- SIMILARITY: Belongs to the WD-repeat striatin family.  
 CC -!- SIMILARITY: Contains 6 WD repeats.  
 CC  
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 CC  
 CC EMBL; AF307777; AAG24454.1; -.  
 CC MGD; MGI:2151064; Strn3.  
 CC InterPro; IPR001680; WD40.  
 CC Pfam; PF00400; WD40; 6.  
 CC PRINTS; PR00320; GPROTEINRPT.  
 CC ProDom; PD000018; WD40; 2.  
 CC SMART; SM00320; WD40; 7.  
 CC PROSITE; PS00678; WD\_REPEATS\_1; 2.  
 CC PROSITE; PS50082; WD\_REPEATS\_2; 4.  
 CC PROSITE; PS50294; WD\_REPEATS\_REGION; 1.  
 CC Calmodulin-binding; Repeat; WD repeat; Coiled coil; Antigen.  
 KW DOMAIN 77 136 COILED COIL (POTENTIAL).  
 FT DOMAIN 166 183 CALMODULIN-BINDING (POTENTIAL).  
 FT REPEAT 477 516 WD 1.  
 FT REPEAT 530 569 WD 2.  
 FT REPEAT 583 622 WD 3.  
 FT REPEAT 678 717 WD 4.  
 FT REPEAT 720 759 WD 5.  
 FT REPEAT 766 795 WD 6.  
 FT DOMAIN 6 13 POLY-GLY.  
 FT SITE 71 79 CAVESOLIN-BINDING (POTENTIAL).  
 SQ SEQUENCE 796 AA; 87150 MW; 161FAF5DDEBE23DD CRC64;  
 Query Match 52.1%; Score 37; DB 1; Length 796;  
 Best Local Similarity 70.0%; Pred. No. 85;  
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 HEGCRSGEAE 11  
 Db 405 HEGARAEAE 414  
 ||| | | |  
 RESULT 12  
 STR3 HUMAN  
 ID STR3\_HUMAN STANDARD; PRT; 797 AA.  
 AC Q13033; Q9NR45;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Striatin 3 (Cell-cycle autoantigen SG2NA) (S/G2 antigen).  
 GN STRN3 OR SG2NA OR GS2NA.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).  
 RC TISSUE=Liver;  
 RX MEDLINE=95169142; PubMed=7864889;  
 RA Muro Y., Chan E.K., Landberg G., Tan E.M.;  
 RT "A cell-cycle nuclear autoantigen containing WD-40 motifs expressed  
 RT mainly in S and G2 phase cells.";  
 RL Biochem. Biophys. Res. Commun. 207:1029-1037(1995).  
 RN [2]  
 RP SEQUENCE OF 120-797 FROM N.A. (ISOFORM BETA).  
 RX MEDLINE=20347911; PubMed=10748158;  
 RA Castets F., Rakitina T., Gaillard S., Moqrigh A., Mattei M.-G.,  
 RA Monneron A.;  
 RT "Zinedin, SG2NA, and striatin are calmodulin-binding, WD repeat  
 RT proteins principally expressed in the brain.";

RL J. Biol. Chem. 275:19970-19977(2000).

CC -!- FUNCTION: Binds calmodulin in a calcium dependent manner. May

CC function as scaffolding or signaling protein.

CC -!- SUBUNIT: INTERACTS WITH PROTEIN PHOSPHATASE 2A (PP2A) (POTENTIAL).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic and membrane-bound (By

CC similarity).

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Comment=Additional isoforms seem to exist;

CC Name=Beta;

CC IsoId=Q13033-1; Sequence=Displayed;

CC Name=Alpha;

CC IsoId=Q13033-2; Sequence=VSP\_006786;

CC -!- SIMILARITY: Belongs to the WD-repeat striatin family.

CC -!- SIMILARITY: Contains 6 WD repeats.

CC -!- CAUTION: Was originally (Ref.1) thought to be nuclear.

CC

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CC -----

DR EMBL; U17989; AAB81551.1; -.

DR EMBL; AF243424; AAF81201.1; -.

DR PIR; JC2522; JC2522.

DR Genew; HGNC:15720; STRN3.

DR GO; GO:0005829; C:cytosol; NAS.

DR GO; GO:0005624; C:membrane fraction; NAS.

DR GO; GO:0005634; C:nucleus; IDA.

DR GO; GO:0005516; P:calmodulin binding; NAS.

DR GO; GO:0007049; P:cell cycle; IDA.

DR InterPro; IPR001680; WD40.

DR Pfam; PF00400; WD40; 6.

DR PRINTS; PR00320; GPROTEINRPT.

DR ProDom; PD000018; WD40; 2.

DR SMART; SM00320; WD40; 2.

DR PROSITE; PS00678; WD\_REPEATS\_1; 2.

DR PROSITE; PS00678; WD\_REPEATS\_2; 4.

DR PROSITE; PS50082; WD\_REPEATS\_2; 4.

DR PROSITE; PS50294; WD\_REPEATS\_REGION; 1.

DR Calmodulin-binding; Repeat; WD repeat; Coiled coil; Antigen;

KW Alternative splicing.

KW DOMAIN 77 136 COILED COIL (POTENTIAL).

FT DOMAIN 166 183 CALMODULIN-BINDING (POTENTIAL).

FT REPEAT 478 517 WD 1.

FT REPEAT 531 570 WD 2.

FT REPEAT 584 623 WD 3.

FT REPEAT 679 718 WD 4.

FT REPEAT 721 760 WD 5.

FT REPEAT 767 796 WD 6.

FT DOMAIN 6 13 POLY-GLY.

FT SITE 71 79 CAVEOLIN-BINDING (POTENTIAL).

FT VARSPPLIC 330 413 Missing (in isoform Alpha).

FT /FTID=VSP\_006786.

SQ SEQUENCE 797 AA; 87133 MW; AD83F255CC52185D CRC64;

Query Match 52.1%; Score 37; DB 1; Length 797;

Best Local Similarity 70.0%; Pred. No. 85;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 HEGCRSGEAE 11

Db 406 HEGARAEAE 415

RESULT 13

ALK\_MOUSE

ID ALK\_MOUSE STANDARD; PRT; 1621 AA.

AC P97793;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE ALK tyrosine kinase receptor precursor (EC 2.7.1.112) (Anaplastic

DE lymphoma kinase).

GN ALK.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_taxid=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain, and Testis;

RX MEDLINE=97178963; PubMed=9053841;

RA Iwahara T., Fujimoto J., Wen D., Cupples R., Bucay N., Arakawa T.,

RA Mori S., Ratzkin B., Yamamoto T.;

RT "Molecular characterization of ALK, a receptor tyrosine kinase

RT expressed specifically in the nervous system.";

RL Oncogene 14:439-449(1997).

CC -!- FUNCTION: Orphan receptor with a tyrosine-protein kinase activity.

CC Appears to play an important role in the normal development and

CC function of the nervous system.

CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein

CC tyrosine phosphate.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).

CC -!- SIMILARITY: Belongs to the Tyr family of protein kinases. Insulin

CC receptor subfamily.

CC -!- SIMILARITY: Contains 1 LDL-receptor class A domain.

CC -!- SIMILARITY: Contains 2 MAM domains.

CC

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CC -----

DR EMBL; D83002; BAAL1673.1; -.

DR PIR; T30200; T30200.

DR HSP; P08631; IAD5.

DR MGD; MGI:103305; ALK.

DR InterPro; IPR002172; LDL receptor\_A.

DR InterPro; IPR000598; MAM\_domain.

DR InterPro; IPR000719; Prot\_kinase.

DR InterPro; IPR002011; RecepttyrkinaI.

DR InterPro; IPR001245; Tyr\_kinase.

DR InterPro; IPR008266; Tyr\_kinase\_AS.

DR Pfam; PF00629; MAM; 1.

DR Pfam; PF00669; pkinase; 1.

DR PRINTS; PR00109; TYRKINASE.

DR ProDom; PD000001; Prot\_kinase; 1.

DR SMART; SM00192; LDLA; 1.

DR SMART; SM00219; TyrK; 1.

DR PROSITE; PS00740; MAM\_1; FALSE\_NEG.

DR PROSITE; PS50060; MAM\_2; 2.

DR PROSITE; PS01209; LDLRA\_1; FALSE\_NEG.

DR PROSITE; PS50068; LDLRA\_2; FALSE\_NEG.

DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.

DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.

DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.

DR PROSITE; PS00239; RECEPTOR\_TYR\_KIN\_II; 1.

KW Transferase; Tyrosine-protein kinase; Transmembrane; ATP-binding;

KW Phosphorylation; Receptor; Glycoprotein; Repeat; Signal.

FT SIGNAL 1 18

FT CHAIN 19 1621 ALK TYROSINE KINASE RECEPTOR.

FT DOMAIN 19 1042 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 1043 1063 POTENTIAL.

FT DOMAIN 1064 1621 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 268 431 MAM 1.

FT DOMAIN 441 477 LDL-RECEPTOR CLASS A.

FT DOMAIN 482 640 MAM 2.

FT DOMAIN 1120 1396 PROTEIN KINASE.

FT DOMAIN 820 944 GLY-RICH.

FT NP\_BIND 1126 1134 ATP (BY SIMILARITY).



```

FT BINDING 1154 1154 ATP (BY SIMILARITY).
FT ACT_SITE 1253 1253 BY SIMILARITY.
FT MOD_RES 1286 1286 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CARBOHYD 174 174 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 248 248 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 328 328 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 415 415 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 428 428 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 449 449 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 567 567 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 575 575 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 631 631 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 673 673 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 713 713 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 812 812 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 868 868 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 890 890 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 990 990 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 1621 AA; 174919 MW; 16E252BF21AADE22 CRC64;

Query Match 52.1%; Score 37; DB 1; Length 1621;
Best Local Similarity 54.5%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 HEGCRSGEAG 12
Db 462 HQDCAQGEDEG 472

RESULT 14
YQJI_ECOLI
ID YQJI_ECOLI STANDARD; PRT; 207 AA.
AC Q46872;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical protein YQJI.
GN YQJI OR B3071 OR SF3112 OR S3318.
OS Escherichia coli, and
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562, 623;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RL "The complete genome sequence of Escherichia coli K-12.";
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
RX MEDLINE=2272406; PubMed=12384590;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157.";
RL Nucleic Acids Res. 30:4432-4441(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=S.flexneri; STRAIN=2457T / ATCC 700930 / Serotype 2a;
RX MEDLINE=22590274; PubMed=12704152;
RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
RA Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
Schwartz D.C., Blattner F.R.;
RT "Complete genome sequence and comparative genomics of Shigella
RT flexneri serotype 2a strain 2457T.";
RL Infect. Immun. 71:2775-2786(2003).
CC -----
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CC -----
CC EMBL; U28379; AAA89150.1; -.
CC EMBL; AE000389; AAC76106.1; -.
CC EMBL; AE015322; AAN44586.1; -.
CC EMBL; AE016988; AAP18398.1; -.
CC PIR; D65095; D65095.
CC EcoGene; EG12954; YQJI.
CC InterPro; IPR005149; PadR.
CC Pfam; PF03551; PadR; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 207 AA; 23401 MW; DD3D108D83E087F7 CRC64;

Query Match 50.7%; Score 36; DB 1; Length 207;
Best Local Similarity 75.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 HEGCRSGE 9
Db 17 HEGCKGGE 24

RESULT 15
DAPB_LISIN
ID DAPB_LISIN STANDARD; PRT; 263 AA.
AC Q92AA1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Dihydropicolinate reductase (EC 1.3.1.26) (DHPR).
GN DAPB OR LIN2021.
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1642;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIP 11262 / Serovar 6a;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaser P., Frangoul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kneft J., Kuhn M., Kunst F., Kurapkai G.,
RA Madueno E., Maitournan A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordisiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehlend J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
CC -!- CATALYTIC ACTIVITY: 2,3,4,5-tetrahydropicolinate + NAD(P)(+) =
CC 2,3-dihydropicolinate + NAD(P)H.
CC -!- PATHWAY: Biosynthesis of diaminopimelate and lysine from aspartate
CC semialdehyde; second step.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the dihydropicolinate reductase family.
CC -----
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FT CHAIN 55 451 MITOCHONDRIAL.
FT CYSTEINE DESULFURASE, ISOFORM
FT CYTOPLASMIC.
FT INIT MET 55 55 FOR ISOFORM CYTOPLASMIC.
FT BINDING 252 252 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
FT ACT SITE 375 375 BY SIMILARITY.
SQ SEQUENCE 451 AA; 50012 MW; 8E9083D6222F3087 CRC64;

Query Match 50.7%; Score 36; DB 1; Length 451;
Best Local Similarity 70.0%; Pred. No. 71;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 EGCGRGEAEG 12
Db 155 DSCRSLAEAG 164

RESULT 18
ID NFS1_HUMAN STANDARD; PRT; 457 AA.
AC Q9Y697; Q9NTZ5; Q9Y481;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cysteine desulfurase, mitochondrial precursor (EC 4.4.1.1-) (HUSSY-08).
GN NFS1 OR NIFS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99102954; PubMed=9885568;
RA Land T., Rouault T.A.;
RT "targeting of a human iron-sulfur cluster assembly enzyme, nifs, to
RT different subcellular compartments is regulated through alternative
RT AUG utilization.";
RL Mol. Cell 2:807-815(1998).
RN [2]
RP REVISIONS TO 380-402.
RA Land T., Rouault T.A.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE OF 140-457 FROM N.A.
RX MEDLINE=21064499; PubMed=11124703;
RA Stanchi F., Bertocco E., Toppo S., Dioguardi R., Simionati B.,
RA Canata N., Zimbello R., Lanfranchi G., Valle G.;
RT "Characterization of 16 novel human genes showing high similarity to
RT yeast sequences.";
RL Yeast 18:69-80(2001).
RN [4]
RP SEQUENCE OF 137-457 FROM N.A.
RA Laird G.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: Catalyzes the removal of elemental sulfur from cysteine
CC to produce alanine. It supplies the inorganic sulfur for iron-
CC sulfur (Fe-S) clusters.
CC -!- COFACTOR: Pyridoxal phosphate (By similarity).
CC -!- SUBCELLULAR LOCATION: Mitochondrial and cytoplasmic.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative initiation;
CC Comment=2 isoforms, Mitochondrial (shown here) and Cytoplasmic,
CC are produced by alternative initiation;
CC -!- TISSUE SPECIFICITY: Predominantly expressed in heart and skeletal
CC muscle. Also found in brain, liver and pancreas.
CC -!- SIMILARITY: Belongs to class-V of pyridoxal-phosphate-dependent
CC aminotransferases. Nifs/iscs subfamily.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF097025; AAD09187.2; -.
DR EMBL; AJ010952; CAA09424.1; -.
DR EMBL; AL109827; CAB87612.1; -.
DR Genew; HGNC:15910; NFS1.
DR MIM; 603485; -.
DR GO; GO:0005829; C:cytosol; TAS.
DR GO; GO:0005739; C:mitochondrion; TAS.
DR GO; GO:0005634; C:nucleus; TAS.
DR GO; GO:0006461; P:protein complex assembly; TAS.
DR GO; GO:0000936; P:sulfur amino acid metabolism; TAS.
DR InterPro; IPR000192; Aminotrans_V.
DR Pfam; PF00266; aminotran_5; 1.
DR PROSITE; PS00595; AA_TRANSFER_CLASS_5; 1.
KW Lyase; Pyridoxal phosphate; Mitochondrion; Transit peptide;
KW Alternative initiation.
FT TRANSIT 1 ?
FT CHAIN ? 457
FT CHAIN 61 457
FT INIT MET 61 61
FT BINDING 258 258 FOR ISOFORM CYTOPLASMIC.
FT ACT SITE 381 381 BY SIMILARITY.
FT CONFLICT 412 412 R -> A (IN REF. 1).
FT CONFLICT 431 431 K -> N (IN REF. 1).
SQ SEQUENCE 457 AA; 50253 MW; 03FDBFFCA0089669 CRC64;

Query Match 50.7%; Score 36; DB 1; Length 457;
Best Local Similarity 70.0%; Pred. No. 72;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 EGCGRGEAEG 12
Db 161 DSCRSLAEAG 170

RESULT 19
ID Y410_ARATH STANDARD; PRT; 594 AA.
AC P16128; Q9SB82;
DT 01-APR-1990 (Rel. 14, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical protein At4g18490.
GN AT4G18490 OR F28J12.150.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsia.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083488; PubMed=10617198;
RA Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N.,
RA Harris B., Ansgore W., Brandt P., Grivell L.A., Rieger M.,
RA Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,
RA Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidheini T.,
RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
RA Vos P., Hohnsels J., Zimmermann W., Wedler H., Robben J.,
RA Langham S.-A., McCullagh B., Bilham L., Chuang Y.-J., Vandenbussche F.,
RA Van der Schueren J., Grymonprez B., Baatens I., Aert R., Defoor E.,
RA Braeken M., Weltjens I., Voet M., Baatens I., Hilbert H., Braun M.,
RA Weitzenegger T., Bothe G., Ransperger U., Staveren M., Dirkse W.,
RA Holzer E., Brandt A., Peters S., van Staveren M., Koetter P.,
RA Moolman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
RA Berner S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
RA De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R.,
RA Van Montagu M., Rogers J., Cronin A., Quail M.A., Bray-Allen S.,

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Clark L., Doggett J., Hall S., Kay M., Lennard N., McLeay K., Mayes R.,  
 Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,  
 Borkova D., Bloeker H., Scharfe M., Grimm M., Loehner T.-H.,  
 Gabel C., Fuchs M., Maarse A.C., Schaefer M., Mueller-Auer S.,  
 Neumann S., Argirou A., Vitale D., Granderath K., Dauner D., Herzl A.,  
 Masenat O., Quigley F., Ciba G., Muendlein A., Felber R.,  
 Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,  
 Chedof F., Cooke R., Berger C., Monfort A., Casacuberta E.,  
 Gibbons T., Weber N., Vandenbol M., Barges M., Terol J., Torres A.,  
 Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,  
 Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bielek C.,  
 Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,  
 Zaccaria P., Devan M., Wilson R.K., de la Bastide M., Habermann K.,  
 Parnell L., Dedha N., Gnoj L., Schutz K., Huang E., Spiegel L.,  
 Stokem M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,  
 Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,  
 Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,  
 Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,  
 Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.W.,  
 Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,  
 Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,  
 Antonolu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,  
 Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,  
 Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,  
 Granat S., Shoddy N., Hasegawa A., Hameed A., Lodi M., Johnson A.,  
 Chen E., Marra M.A., Martensen R., McCombie W.R.,  
 "Sequence and analysis of chromosome 4 of the plant Arabidopsis  
 thaliana";  
 RL Nature 402:769-777(1999).  
 RL [2]  
 RP SEQUENCE OF 1-290 FROM N.A.  
 RC STRAIN-cv. Columbia;  
 EX MEDLINE=90228329; PubMed=2158442;  
 RA Koncz C., Mayerhofer R., Koncz-Kalman Z., Nawrath C., Reiss B.,  
 Redei G.P., Schell J.;  
 RT "Isolation of a gene encoding a novel chloroplast protein by T-DNA  
 tagging in Arabidopsis thaliana";  
 RL EMBO J. 9:1337-1346(1990).  
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 CC -----  
 DR EMBL; AL021710; CAA16729.1; -;  
 DR EMBL; AL161548; CAB78851.1; -;  
 DR EMBL; X51799; CAA36096.1; -;  
 DR PIR; T04545; T04545.  
 KW Hypothetical protein.  
 SQ SEQUENCE 594 AA; 65822 MW; 39618B936AC3C34E CRC64;  
 Query Match 50.7%; Score 36; DB 1; Length 594;  
 Best Local Similarity 70.0%; Pred. No. 94;  
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 HEGCRSGEAE 11  
 DB 180 HELCRSGTKE 189  
 RESULT 20  
 E2KI RABIT  
 ID E2KI RABIT STANDARD; PRT; 626 AA.  
 AC P33279;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Eukaryotic translation initiation factor 2 alpha kinase 1  
 DE (EC 2.7.1.37) (Heme-regulated eukaryotic initiation factor eIF-2-alpha

kinase) (Heme-regulated inhibitor) (Heme-controlled repressor) (HCR)  
 DE (Hemin-sensitive initiation factor-2 alpha kinase).  
 GN EIF2AK1 OR HRI.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9996;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Reticulocytes;  
 RX MEDLINE=91352063; PubMed=1679235;  
 RA Chen J.-J., Throop M.S., Gehrke L., Kuo I., Pal J.K., Brodsky M.,  
 London I.M.;  
 RT "Cloning of the cDNA of the heme-regulated eukaryotic initiation  
 factor 2 alpha (eIF-2 alpha) kinase of rabbit reticulocytes: homology  
 RT to yeast GCN2 protein kinase and human double-stranded-RNA-dependent  
 RT eIF-2 alpha kinase";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:7729-7733(1991).  
 RN [2]  
 RP SEQUENCE OF 166-178; 454-467 AND 506-525.  
 RC TISSUE=Reticulocytes;  
 RX MEDLINE=91110520; PubMed=1671169;  
 RA Chen J.-J., Pal J.K., Petryshyn R., Kuo I., Yang J.M., Throop M.S.,  
 Gehrke L., London I.M.;  
 RT "Amino acid microsequencing of internal tryptic peptides of heme-  
 RT regulated eukaryotic initiation factor 2 alpha subunit kinase:  
 RT homology to protein kinases";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:315-319(1991).  
 RN [3]  
 RP PHOSPHORYLATION OF EIF2S1 AT SER-48.  
 RC TISSUE=Reticulocytes;  
 RX MEDLINE=86304412; PubMed=3745199;  
 RA Wettenhall R.B.H., Kudlicki W., Kramer G., Hardesty B.;  
 RT "The NH2-terminal sequence of the alpha and gamma subunits of  
 RT eukaryotic initiation factor 2 and the phosphorylation site for the  
 RT heme-regulated eIF-2 alpha kinase";  
 RL J. Biol. Chem. 261:12444-12447(1986).  
 RN [4]  
 RP REVIEW.  
 RX MEDLINE=95201039; PubMed=7893826;  
 RA Chen J.-J., Crosby J.S., London I.M.;  
 RT "Regulation of heme-regulated eIF-2 alpha kinase and its expression  
 RT in erythroid cells";  
 RL Biochimie 76:761-769(1994).  
 RN [5]  
 RP MUTAGENESIS OF LYS-199, AUTOPHOSPHORYLATION, AND HEME-BINDING.  
 RX MEDLINE=20138267; PubMed=10671563;  
 RA Rafie-Kolpin M., Chafalo P.J., Hussain Z., Hahn J., Uma S.,  
 Matts R.L., Chen J.-J.;  
 RT "Two heme-binding domains of heme-regulated eukaryotic initiation  
 RT factor-2alpha kinase. N terminus and kinase insertion";  
 RL J. Biol. Chem. 275:5171-5178(2000).  
 RN [6]  
 RP INTERACTION WITH A MULTIPROTEIN COMPLEX CONTAINING HSP90; PPP5C AND  
 RP CDC37.  
 RX MEDLINE=22017694; PubMed=12022881;  
 RA Shao J., Hartson S.D., Matts R.L.;  
 RT "Evidence that protein phosphatase 5 functions to negatively modulate  
 RT the maturation of the Hsp90-dependent heme-regulated eIF2alpha  
 RT kinase";  
 RL Biochemistry 41:6770-6779(2002).  
 RN [7]  
 RP REGULATION BY NITRIC OXIDE AND CARBON MONOXIDE.  
 RX MEDLINE=22319058; PubMed=12431098;  
 RA Ishikawa H., Yun B.-G., Takahashi S., Hori H., Matts R.L.,  
 Ishimori K., Morishima I.;  
 RT "NO-induced activation mechanism of the heme-regulated eIF2alpha  
 RT kinase";  
 RL J. Am. Chem. Soc. 124:13696-13697(2002).  
 CC -1- FUNCTION: Mediates down-regulation of protein synthesis in heme-  
 CC deficient reticulocytes and in response to various stress  
 CC conditions by the phosphorylation of EIF2S1 at Ser-48 and Ser-51.  
 CC Protein synthesis is inhibited at the level of initiation.

CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
 CC -!- ENZYME REGULATION: Hemin inactivates EIP2AK1 by promoting the  
 CC formation of a disulfide-linked homodimer. Binding of nitric oxide  
 CC (NO) to the heme iron in the N-terminal heme-binding domain  
 CC activates the kinase activity, while binding of carbon monoxide  
 CC (CO) suppresses kinase activity.  
 CC -!- SUBUNIT: Synthesized in an inactive form that binds to the N-  
 CC terminal domain of CDC37. Has to be associated with a multiprotein  
 CC complex containing Hsp90, CDC37 and PPP5C for maturation and  
 CC activation by autophosphorylation. The phosphatase PPP5C modulates  
 CC this activation. Homodimer; non-covalently bound in the absence of  
 CC hemin. Converted to an inactive disulfide linked homodimer in the  
 CC presence of hemin.  
 CC -!- TISSUE SPECIFICITY: Reticulocytes.  
 CC -!- PTM: Activated by autophosphorylation (at least 5 moles of  
 CC phosphate per mole of enzyme). Phosphorylated predominantly on  
 CC serine and threonine residues, but also on tyrosine residues (By  
 CC similarity).  
 CC -!- MISCELLANEOUS: Can bind 2 molecules of heme per polypeptide chain.  
 CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. GCN2  
 CC subfamily.  
 CC -!- SIMILARITY: Contains 2 heme regulatory motif (HRM) repeats.  
 CC -----  
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 CC -----  
 CC EMBL; M69035; AA31241.1; -.  
 CC F1R; A41284; A41284.  
 CC DR GO; GO:0005737; C:cytoplasm; ISS.  
 CC DR GO; GO:0005524; F:ATP binding; NAS.  
 CC DR GO; GO:0004694; F:eukaryotic translation initiation factor 2a. . . ; IDA.  
 CC DR GO; GO:0020037; F:heme binding; ISS.  
 CC DR GO; GO:0042803; F:protein homodimerization activity; ISS.  
 CC DR GO; GO:0046777; F:autophosphorylation; ISS.  
 CC DR GO; GO:0008285; P:negative regulation of cell proliferation; ISS.  
 CC DR GO; GO:0046986; P:negative regulation of hemoglobin biosynthesis; ISS.  
 CC DR GO; GO:0045993; P:negative regulation of translational initia. . . ; ISS.  
 CC DR GO; GO:0018105; P:peptidyl-serine phosphorylation; IDA.  
 CC DR GO; GO:0006411; P:regulation of protein biosynthesis; NAS.  
 CC DR GO; GO:0009605; P:response to external stimulus; ISS.  
 CC DR GO; GO:0006950; P:response to stress; ISS.  
 CC DR InterPro; IPR000719; Prot kinase.  
 CC DR InterPro; IPR008271; Ser Thr\_pkin\_AS.  
 CC DR Pfam; PF00069; pkinase; 1.  
 CC DR ProDom; PD000001; Prot\_kinase; 2.  
 CC DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 CC DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 CC DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
 CC DR Transferrase; Kinase; Serine/threonine-protein kinase;  
 CC Protein synthesis inhibitor; ATP-binding; Repeat; Phosphorylation.  
 CC FT DOMAIN 170 578  
 CC NP\_BIND 176 184 ATP (BY SIMILARITY).  
 CC FT BINDING 199 199 ATP (BY SIMILARITY).  
 CC FT ACT\_SITE 437 437 BY SIMILARITY.  
 CC FT REPEAT 405 410 HRM 1.  
 CC FT REPEAT 547 552 HRM 2.  
 CC FT MOD\_RES 483 483 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 CC FT MUTAGEN 199 199 K->R; ABOLISHES KINASE ACTIVITY.  
 CC SQ SEQUENCE 626 AA; 70274 MW; 4E47CC0173289B57 CRC64;

Query Match 50.7%; Score 36; DB 1; Length 626;  
 Best Local Similarity 77.8%; Pred. No. 99;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 4 GCRSGEAG 12  
 | | | | |  
 Db 7 GTRGGEAG 15

RESULT 21  
 FBL1\_CHICK  
 ID FBL1\_CHICK STANDARD; PRT; 704 AA.  
 AC 073775; 073774;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Fibulin-1 precursor.  
 GN FBLN1.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS C AND D).  
 RC TISSUE=Embryo;  
 RX MEDLINE=99120531; PubMed=9923656;  
 RA Barth J.L., Argraves K.M., Roark E.F., Little C.D., Argraves W.S.;  
 RT "Identification of chicken and C. elegans fibulin-1 homologs and  
 RL characterization of the C. elegans fibulin-1 gene.";  
 RL Matrix Biol. 17:635-646(1998).  
 CC -!- FUNCTION: Incorporated into fibronectin-containing matrix fibers.  
 CC May play a role in cell adhesion and migration along protein  
 CC fibers within the extracellular matrix (ECM). Could be important  
 CC for certain developmental processes and contribute to the  
 CC supramolecular organization of ECM architecture, in particular to  
 CC those of basement membranes.  
 CC -!- SUBUNIT: Interacts with itself and with various extracellular  
 CC matrix components (by similarity).  
 CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=D;  
 CC IsoId=073775-2; Sequence=Displayed;  
 CC Name=C;  
 CC IsoId=073775-1; Sequence=VSP\_007378;  
 CC -!- SIMILARITY: Belongs to the fibulin family.  
 CC -!- SIMILARITY: Contains 3 anaphylatoxin-like domains.  
 CC -!- SIMILARITY: Contains 9 EGF-like domains.  
 CC -----  
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 CC -----  
 CC EMBL; AF051399; AAC05387.1; -.  
 CC DR EMBL; AF051400; AAC05388.1; -.  
 CC DR HSP; P00742; IHCG.  
 CC DR InterPro; IPR000020; Anaphylatoxin.  
 CC DR InterPro; IPR000152; Asx hydroxyl\_S.  
 CC DR InterPro; IPR001881; EGF\_Ca.  
 CC DR InterPro; IPR006209; EGF\_like.  
 CC DR InterPro; IPR006210; IEGF.  
 CC DR Pfam; PF01821; ANATO; 2.  
 CC DR Pfam; PF00008; EGF; 6.  
 CC DR SMART; SM00104; ANATO; 3.  
 CC DR SMART; SM00181; EGF; 9.  
 CC DR SMART; SM00179; EGF\_CA; 8.  
 CC DR PROSITE; PS01177; ANAPHYLATOXIN\_1; 1.  
 CC DR PROSITE; PS01178; ANAPHYLATOXIN\_2; 2.  
 CC DR PROSITE; PS00010; ASX\_HYDROXYL; 5.  
 CC DR PROSITE; PS00022; EGF\_1; FALSE\_NEG.  
 CC DR PROSITE; PS01186; EGF\_2; 3.  
 CC DR PROSITE; PS50026; EGF\_3; 5.  
 CC DR PROSITE; PS01187; EGF\_CA; 8.  
 CC KW Signal; Alternative splicing; Glycoprotein; Extracellular matrix;  
 CC Repeat; EGF-like domain; Calcium-binding.  
 CC FT SIGNAL 1 25  
 CC POTENTIAL.

FT CHAIN 26 704  
 FT DOMAIN 33 74  
 FT DOMAIN 75 109  
 FT DOMAIN 110 142  
 FT DOMAIN 117 216  
 FT DOMAIN 217 262  
 FT DOMAIN 263 308  
 FT DOMAIN 309 356  
 FT DOMAIN 357 399  
 FT DOMAIN 400 441  
 FT DOMAIN 442 481  
 FT DOMAIN 482 525  
 FT DOMAIN 526 579  
 FT DOMAIN 579 641  
 FT DISULFID 33 59  
 FT DISULFID 34 66  
 FT DISULFID 47 67  
 FT DISULFID 76 107  
 FT DISULFID 89 108  
 FT DISULFID 110 134  
 FT DISULFID 111 141  
 FT DISULFID 124 142  
 FT DISULFID 181 191  
 FT DISULFID 187 200  
 FT DISULFID 202 215  
 FT DISULFID 221 234  
 FT DISULFID 228 243  
 FT DISULFID 249 261  
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 FT DISULFID 274 289  
 FT DISULFID 295 307  
 FT DISULFID 313 326  
 FT DISULFID 320 335  
 FT DISULFID 342 355  
 FT DISULFID 361 374  
 FT DISULFID 368 383  
 FT DISULFID 385 398  
 FT DISULFID 404 416  
 FT DISULFID 412 425  
 FT DISULFID 427 440  
 FT DISULFID 446 455  
 FT DISULFID 451 464  
 FT DISULFID 466 480  
 FT DISULFID 486 499  
 FT DISULFID 495 508  
 FT DISULFID 510 524  
 FT DISULFID 530 543  
 FT DISULFID 537 552  
 FT DISULFID 557 578  
 FT CARBOHYD 96 96  
 FT CARBOHYD 536 536  
 FT CARBOHYD 540 540  
 FT VARSPIC 568 704

Query Match 50.7%; Score 36; DB 1; Length 704;  
 Best Local Similarity 71.4%; Pred. No. 1.1e+02;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 HEGCRSG 8  
 | : | | |  
 Db 178 HDGCRGG 184

RESULT 22

2142\_HUMAN STANDARD; PRT; 1687 AA.  
 ID Z142\_HUMAN  
 AC P52746; Q92510;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Zinc finger protein 142 (HA4654).  
 GN ZNF142 OR KIAA0236.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Bone marrow;  
 RX MEDLINE=97191544; PubMed=9039502;  
 RA Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawarabayashi Y.,  
 RA Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.;  
 RT "Prediction of the coding sequences of unidentified human genes. VI.  
 RT The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by  
 RT analysis of cDNA clones from cell line KG-1 and brain.";  
 RL DNA Res. 3:321-329(1996).  
 RN [2]  
 RP SEQUENCE OF 460-632 FROM N.A.  
 RC TISSUE=Insulinoma;  
 RX MEDLINE=96044430; PubMed=7557990;  
 RA Tommerup N., Vissing H.;  
 RT "Isolation and fine mapping of 16 novel human zinc finger-encoding  
 RT cDNAs identify putative candidate genes for developmental and  
 RT malignant disorders.";  
 RL Genomics 27:259-264(1995).  
 CC -!- FUNCTION: May be involved in transcriptional regulation.  
 CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).  
 CC -!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-  
 CC FINGER PROTEINS.  
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 DR EMBL; D87073; BAA13242.1; -;  
 DR EMBL; U09849; AAC50265.1; -;  
 DR PIR; I38617; I38617.  
 DR Genew; HGNC:12927; ZNF142.  
 DR MIM; 604083; -;  
 DR GO; GO:0003700; F:transcription factor activity; TAS.  
 DR InterPro; IPR007087; Znf\_C2H2.  
 DR Pfam; PF00096; zf-C2H2; 31.  
 DR SMART; SM00355; Znf\_C2H2; 34.  
 DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 17.  
 DR PROSITE; PS00157; ZINC\_FINGER\_C2H2\_2; 18.  
 KW Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;  
 KW Nuclear protein; Repeat.  
 FT ZN FING 163 185 C2H2-TYPE.  
 FT ZN FING 219 242 C2H2-TYPE.  
 FT ZN FING 253 275 C2H2-TYPE.  
 FT ZN FING 286 311 C2H2-TYPE (ATYPICAL).  
 FT ZN FING 316 340 C2H2-TYPE.  
 FT ZN FING 343 366 C2H2-TYPE.  
 FT ZN FING 372 395 C2H2-TYPE.  
 FT ZN FING 401 423 C2H2-TYPE.  
 FT ZN FING 429 451 C2H2-TYPE.  
 FT ZN FING 457 479 C2H2-TYPE.  
 FT ZN FING 485 507 C2H2-TYPE.  
 FT ZN FING 512 536 C2H2-TYPE.  
 FT ZN FING 544 567 C2H2-TYPE.  
 FT ZN FING 573 596 C2H2-TYPE.  
 FT ZN FING 1158 1194 C2H2-TYPE.  
 FT ZN FING 1171 1194 C2H2-TYPE.

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FT ZN_FING 1200 1222 C2H2-TYPE.
FT ZN_FING 1228 1251 C2H2-TYPE.
FT ZN_FING 1257 1280 C2H2-TYPE.
FT ZN_FING 1286 1309 C2H2-TYPE.
FT ZN_FING 1328 1351 C2H2-TYPE.
FT ZN_FING 1354 1377 C2H2-TYPE.
FT ZN_FING 1380 1403 C2H2-TYPE.
FT ZN_FING 1424 1446 C2H2-TYPE.
FT ZN_FING 1452 1474 C2H2-TYPE.
FT ZN_FING 1480 1502 C2H2-TYPE.
FT ZN_FING 1508 1530 C2H2-TYPE.
FT ZN_FING 1536 1559 C2H2-TYPE.
FT ZN_FING 1565 1587 C2H2-TYPE.
FT ZN_FING 1593 1615 C2H2-TYPE.
FT ZN_FING 1621 1643 C2H2-TYPE.
FT CONFLICT 460 463 TECG -> LKGS (IN REF. 2).
FT CONFLICT 541 541 S -> A (IN REF. 2).
SQ SEQUENCE 1687 AA; 187865 MW; 42847520F04D38E7 CRC64;

Query Match 50.7%; Score 36; DB 1; Length 1687;
Best Local Similarity 57.1%; Pred. No. 2.8e+02;
Matches 8; Conservative 0; Mismatches 4; Indels 2; Gaps 1;

QY 1 SH-EGCRSGAEG 12
|| ||||| |
Db 1043 SHVAEGCRGCGG 1056

RESULT 23
MT12 MYTED STANDARD; PRT; 72 AA.
ID _TUBE MYCTU STANDARD; PRT; 72 AA.
AC P80247; O62555;
DT 01-FEB-1994 (Rel. 28, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Metallothionein 10-II (MT-10-II).
OS Mytilus edulis (Blue mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloida;
OC Mytiloidae; Mytilidae; Mytilus.
OX NCBI_TaxID=6550;
RN [1]
RP SEQUENCE.
RX MEDLINE=94062828; PubMed=8243463;
RA Mackay E.A., Overnell J., Dunbar B., Davidson I., Hunziker P.E.,
RA Kaegi J.H.R., Fothergill J.E.;
RT "Complete amino acid sequences of five dimeric and four monomeric
RT forms of metallothionein from the edible mussel Mytilus edulis."
RL Eur. J. Biochem. 218:183-194(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Digestive gland;
RX MEDLINE=99206055; PubMed=10190057;
RA Barsyte D., White K.N., Lovejoy D.A.;
RT "Cloning and characterization of metallothionein cDNAs in the mussel
RT Mytilus edulis L. digestive gland";
RL Comp. Biochem. Physiol. 122C:287-296(1999).
CC -!- FUNCTION: The metallothioneins are involved in the cellular
CC sequestration of toxic metal ions.
CC -!- SUBUNIT: Monomer.
CC -!- INDUCTION: By cadmium.
CC -!- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 2.
CC
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CC
CC -----
DR EMBL; AJ005453; CAA06550.1; -
DR PIR; S39417; S39417.
DR InterPro; IPR003019; Metallthion_

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DR InterPro; IPR001008; Metallthion_2.
DR Pfam; PF00131; metalthio; 1.
DR PRINTS; PR00875; MTMOLLUSC.
KW Metal-binding; Metal-thiolate cluster; Cadmium.
FT INIT MET 0
FT CONFLICT 21 21 D -> E (IN REF. 1).
SQ SEQUENCE 72 AA; 7022 MW; 7FA99D945C35DE19 CRC64;

Query Match 49.3%; Score 35; DB 1; Length 72;
Best Local Similarity 60.0%; Pred. No. 16;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SHEGCRSGEA 10
|:|:|:|:|
Db 19 SGDCRCGDA 28

RESULT 24
TUBE MYCTU STANDARD; PRT; 89 AA.
ID _TUBE MYCTU STANDARD; PRT; 89 AA.
AC P02944;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-NOV-1988 (Rel. 09, Last annotation update)
DE Tuberculin-active protein.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE.
RC STRAIN=Human type Aoyama/B;
RX MEDLINE=75133468; PubMed=804477;
RA Kuwabara S.;
RT "Amino acid sequence of tuberculin-active protein from Mycobacterium
RT tuberculosis."
RL J. Biol. Chem. 250:2563-2568(1975).
CC -!- FUNCTION: TUBERCULIN IS THE SOLUBLE, PROTEINACEOUS CELL SUBSTANCE
CC OF THE BACTERIUM, TO WHICH INFECTED ANIMALS BECOME HYPERSENSITIVE
CC AND REACT CHARACTERISTICALLY TO DERMAL INJECTIONS.
CC -!- MISCELLANEOUS: THIS PROTEIN IS THE MOST POTENT COMPONENT WITH
CC TUBERCULIN ACTIVITY SO FAR PURIFIED AND CHARACTERIZED.
DR PIR; A03444; TKMT. 59
FT DISULFID 27
SQ SEQUENCE 89 AA; 9493 MW; 91DA5EBB044660F1 CRC64;

Query Match 49.3%; Score 35; DB 1; Length 89;
Best Local Similarity 61.5%; Pred. No. 19;
Matches 8; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 2 HEGCRSG--EAG 12
||| ||| |
Db 56 HEICRDGSGSEG 68

RESULT 25
YOR2 AZOVI
ID YOR2 AZOVI STANDARD; PRT; 164 AA.
AC O69219;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Hypothetical 17.8 kDa protein (ORF2).
OS Azotobacter vinelandii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Azotobacter.
OX NCBI_TaxID=354;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DJ116;
RX MEDLINE=98250785; PubMed=9582371;
RA Zheng L., Cash V.L., Flint D.H., Dean D.R.;
RT "Assembly of iron-sulfur clusters. Identification of an iscSUA-hscRA-

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RT fdx gene cluster from Azotobacter vinelandii.";
RL J. Biol. Chem. 273:13264-13272(1998).
CC -!- SIMILARITY: Belongs to the UPF0074 (rff2) family.
CC -----
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CC -----
DR EMBL: AF010139; AAC24480.1; -.
DR FIR: T44280; T44280.
DR InterPro: IPR000944; UPF0074.
DR Pfam: PF02082; Rff2; 1.
DR ProDom: PD003632; UPF0074; 1.
DR TIGRFAMs: TIGR00738; rff2 super; 1.
DR PROSITE: PS01332; UPF0074; 1.
KW Hypothetical protein.
SQ SEQUENCE 164 AA; 17831 MW; B03C777BF30654CE CRC64;
Query Match 49.3%; Score 35; DB 1; Length 164;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 GCRSGE 9
Db 97 GCRSGE 102
RESULT 26
ID BGB DROME STANDARD; PRT; 184 AA.
AC Q24040; Q9W0B9;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Big brother protein.
GN BGB OR CG7959.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96182097; PubMed=8622696;
RA Golling G., Li L., Pepling M., Stebbins M., Gergen J.P.;
RT "Drosophila homologs of the proto-oncogene product PEBP2/CBF beta
RL Mol. Cell. Biol. 16:932-942(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=Berkley;
RC MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Rogers J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Wortman J.R., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Chery J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

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RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kammel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Li X., Mattei B., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kimms I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Voh R.-P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
CC -!- FUNCTION: Regulates the DNA-binding properties of Runt.
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- SIMILARITY: Belongs to the CBF-beta family.
CC -----
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CC -----
DR EMBL: U22177; AAB03676.1; -.
DR EMBL: AE003472; AAF47533.1; ALT_INIT.
DR TRANSFAC: T02222; -.
DR FlyBase: FBgn0013753; Bgb.
DR GO: GO:0005634; C:nucleus; IDA.
DR GO: GO:0003713; F:transcription co-activator activity; IDA.
DR InterPro: IPR003417; CBF_beta.
DR Pfam: PF02312; CBF_beta; 1.
DR Nuclear Protein.
KW CONFLICT 112 112 E -> D (IN REF. 1).
SQ SEQUENCE 184 AA; 21792 MW; 2703C5B91E049D CRC64;
Query Match 49.3%; Score 35; DB 1; Length 184;
Best Local Similarity 60.0%; Pred. No. 42;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 4 GCRSGEAGS 13
Db 47 GCRSGTEAS 56
RESULT 27
YA29 TREPA STANDARD; PRT; 228 AA.
AC O8392;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein TP1029.
GN TP1029.
OS Treponema pallidum.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=160;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Nichols;
RX MEDLINE=98332770; PubMed=9665876;
RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
RA Dodson R., Gwinn M., Hackey E.K., Clayton R., Ketchum K.A.,
RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,

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RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,  
RA McDonald L., Artach P., Bowman C., Cotton M.D., Fujii C., Garland S.,  
RA Hatch B., Horet K., Roberts K., Sandueky M., Weidman J., Smith H.O.,  
RA Venter J.C.;  
RT "Complete genome sequence of Treponema pallidum, the syphilis  
RL spirochete.";  
RL Science 281:375-388(1998).  
CC -----  
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CC -----  
DR EMBL; AE001270; AAC65982.1; -.  
DR PIR; H71251; H71251.  
DR TIGR; TP1029; -.  
DR InterPro; IPR005580; DbpA.  
DR Pfam; PF03880; DbpA; 1.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 228 AA; 25186 MW; 39EB5D6EEAE1846A CRC64;  
  
Query Match 49.3%; Score 35; DB 1; Length 228;  
Best Local Similarity 46.2%; Pred. No. 52;  
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
  
QY 1 SHEGCRSGEAGS 13  
: |||: |||  
Db 60 ANTHCRAGATAGS 72  
  
RESULT 28  
P2IN LACLA  
ID P2IN LACLA STANDARD; PRT; 382 AA.  
AC Q9C163;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Prophage ps2 probable integrase (Int-TnX).  
GN PS201 OR INT201 OR IL1403.  
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).  
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.  
OX NCBI\_TaxID=1360;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=IL1403;  
RX MEDLINE=20000172; PubMed=10532372;  
RA Bolotin A., Mauger S., Malarne K., Ehrlich S.D., Sorokin A.;  
RT "Low-redundancy sequencing of the entire Lactococcus lactis IL1403  
RT genome.";  
RL Antonie Van Leeuwenhoek 76:27-76(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=IL1403;  
RX MEDLINE=21235186; PubMed=11337471;  
RA Bolotin A., Wincker P., Mauger S., Jaillon O., Malarne K.,  
RA Weissenbach J., Ehrlich S.D., Sorokin A.;  
RT "The complete genome sequence of the lactic acid bacterium Lactococcus  
RT lactis ssp. lactis IL1403.";  
RL Genome Res. 11:731-753(2001).  
CC -----  
CC -!- SIMILARITY: Belongs to the "phage" integrase family.  
CC -----  
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CC -----  
DR EMBL; AF320916; AAK08223.1; -.  
DR

DR EMBL; AE006285; AAK04601.1; -.  
DR PIR; G86687; G86687.  
DR InterPro; IPR002104; Phage integrase.  
DR Pfam; PF00589; Phage\_integrase; 1.  
KW Hypothetical protein; DNA recombination; DNA integration;  
KW Complete proteome.  
FT ACT\_SITE 363  
FT TRANSIENT COVALENT LINKAGE TO DNA DURING  
FT STRAND CLEAVAGE AND REJOINING (BY  
FT SIMILARITY).  
SQ SEQUENCE 382 AA; 43958 MW; 07A4C4F02B9F738A CRC64;  
  
Query Match 49.3%; Score 35; DB 1; Length 382;  
Best Local Similarity 70.0%; Pred. No. 89;  
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 SHEGCRSGEA 10  
: |||: |||  
Db 204 SLNGCRMGEA 213  
  
RESULT 29  
DBDR\_RAT  
ID DBDR\_RAT STANDARD; PRT; 475 AA.  
AC P25115;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 01-MAY-1992 (Rel. 22, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE D(1B) dopamine receptor (D(5) dopamine receptor).  
GN DRD5.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley;  
RX MEDLINE=91352014; PubMed=1831904;  
RA Tiberi M., Jarvie K.R., Silvia C., Palardeau P., Gingrich J.A.,  
RA Godinot N., Bertrand L., Yang-Feng T.L., Fremieu R.T. Jr.,  
RA Caron M.G.;  
RT "Cloning, molecular characterization, and chromosomal assignment of a  
RT gene encoding a second D1 dopamine receptor subtype: differential  
RT expression pattern in rat brain compared with the D1A receptor.";  
RL Proc. Natl. Acad. Sci. U.S.A. 88:7491-7495(1991).  
CC -!- FUNCTION: This is one of the five types (D1 to D5) of receptors  
CC for dopamine. The activity of this receptor is mediated by G  
CC proteins which activate adenylyl cyclase.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- TISSUE SPECIFICITY: Brain, in the lateral mammillary nuclei, the  
CC anterior prefrontal nuclei, and several layers of the hippocampus.  
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
CC -----  
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CC -----  
DR EMBL; M69118; AAA41072.1; -.  
DR PIR; A41271; A41271.  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PR00237; GPCRHOODPSN.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE; PS0262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
KW Multigene family; Lipoprotein; Palmitate.  
FT DOMAIN 1 38 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 39 64 1 (POTENTIAL).  
FT DOMAIN 65 75 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 76 102 2 (POTENTIAL).  
FT



FT DOMAIN 103 111 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 112 134 3 (POTENTIAL).  
 FT DOMAIN 135 153 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 154 179 4 (POTENTIAL).  
 FT DOMAIN 180 215 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 216 240 5 (POTENTIAL).  
 FT DOMAIN 241 269 6 (POTENTIAL).  
 FT TRANSMEM 290 317 6 (POTENTIAL).  
 FT DOMAIN 318 335 7 (POTENTIAL).  
 FT TRANSMEM 336 357 7 (POTENTIAL).  
 FT CARBOHYD 358 475 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT DISULFID 111 211 BY SIMILARITY.  
 FT LIPID 370 370 S-palmitoyl cysteine (By similarity).  
 SQ SEQUENCE 475 AA; 52830 MW; 4B0C004539540D82 CRC64;

Query Match 49.3%; Score 35; DB 1; Length 475;  
 Best Local Similarity 75.0%; Pred. No. 1.1e+02;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 CRSGBAEG 12  
 | | | | |  
 Db 316 CSSGDAEG 323

RESULT 30  
 OPT\_DROME STANDARD; PRT; 487 AA.  
 ID Q95RW8; O76291; Q8MKN3; Q9UA64; Q9V355;  
 AC Q95RW8; O76291; Q8MKN3; Q9UA64; Q9V355;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Optix protein (Homeobox protein SIX3).  
 GN OPTIX OR SIX3 OR OPT OR CGI8455.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM B), AND DEVELOPMENTAL STAGE.  
 RC STRAIN=Canton-S; TISSUE=Larva;  
 RX MEDLINE=99310670; PubMed=10381573;  
 RA Seo H.-C., Curtiss J., Mlodzik M., Fjose A.;  
 RT "Six class homeobox genes in Drosophila belong to three distinct  
 RT families and are involved in head development.";  
 RL Mech. Dev. 83:127-139(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkely;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Branton R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt J.G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster.";  
 RL Science 287:2185-2195(2000).  
 RN [3]  
 RP REVISIONS, AND ALTERNATIVE SPLICING.  
 RX MEDLINE=2426069; PubMed=12537572;  
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,  
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
 RA Battencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,  
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
 RA Lewis S.E.;  
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a  
 RT systematic review.";  
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM A).  
 RC STRAIN=Berkely; TISSUE=Embryo;  
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.W.,  
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.A.,  
 RA Gonzalez M., Guarin H., Li P.W., Liao G., Miranda A., Mungall C.J.,  
 RA Nunoo J., Pacleb J.M., Paragas V., Park S., Phouanavong S.,  
 RA Wan K.H., Yu C., Lewis S.E., Rubin G.M., Celniker S.E.;  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE OF 155-214 FROM N.A., AND DEVELOPMENTAL STAGE.  
 RX MEDLINE=98393698; PubMed=9724757;  
 RA Toy J., Yang J.-M., Leppert G.S., Sundin O.H.;  
 RT "The optx2 homeobox gene is expressed in early precursors of the eye  
 RT and activates retina-specific genes.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:10643-10648(1998).  
 CC -!- FUNCTION: May be involved in head or eye development.  
 CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=3;  
 CC Comment=Experimental confirmation may be lacking for some  
 CC isoforms;  
 CC Name=A;  
 CC IsoId=Q95RW8-1; Sequence=Displayed;  
 CC Name=B;  
 CC IsoId=Q95RW8-2; Sequence=VSP\_002258;  
 CC Name=C;  
 CC IsoId=Q95RW8-3; Sequence=VSP\_002259;  
 CC -!- DEVELOPMENTAL STAGE: Expressed during early development of the  
 CC head. First expression in a band around the head end of the stage  
 CC 5 blastoderm embryo, at 93% to 85% egg length. By the gastrula  
 CC stage, the site of expression shifts to the dorsal-anterior  
 CC region. At stage 12, expression is found in the clypeolabrum, the  
 CC stomodaeum, and in ectoderm dorsal to the future supraesophageal  
 CC ganglion.  
 CC -!- SIMILARITY: Belongs to the SIX/Sine oculis homeobox family.  
 CC -!- SIMILARITY: Contains 1 homeobox domain.  
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CC -----
CC EMBL; AF099184; AAD39863.1; -
DR EMBL; AE003839; AAF59147.3; -
DR EMBL; AE003839; AAM68882.1; -
DR EMBL; AY061077; AAL28625.1; -
DR EMBL; AF050132; AAC33852.1; -
DR FlyBase; FBgn0025360; Optix.
DR GO; GO:0005634; C:nucleus; ISS.
DR GO; GO:0003677; C:nucleus; ISS.
DR GO; GO:0007456; P:eye morphogenesis (sensu Drosophila); IEP.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR007105; SIX.
DR InterPro; IPR007106; SIX_SINE_homeo.
DR Pfam; PF00046; homeobox.1.
DR ProDom; PD000010; Homeobox; 1.
DR PROSITE; PS00027; HOMEBOX_1; FALSE_NEG.
DR PROSITE; PS00711; HOMEBOX_2; 1.
KW Developmental protein; DNA-binding; Homeobox; Nuclear protein;
KW Alternative splicing.
FT DNA_BIND 154 214
FT VARSPPLIC 221 382
FT Missing (in isoform B).
FT /FTid=VSP 002258.
FT Missing (in isoform C).
FT /FTid=VSP 002259.
FT G -> R (IN REF. 1).
FT CONFLICT 446 446
FT CONFLICT 455 487
FT CONFLICT 455 487 MISSING (IN REF. 1).
SQ SEQUENCE 487 AA; 52419 MW; ECA9FD59F171E599 CRC64;

Query Match 49.3%; Score 35; DB 1; Length 487;
Best Local Similarity 60.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCRSGEAGS 13
DB 230 GCRSRADGA 239

RESULT 31
WD21 HUMAN
ID WD21_HUMAN STANDARD; PRT; 495 AA.
AC Q8WV16; Q96K22; Q9Y4P5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE WD-repeat protein 21.
GN WDR21.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovarian carcinoma;
RA Isoqai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Wagatsuma M., Hosoi T., Raku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA Ninomiya K., Iwayanagi T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBSJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,

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RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buttefield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE OF 4-433 FROM N.A.
RC TISSUE=Testis;
RA Wambutt R., Heubner D., Mewes H.-W., Gassenhuber J., Wiemann S.;
RA Submitted (JUN-1999) to the EMBL/GenBank/DBSJ databases.
CC -1- SIMILARITY: Contains 2 WD repeats.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AK027745; BAB55337.1; -
DR EMBL; BC018979; AAH18979.1; -
DR EMBL; AL080157; CAB45748.1; -
DR PIR; T12541; T12541.
DR Genew; HGNC:20229; WDR21.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 2.
DR SMART; SM00320; WD40; 2.
DR PROSITE; PS00678; WD_REPEATS_1; FALSE_NEG.
DR PROSITE; PS00082; WD_REPEATS_2; 1.
DR PROSITE; PS0294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
FT REPEAT 368 407
FT REPEAT 410 451
FT CONFLICT 4 4 S -> G (IN REF. 3).
FT CONFLICT 35 35 R -> Q (IN REF. 1).
FT CONFLICT 45 45 H -> Y (IN REF. 1).
FT CONFLICT 65 65 E -> G (IN REF. 1).
FT CONFLICT 193 193 T -> K (IN REF. 1).
FT CONFLICT 269 269 P -> PA (IN REF. 1).
FT CONFLICT 328 334 MISSING (IN REF. 1).
FT CONFLICT 432 433 VG -> GT (IN REF. 3).
FT CONFLICT 439 439 I -> R (IN REF. 1).
SQ SEQUENCE 495 AA; 55657 MW; 0F084922B635750A CRC64;

Query Match 49.3%; Score 35; DB 1; Length 495;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCRSGE 9
DB 342 GCRSGE 347

RESULT 32
TPP1 MOUSE
ID TPP1_MOUSE STANDARD; PRT; 562 AA.
AC O89023; Q9QUS7;
DT 15-DEC-1998 (Rel. 37, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tripeptidyl-peptidase I precursor (EC 3.4.14.9) (TPP-I) (Tripeptidyl
DE aminopeptidase) (Lysosomal peptatin insensitive protease) (LIPIC).
GN CLN2 OR TPP1.

```

OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;  
 OX NCBI\_TaxID=10090;  
 RN (1)  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=99142696; PubMed=9989590;  
 RA Vines D.J., Warburton M.J.;  
 RT "Classical late infantile neuronal ceroid lipofuscinosis fibroblasts  
 are deficient in lysosomal tripeptidyl peptidase I.";  
 RL FEBS Lett. 443:131-135(1999).  
 RN (2)  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=20028316; PubMed=10556422;  
 RA Katz M.L., Liu P.-C., Grob-Nunn S.E., Shibuya H., Johnson G.S.;  
 RT "Characterization and chromosomal mapping of a mouse ortholog of the  
 late-infantile ceroid-lipofuscinosis gene CLN2.";  
 RL Mamm. Genome 10:1050-1053(1999).  
 RN (3)  
 RN SEQUENCE FROM N.A.  
 RP Slet D.E., Lobel P.;  
 RA "Murine homologue of the lysosomal pepstatin insensitive protease  
 which is deficient in human classical late infantile neuronal ceroid  
 lipofuscinosis.";  
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
 RN (4)  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=C57BL/6J; TISSUE=Kidney;  
 RC MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Glessi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,  
 RA Hayashizaki Y.;  
 RA "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 CC -!- FUNCTION: Lysosomal serine protease with tripeptidyl-peptidase I  
 activity. May act as a non-specific lysosomal peptidase which  
 generates tripeptides from the breakdown products produced by  
 lysosomal proteinases. Requires substrates with an unsubstituted  
 N-terminus (By similarity).  
 CC -!- CATALYTIC ACTIVITY: Release of an N-terminal tripeptide from a  
 polypeptide, but also has endopeptidase activity.  
 CC -!- SUBCELLULAR LOCATION: Lysosomal.  
 CC -!- PTM: Activated by autocatalytic proteolytical processing upon  
 acidification (By similarity).  
 CC -!- SIMILARITY: Belongs to peptidase family S53.  
 CC  
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 CC  
 CC EMBL; AJ011912; CAA09863.1; ALT\_INIT.  
 CC EMBL; AF124599; RAD32573.1; --  
 CC EMBL; AF111172; RAD03083.1; --  
 CC EMBL; AK002418; BAB22085.1; --

DR MEROPS; S53.003; --  
 DR MGD; MGI:1336194; Cln2.  
 KW Hydrolyase; Protease; Serine protease; Zymogen; Signal; Lysosome;  
 KW Glycoprotein.  
 FT SIGNAL 1 19 BY SIMILARITY.  
 FT PROPEP 20 194 REMOVED IN MATURE FORM (BY SIMILARITY).  
 FT CHAIN 195 562 TRIPEPTIDYL-PEPTIDASE I.  
 FT ACT\_SITE 271 275 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 275 275 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT CARBOHYD 209 209 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 221 221 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 285 285 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 312 312 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 442 442 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CONFLICT 1 1 M -> V (IN REF. 1).  
 FT CONFLICT 562 562 P -> LDPFVP (IN REF. 1).  
 SQ SEQUENCE 562 AA; 61342 MW; 0AF8163E1A166396 CRC64;

Query Match 49.3%; Score 35; DB 1; Length 562;  
 Best Local Similarity 54.5%; Pred. No. 1.3e+02;  
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 2 HEGCSGREG 12  
 ||| : |||

DB 522 HESCLNEVEG 532

RESULT 33  
 ID TPPI\_RAT  
 AC Q9EQV6; STANDARD; PRT; 563 AA.  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Tripeptidyl-peptidase I precursor (EC 3.4.14.9) (TPP-I) (Tripeptidyl  
 aminopeptidase) (lysosomal pepstatin insensitive protease) (LIPIC).  
 GN CLN2 OR TPPI.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RA Du P., Kato S., Li Y., Maeda T., Yamane T., Yamamoto S., Fujiwara M.,  
 RA Yamamoto Y., Nishi K., Ohkubo I.;  
 RT "Rat tripeptidyl peptidase I: its purification and molecular  
 cloning.";  
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
 RN (2)  
 RP SEQUENCE OF 196-217; 374-392 AND 395-429, AND CHARACTERIZATION.  
 RC TISSUE=Spleen;  
 RA Vines D.J., Warburton M.J.;  
 RT "Purification and characterisation of a tripeptidyl aminopeptidase I  
 from rat spleen.";  
 RL Biochim. Biophys. Acta 1384:233-242(1998).  
 CC -!- FUNCTION: Lysosomal serine protease with tripeptidyl-peptidase I  
 activity. May act as a non-specific lysosomal peptidase which  
 generates tripeptides from the breakdown products produced by  
 lysosomal proteinases. Requires substrates with an unsubstituted  
 N-terminus. Maximum activity at pH 4, unstable above pH 7.  
 CC -!- CATALYTIC ACTIVITY: Release of an N-terminal tripeptide from a  
 polypeptide, but also has endopeptidase activity.  
 CC -!- SUBCELLULAR LOCATION: Lysosomal.  
 CC -!- PTM: Activated by autocatalytic proteolytical processing upon  
 acidification (By similarity).  
 CC -!- SIMILARITY: Belongs to peptidase family S53.  
 CC  
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EMBL; AB043870; BAB18570.1; -.  
KW Hydrolase; Protease; Serine protease; Zymogen; Signal; Lysosome;  
FT SIGNAL 1 19 BY SIMILARITY  
FT PROPEP 20 195 REMOVED IN MATURE FORM.  
FT CHAIN 196 563 TRIPEPTIDYL-PEPTIDASE 1.  
FT ACT SITE 272 272 CHARGE RELAY SYSTEM (BY SIMILARITY).  
FT ACT SITE 276 276 CHARGE RELAY SYSTEM (BY SIMILARITY).  
FT ACT SITE 475 475 CHARGE RELAY SYSTEM (BY SIMILARITY).  
FT CARBOHYD 210 210 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 222 222 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 286 286 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 313 313 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 443 443 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CONFLICT 210 210 N -> A (IN REF. 2).  
FT CONFLICT 216 217 VG -> SQ (IN REF. 2).  
FT CONFLICT 389 391 GGT -> SPP (IN REF. 2).  
SQ SEQUENCE 563 AA; 61332 MW; B54F3C86205DFEC1 CRC64;

Query Match 49.3%; Score 35; DB 1; Length 563;  
Best Local Similarity 54.5%; Pred. No. 1.3e+02;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 2 HEGCRSGEABG 12  
|||:|  
Db 523 HESCLNEVEEG 533

RESULT 34  
TAN ASPOR STANDARD; PRT; 588 AA.  
AC P78581;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2004 (Rel. 41, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Tannase precursor (EC 3.1.1.20).  
OS Aspergillus oryzae.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
OC Euryales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.  
OX NCBI\_TaxID=5062;  
RN [1]  
SEQUENCE FROM N.A., AND SEQUENCE OF 19-43; 159-166; 317-327; 424-426  
AND 456-471.  
RC STRAIN=TH;  
RX MEDLINE=97074675; PubMed=8917102;  
RA Hatamoto O., Watarai T., Kikuchi M., Mizusawa K., Sekine H.;  
RT "Cloning and sequencing of the gene encoding tannase and a structural  
study of the tannase subunit from Aspergillus oryzae.";  
RL Gene 175:215-221(1996).  
CC -! FUNCTION: Hydrolyzes ester bonds of tannic acid to produce gallic  
acid and glucose.  
CC -! CATALYTIC ACTIVITY: Digallate + H(2)O = 2 gallate.  
CC -! SUBUNIT: Heterooctamer of 4 33 kDa and 4 30 kDa subunits linked by  
disulfide bond(s).  
CC -! PTM: The protein is glycosylated to a carbohydrate content of  
22.7%.

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EMBL; D63338; BAA09656.1; -.  
DR PIR; JC5087; JC5087.  
KW Hydrolase; Glycoprotein; Signal.

FT SIGNAL 1 18  
FT CHAIN 19 316 TANNASE 33 kDa SUBUNIT.  
FT CHAIN 317 588 TANNASE 30 kDa SUBUNIT.  
FT SITE 315 316 CLEAVAGE.  
FT MOD RES 317 317 BLOCKED (PROBABLE).  
SQ SEQUENCE 588 AA; 64095 MW; 24DB928DB02BE77D CRC64;

Query Match 49.3%; Score 35; DB 1; Length 588;  
Best Local Similarity 54.5%; Pred. No. 1.4e+02;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 2 HEGCRSGEABG 12  
|||:|  
Db 191 YEGCSDGGREG 201

RESULT 35  
PO23 POPJA STANDARD; PRT; 606 AA.  
ID PO23 POPJA STANDARD; PRT; 606 AA.  
AC Q05118;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Retrovirus-related POL polyprotein from type I retrotransposable element R2 [Contains: Reverse transcriptase (EC 2.7.7.49);  
DE Endonuclease] (Fragment).  
DE Popillia japonica (Japanese beetle).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Scarabaeiformia;  
OC Scarabaeidae; Rutelinae; Popillia.  
OX NCBI\_TaxID=7064;  
RN [1]  
SEQUENCE FROM N.A.  
RX MEDLINE=93196484; PubMed=8383793;  
RA Burke W.D., Eickbush D.G., Xiong Y., Jakubczak J.L., Eickbush T.H.;  
RT "Sequence relationship of retrotransposable elements R1 and R2 within  
and between divergent insect species.";  
RL Mol. Biol. Evol. 10:163-185(1993).  
CC -! CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate  
+ {DNA} (N).

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EMBL; L00948; AAA29786.1; -.  
DR InterPro; IPR000477; RVTse.  
DR Pfam; PF00078; rvt; 1.  
KW Transferase; RNA-directed DNA polymerase; Transposable element;  
KW Hydrolase; Nuclease; Endonuclease.  
FT NON\_TER 1 1  
FT DOMAIN <1 330 REVERSE TRANSCRIPTASE.  
FT DOMAIN 331 606 NUCLEIC ACID-BINDING ENDONUCLEASE.  
SQ SEQUENCE 606 AA; 68367 MW; B70DB4D5B099069C CRC64;

Query Match 49.3%; Score 35; DB 1; Length 606;  
Best Local Similarity 71.4%; Pred. No. 1.4e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 HEGCRSG 8  
|||:|  
Db 419 HRCGRNG 425

RESULT 36  
ACH4 CHICK STANDARD; PRT; 622 AA.  
ID ACH4 CHICK STANDARD; PRT; 622 AA.  
AC P09482;  
DT 01-MAR-1989 (Rel. 10, Created)



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Db          410 ECGTTGGSGA 420

RESULT 38
PRID SCHPO
ID PRHI SCHPO STANDARD; PRT; 719 AA.
AC Q03319;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable ATP-dependent RNA helicase prhi.
GN PRHI OR SPAC2G11.11C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN SEQUENCE FROM N.A.
RN MEDLINE=93087203; PubMed=1454545;
RA Inoue S.B., Sakamoto H., Sawa H., Shimura Y.;
RT "Nucleotide sequence of a fission yeast gene encoding the DEAH-box
RL Nucleic Acids Res. 20:5841-5841(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gilliam R., Rajadream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volktaert G., Aert R., Robben J., Grymonprez B.,
RA Welljans I., Volckaert E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer C., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Leirach E., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RL Nature 415:871-880(2002).
CC "The genome sequence of Schizosaccharomycetes pombe."
CC -!- FUNCTION: May be involved in pre-mRNA splicing.
CC -!- SIMILARITY: Belongs to the DEAD box helicase family. DEAH
CC subfamily.
CC
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CC -----
CC EMBL; D13249; BAA02516.1; -
CC EMBL; 254354; CAA91176.1; -
CC PIR; S35546; S35546.
CC PIR; S62466; S62466.
CC GeneDB Spombe; SPAC2G11.11C; -.
CC InterPro; IPR003593; AAA ATPase.
CC InterPro; IPR001410; DEAD.

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DR InterPro; IPR002464; DEAH_box.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR007502; Helicase_dom.
DR Pfam; PF04408; HA2; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR SMART; SM00382; AAA; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
DR PROSITE; PS00690; DEAH_ATP_HELICASE; 1.
KW Helicase; ATP-binding; RNA-binding; mRNA processing.
FT NP_BIND 119 126 ATP (BY SIMILARITY).
FT SITE 216 219 DEAH_BOX.
FT CONFLICT 719 719 T -> HLTFFQLKKIKKAHLSHYLVNLETTIF
FT (IN REF. 1).
SQ SEQUENCE 719 AA; 80605 MW; E6EB16EEED852115 CRC64;

Query Match 49.3%; Score 35; DB 1; Length 719;
Best Local Similarity 50.0%; Pred. NO. 1.7e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 SHEGCRSGEARG 12
   : : ||| || |
Db 163 AEQGRLGEQVG 174

RESULT 39
SP4_MOUSE
ID SP4_MOUSE STANDARD; PRT; 782 AA.
AC Q62445;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Transcription factor Sp4.
GN SP4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
OX [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=96239580; PubMed=8660867;
RX Supp D.M., Witte D.P., Branford W.W., Smith E.P., Potter S.S.;
RT "Sp4, a member of the Sp1-family of zinc finger transcription
RT factors, is required for normal murine growth, viability, and male
RT fertility.";
RL Dev. Biol. 176:284-299(1996).
CC -!- FUNCTION: Binds to GT and GC boxes promoters elements. Probable
CC transcriptional activator. Required for normal male reproductive
CC behavior.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: Expressed in many tissues.
CC -!- DEVELOPMENTAL STAGE: Highly expressed in embryos in the developing
CC central nervous system (CNS). Expression is seen as early as day 9
CC of development, where transcripts are abundant in the posterior
CC neuropore. Expression in later embryos is detected throughout the
CC CNS as well as in other structures.
CC -!- SIMILARITY: BELONGS TO THE SPI FAMILY OF C2H2-TYPE ZINC-FINGER
CC PROTEINS.
CC -!- SIMILARITY: Contains 3 C2H2-type zinc fingers.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U62522; AAC52653.1; -
CC HSPF; F08047; ISF1.
CC TRANSFAC; T02414; -.
CC MGD; MGI:107595; Sp4.
CC GO; GO:0008016; P:regulation of heart rate; IMP.

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DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF00096; zf-C2H2; 3.
DR ProDom; PD000003; Znf_C2H2; 2.
DR SMART; SM00355; Znf_C2H2; 3.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 3.
DR Transcription regulation; Activator; Zinc-finger; Metal-binding;
KW DNA-binding; Nuclear protein; Repeat.
FT ZN_FING 645 669 C2H2-TYPE 1.
FT ZN_FING 675 699 C2H2-TYPE 2.
FT ZN_FING 705 727 C2H2-TYPE 3.
FT DOMAIN 7 11 POLY-GLU.
FT DOMAIN 12 17 POLY-ALA.
FT DOMAIN 120 128 POLY-SER.
FT DOMAIN 285 POLY-THR.
SQ SEQUENCE 782 AA; 81966 MW; 50BDA3D6C0848A4F CRC64;

Query Match 49.3%; Score 35; DB 1; Length 782;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CRSGEAEGS 13
||| |||
DB 628 CREGEGRGS 636

RESULT 40
SP4_HUMAN STANDARD; PRT; 784 AA.
AC Q02I46; O60402;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Transcription factor Sp4 (SPR-1).
GN SP4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX MEDLINE=93087156; PubMed=1454515;
RA Hagen G., Mueller S., Beato M., Suske G.;
RT "Cloning by recognition site screening of two novel GT box binding
RT proteins: a family of Sp1 related genes.";
RL Nucleic Acids Res. 20:5519-5525(1992).
RN [2]
RP SEQUENCE FROM N.A.
RA Ozersky P., Holmes A.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Binds to GT and GC boxes promoters elements. Probable
CC transcriptional activator.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: ABUNDANT IN BRAIN.
CC -!- SIMILARITY: BELONGS TO THE SP1 FAMILY OF C2H2-TYPE ZINC-FINGER
CC PROTEINS.
CC -!- SIMILARITY: Contains 3 C2H2-type zinc fingers.
-----
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-----
DR EMBL; X68561; CAA48563.1; -.
DR EMBL; AC004595; AAD12226.1; -.
DR PIR; S26638; S26638.
DR HSP; P08047; 1SP1.
DR TRANSFAC; T02339; -.
DR Genew; HGNC:11209; SP4.

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DR MIM; 600540; -.
DR GO; GO:0003702; F:RNA polymerase II transcription factor acti. . .; TAS.
DR GO; GO:0003713; F:transcription co-activator activity; TAS.
DR GO; GO:0006357; P:regulation of transcription from Pol II pro. . .; TAS.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF00096; zf-C2H2; 3.
DR ProDom; PD000003; Znf_C2H2; 2.
DR SMART; SM00355; Znf_C2H2; 3.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 3.
DR Transcription regulation; Activator; Zinc-finger; Metal-binding;
KW DNA-binding; Nuclear protein; Repeat.
FT ZN_FING 647 671 C2H2-TYPE 1.
FT ZN_FING 677 701 C2H2-TYPE 2.
FT ZN_FING 707 729 C2H2-TYPE 3.
FT DOMAIN 7 11 POLY-GLU.
FT DOMAIN 12 19 POLY-ALA.
FT DOMAIN 122 130 POLY-SER.
FT DOMAIN 185 188 POLY-SER.
FT CONFLICT 197 197 K -> Q (IN REF. 2).
FT CONFLICT 379 380 HA -> QP (IN REF. 2).
FT CONFLICT 386 386 Q -> A (IN REF. 2).
SQ SEQUENCE 784 AA; 82025 MW; 3C4AE28CB2B81FB CRC64;

Query Match 49.3%; Score 35; DB 1; Length 784;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CRSGEAEGS 13
||| |||
DB 630 CREGEGRGS 638

RESULT 41
PRGR_HUMAN STANDARD; PRT; 933 AA.
AC P06401; Q9UPF7;
DT 01-JAN-1988 (Rel. 06, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Progesterone receptor (PR).
GN PR OR NR3C3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND VARIANTS THR-344
RP AND VAL-660.
RX MEDLINE=90228361; PubMed=2328727;
RA Kastner P., Krust A., Turcotte B., Stropp U., Tora L., Gronemeyer H.,
RA Chambon P.;
RT "Two distinct estrogen-regulated promoters generate transcripts
RT encoding the two functionally different human progesterone receptor
RT forms A and B.";
RL EMBO J. 9:1603-1614(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87184565; PubMed=3551956;
RA Misrahi M., Atger M., D'Auriol L., Loosfelt H., Meriel C.,
RA Fridlansky F., Guiochon-Mantel A., Galibert F., Milgrom E.;
RT "Complete amino acid sequence of the human progesterone receptor
RT deduced from cloned cDNA.";
RL Biochem. Biophys. Res. Commun. 143:740-748(1987).
RN [3]
RP SEQUENCE FROM N.A.
RA Kieback D.G., Agoulnik I.U., Tong X.-W.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 682-933.
RX MEDLINE=98282128; PubMed=9620806;
RA Williams S.P., Sigler P.B.;
RT "Atomic structure of progesterone complexed with its receptor.";

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 CC -----

DR EMBL; M80547; AAB05617.1; -;  
 DR PIR; S27473; S27473.  
 DR HSP; P17679; 1GNP.  
 DR TRANSFAC; T02406; -;  
 DR InterPro; IPR000679; Znf\_GATA.  
 DR Pfam; PF00320; GATA; 2; GATA.  
 DR PRINTS; PR00619; GATAZNFINGER.  
 DR SMART; SM00401; Znf\_GATA; 2.  
 DR PROSITE; PS00344; GATA\_ZNFINGER\_1; 2.  
 DR PROSITE; PS0114; GATA\_ZNFINGER\_2; 2.  
 KW DNA-binding; Zinc-finger; Transcription regulation; Repressor;  
 KW Nuclear protein.  
 FT ZN\_FING 338 362 GATA-TYPE 1.  
 FT ZN\_FING 482 506 GATA-TYPE 2.  
 FT DOMAIN 24 27 POLY-ALA.  
 FT DOMAIN 28 36 POLY-SER.  
 FT DOMAIN 487 490 POLY-THR.  
 FT DOMAIN 753 780 HIS-RICH.  
 FT DOMAIN 902 906 POLY-SER.  
 SQ SEQUENCE 950 AA; 101427 MW; F969C6DA09A78C12 CRC64;

Query Match 49.3%; Score 35; DB 1; Length 950;  
 Best Local Similarity 53.8%; Pred. No. 2.3e+02;  
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 SHEGCRSGEAGS 13  
 ||||| :|||  
 Db 857 SHESPTGSAQGS 869

## RESULT 43

ID KCH3 HUMAN STANDARD; PRT; 1083 AA.  
 AC Q9ULJ8; Q9UQ06;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Potassium voltage-gated channel subfamily H member 3 (Ether-a-go-go-  
 DE like potassium channel 2) (ELK channel 2) (ELK2) (Brain-specific eag-  
 DE like channel 1) (BEC1).  
 GN KCHH3 OR KIAA1282.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=93386988; PubMed=10455180;  
 RA Miyake A., Mochizuki S., Yokoi H., Kohda M., Furuichi K.;  
 RT "New ether-a-go-go K+ channel family members localized in human  
 RT telencephalon.";  
 RL J. Biol. Chem. 274:25018-25025 (1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=20039619; PubMed=10574462;  
 RA Nagase T., Ishikawa K.-I., Kikuno R., Hirose M., Nomura N.,  
 RA Ohara O.;  
 RT "Prediction of the coding sequences of unidentified human genes. XV.  
 RT The complete sequences of 100 new cDNA clones from brain which code  
 RT for large proteins in vitro.";  
 RL DNA Res. 6:337-345(1999).  
 CC -!- FUNCTION: Pore-forming (alpha) subunit of voltage-gated potassium  
 CC channel. Elicits an outward current with fast inactivation.  
 CC Channel properties may be modulated by cAMP and subunit assembly.

CC -!- SUBUNIT: The potassium channel is probably composed of a homo- or  
 CC heterotetrameric complex of pore-forming alpha subunits that can  
 CC associate with modulating beta subunits.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- TISSUE SPECIFICITY: Detected only in brain, in particular in the  
 CC telencephalon. Detected in the cerebral cortex, occipital pole,  
 CC frontal and temporal lobe, putamen, amygdala, hippocampus and  
 CC caudate nucleus.  
 CC -!- DOMAIN: The segment S4 is probably the voltage-sensor and is  
 CC characterized by a series of positively charged amino acids at  
 CC every third position.  
 CC -!- SIMILARITY: Belongs to the potassium channel family. H (Eag)  
 CC subfamily.  
 CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.  
 CC -!- SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.  
 CC -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.  
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 CC -----  
 DR EMBL; AB022696; BAA83590.1; -;  
 DR EMBL; AB033108; BAA86596.1; ALT\_INIT.  
 DR Genew; HGNC:6252; KCHH3.  
 DR MIM; 604527; -;  
 DR GO; GO:0016021; C:integral to membrane; NAS.  
 DR GO; GO:0005249; F:voltage-gated potassium channel activity; TAS.  
 DR GO; GO:0006813; P:potassium ion transport; TAS.  
 DR InterPro; IPR000595; cNMP binding.  
 DR InterPro; IPR003967; Brg Channel.  
 DR InterPro; IPR005821; Ion\_trans.  
 DR InterPro; IPR001622; K-channel\_pore.  
 DR InterPro; IPR005820; M-channel\_nlg.  
 DR InterPro; IPR001610; PAC.  
 DR InterPro; IPR000700; PAS-associ C.  
 DR InterPro; IPR000014; PAS domain.  
 DR Pfam; PF00027; cNMP binding; 1.  
 DR Pfam; PF00520; ion\_trans; 1.  
 DR Pfam; PF00785; PAC; 1.  
 DR PRINTS; PR01470; ERGCHANNEL.  
 DR SMART; SM00100; cNMP; 1.  
 DR SMART; SM00086; PAC; 1.  
 DR TIGRFAMs; TIGR00229; sensory\_box; 1.  
 DR PROSITE; PS00888; cNMP\_BINDING\_1; FALSE\_NEG.  
 DR PROSITE; PS00889; cNMP\_BINDING\_2; FALSE\_NEG.  
 DR PROSITE; PS50042; cNMP\_BINDING\_3; 1.  
 DR PROSITE; PS50112; PAS; 1.  
 DR PROSITE; PS50113; PAC; 1.  
 KW Transport; Ion transport; Ionic channel; Voltage-gated channel;  
 KW Potassium channel; Potassium; Potassium transport; Transmembrane;  
 KW Glycoprotein; Multigene family.  
 FT DOMAIN 1 228 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 229 249 SEGMENT S1 (POTENTIAL).  
 FT TRANSMEM 260 280 SEGMENT S2 (POTENTIAL).  
 FT DOMAIN 281 302 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 303 323 SEGMENT S3 (POTENTIAL).  
 FT TRANSMEM 332 352 SEGMENT S4 (POTENTIAL).  
 FT DOMAIN 353 361 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 362 382 SEGMENT S5 (POTENTIAL).  
 FT DOMAIN 454 474 SEGMENT H5 (PORE-FORMING) (POTENTIAL).  
 FT TRANSMEM 480 500 SEGMENT S6 (POTENTIAL).  
 FT DOMAIN 501 1083 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 18 90 PAC.  
 FT DOMAIN 93 145 PRO-RICH.  
 FT DOMAIN 951 1057 cNMP.  
 FT NP\_BIND 582 697  
 FT CARBOHYD 421 421 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 428 428 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 436 436 N-LINKED (GLCNAC. . .) (POTENTIAL).

```
SQ SEQUENCE 1083 AA; 117128 MW; EF35C8968D7418CC CRC64;
Query Match 49.3%; Score 35; DB 1; Length 1083;
Best Local Similarity 63.6%; Pred. No. 2.6e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SHEGCRSGEAE 11
DB 1021 SEEGARTGPAE 1031

RESULT 44
REPT_MOUSE
ID REPT_MOUSE STANDARD; PRT; 1130 AA.
AC P97347;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Repetin.
GN RPTN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=NMRI; TISSUE=Skin;
RX MEDLINE=97422611; PubMed=9268637;
RA Krieg P.; Schuppier M.; Koesters R.; Mincheva A.; Lichter P.;
RA Marks F.;
RT "Repetin (Rptn), a new member of the 'fused gene' subgroup within the
RT S100 gene family encoding a murine epidermal differentiation
RT protein."
RL Genomics 43:339-348(1997).
CC -!- FUNCTION: Novel potential precursor protein of the cornified cell
CC envelope.
CC -!- SIMILARITY: In the N-terminal section; belongs to the S-100
CC family.
CC -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
CC
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CC
CC EMBL; X99251; CAA67624.1; -.
DR PIR; T30251; T30251.
DR HSP; P02633; I1G5.
DR MGD; MGI:1099055; Rptn.
DR InterPro; IPR001751; CAbP_S100.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; ehand; 1.
DR Pfam; PF01023; S_100; 1.
DR Prodom; PD003407; CAbP_S100; 1.
DR PROSITE; PS00018; EF_HAND; 1.
DR PROSITE; PS00303; S100_CABP; 1.
KW Repeat; Calcium-binding.
FT DOMAIN 1 91 S-100 LIKE.
FT CA_BIND 22 33 EF-HAND 1 (LOW AFFINITY) (POTENTIAL).
FT CA_BIND 62 73 EF-HAND 2 (HIGH AFFINITY) (POTENTIAL).
SQ SEQUENCE 1130 AA; 129884 MW; 7D97BDD25151918D CRC64;
Query Match 49.3%; Score 35; DB 1; Length 1130;
Best Local Similarity 46.2%; Pred. No. 2.8e+02;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 SHEGCRSGEAGS 13
DB 773 SHQGQREGQEQNS 785
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RESULT 45
HAIR_MOUSE
ID HAIR_MOUSE STANDARD; PRT; 1182 AA.
AC Q61645; Q80Y47;
DT 01-NOV-1997 (Rel. 35, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hairless protein.
GN HR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BALB/c; TISSUE=Skin;
RX MEDLINE=94329587; PubMed=8052649;
RA Cachon-Gonzalez M.B.; Fenner S.; Coffin J.M.; Moran C.; Best S.;
RA Stoye J.P.;
RT "Structure and expression of the hairless gene of mice."
RL Proc. Natl. Acad. Sci. U.S.A. 91:7717-7721(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6; TISSUE=Retina;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.;
RA Klausner R.D.; Collins F.S.; Wagner L.; Shenmen C.M.; Schuler G.D.;
RA Altschul S.F.; Zeeberg B.; Buetow K.H.; Schaefer C.F.; Bhat N.K.;
RA Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Hsieh F.;
RA Diatchenko L.; Mariusina K.; Farmer A.A.; Rubin G.M.; Hong L.;
RA Stapleton M.J.; Udén T.B.; Toshiyuki S.; Carninci P.; Prange C.;
RA Raha S.S.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullaly S.J.;
RA Bosak S.A.; McSwan P.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.;
RA Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.;
RA Villalon D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;
RA Fahey J.; Helton E.; Kettman M.; Madan A.; Rodrigues S.; Sanchez A.;
RA Whiting M.; Madan A.; Young A.C.; Shevchenko Y.; Souffard G.G.;
RA Blakesley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;
RA Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.;
RA Butterfield Y.S.N.; Krzywinski M.I.; Skalska U.; Smallos D.E.;
RA Schnerch A.; Schein J.E.; Jones S.J.M.; Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: May act as a transcription factor that could act on to
CC regulate one of the phases of hair growth.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: Expressed predominantly in brain, hair
CC follicles and interfollicular epidermis. No expression in
CC dermis.
CC -!- DISEASE: HR MUTATION PRODUCES A NUMBER OF PLEIOTROPIC EFFECTS
CC INCLUDING STRUCTURAL ABNORMALITIES OF EPITHELIAL CELLS IN THE HAIR
CC FOLLICLES, HAIR LOSS TOWARDS THE END OF THE FIRST HAIR GROWTH
CC CYCLE, AND THE FAILURE OF SUBSEQUENT HAIR GROWTH CYCLES. OLDER
CC MICE CARRYING AN HR MUTATION HAVE BEEN REPORTED TO POSSESS ALTERED
CC RATIOS OF T-CELL-DEPENDENT B-CELL RESPONSES. MICE HOMOCYGOUS FOR
CC HR MUTATION ARE UNIQUELY SENSITIVE TO UV AND CHEMICALLY INDUCED
CC SKIN TUMORS.
CC
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CC
CC EMBL; Z32675; CAA83587.1; -.
DR EMBL; BC049182; AAH49182.1; -.
DR PIR; I48378; I48378.
DR MGD; MGI:96223; hr.
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DR InterPro; IPR003347; TF_JmJC.
DR Pfam; PF02373; JmJC; 1.
DR SMART; SM00558; JmJC; 1.
KW Zinc-finger; DNA-binding; Nuclear protein; Transcription regulation;
KW Metal-binding.
FT ZN FING 595 620 C6-TYPE.
FT ZN FING 535 540 POLY-GLY.
FT ZN FING 401 401 P -> S (IN REF. 1).
FT CONFLICT 401 401
SQ SEQUENCE 1182 AA; 127192 MW; 3AFABE96C6EB3241 CRC64;

Query Match
Best Local Similarity 49.3%; Score 35; DB 1; Length 1182;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGRSGRAGS 13
Db ||| :|||
79 EGRNGRKGKS 89

RESULT 46
POLG POWVL STANDARD; PRT; 3415 AA.
AC Q04538;
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Genome polyprotein [Contains: Capsid protein C (Core protein); Matrix
DE protein (Envelope protein M); Major envelope protein E; Nonstructural
DE proteins NS1, NS2A, NS2B, NS4A and NS4B; Protease/helicase
DE (EC 3.4.21.98) (NS3); RNA-directed RNA polymerase (EC 2.7.7.48)
DE (NS5)].
OS Tick-borne poxvirus (strain LB).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus.
OX NCBI_TaxID=39008;
RN [1]
SEQUENCE FROM N.A.
RA MEDLINE=93242744; PubMed=8097605;
RA Mandl C.W., Holzmann H., Kunz C., Heinz P.X.;
RT "Complete genomic sequence of Powassan virus: evaluation of genetic
RT elements in tick-borne versus mosquito-borne flaviviruses.";
RL Virology 194:173-184(1993).
CC -!- FUNCTION: The small proteins NS2A, NS2B, NS4A and NS4B are
CC hydrophobic, suggesting a possible membrane-related function.
CC NS3 and NS5 may play a role in the viral RNA replication.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of four peptide bonds in the viral
CC precursor polyprotein, commonly with Asp or Glu in the P6
CC position, Cys or Thr in P1 and Ser or Ala in P1'.
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC {RNA} (N).
CC -!- SUBUNIT: The virion of this virus is a nucleocapsid covered by a
CC lipoprotein envelope. The envelope consists of two proteins:
CC protein M and glycoprotein E. The nucleocapsid is a complex of
CC protein C and mRNA.
CC
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CC -----
CC EMBL; L06436; AA02739.1; -.
CC F01; A46105; A46105.
CC HSP; P14336; 1SVB.
CC
CC MEROPS; S07.UFW; -.
CC
CC InterPro; IPR009003; Cys Ser tryptase.
CC InterPro; IPR001410; DEAD.
CC InterPro; IPR001122; Flavi_capsidC.
CC InterPro; IPR000336; Flavi_glycoprote.
CC InterPro; IPR000069; Flavi_M.
CC InterPro; IPR001157; Flavi_NS1.

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DR InterPro; IPR000752; Flavi_NS2A.
DR InterPro; IPR000487; Flavi_NS2B.
DR InterPro; IPR000404; Flavi_NS4A.
DR InterPro; IPR001528; Flavi_NS4B.
DR InterPro; IPR000208; Flavi_NS5.
DR InterPro; IPR002535; Flavi_propep.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR001850; Peptidase S7.
DR InterPro; IPR007094; RNA_pol_DS_Ps.
DR InterPro; IPR007095; RNA_pol_PSVir.
DR InterPro; IPR002877; RmJ_FtsJ.
DR Pfam; PF01003; Flavi_capsid; 1.
DR Pfam; PF02832; Flavi_glycop_C; 1.
DR Pfam; PF00869; Flavi_glycoprot; 1.
DR Pfam; PF00949; Flavi_helicase; 1.
DR Pfam; PF01004; Flavi_M; 1.
DR Pfam; PF00948; Flavi_NS1; 1.
DR Pfam; PF01005; Flavi_NS2A; 1.
DR Pfam; PF01002; Flavi_NS2B; 1.
DR Pfam; PF01350; Flavi_NS4A; 1.
DR Pfam; PF01349; Flavi_NS4B; 1.
DR Pfam; PF00972; Flavi_NS5; 1.
DR Pfam; PF01570; Flavi_propep; 1.
DR Pfam; PF01728; FtsJ; 1.
DR Pfam; PF00271; helicase_C; 1.
DR ProDom; PD001556; Flavi_glycoprotE; 1.
DR ProDom; PD001496; Flavi_NS1; 1.
DR SMART; SM00487; DEXDc; 1.
DR SMART; SM00490; HELICc; 1.
DR PROSITE; PS00690; DEAD ATP HELICASE; FALSE NEG.
KW Polyprotein; Glycoprotein; Transferase; RNA-directed RNA polymerase;
KW Core protein; Coat protein; Envelope protein; Helicase;
KW ATP-binding; Transmembrane; Nonstructural protein.
FT CHAIN 3 114
FT PROPEP 115 203
FT CHAIN 204 278
FT CHAIN 279 775
FT CHAIN 776 1128
FT CHAIN 1129 1358
FT CHAIN 1359 1489
FT CHAIN 1490 2111
FT CHAIN 2112 2260
FT CHAIN 2261 2512
FT CHAIN 2513 3415
FT TRANSMEM 101 114
FT TRANSMEM 244 262
FT TRANSMEM 264 278
FT TRANSMEM 727 748
FT TRANSMEM 754 775
FT TRANSMEM 1137 1153
FT TRANSMEM 1160 1179
FT TRANSMEM 1294 1313
FT TRANSMEM 1385 1403
FT TRANSMEM 1453 1473
FT TRANSMEM 2161 2184
FT TRANSMEM 2191 2211
FT TRANSMEM 2244 2260
FT TRANSMEM 2347 2367
FT TRANSMEM 2434 2454
FT NP_BIND 1688 1695
FT SITE 1780 1783
FT DISULFID 281 308
FT DISULFID 338 394
FT DISULFID 352 383
FT DISULFID 370 399
FT DISULFID 464 568
FT DISULFID 585 617
FT CARBOHYD 142 142
FT CARBOHYD 432 432
FT CARBOHYD 860 860
FT CARBOHYD 983 983
FT CARBOHYD 999 999

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SQ SEQUENCE 3415 AA; 378564 MW; E71092FE64049F46 CRC64;
Query Match 49.3%; Score 35; DB 1; Length 3415;
Best Local Similarity 63.6%; Pred. No. 8.7e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 3 EGCGRGEAGS 13
:| | | | |
Db 2508 QGARGGAGS 2518

RESULT 47
ZEP1 HUMAN
ID ZEP1 HUMAN STANDARD; PRT; 2717 AA.
AC P15822;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Zinc finger protein 40 (Human immunodeficiency virus type I enhancer-
DE binding protein 1) (HIV-EPI) (Major histocompatibility complex binding
DE protein 1) (MBP-1) (Positive regulatory domain II binding factor 1)
DE (PRDII-BFI).
GN HIVEP1 OR ZNF40.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RW SEQUENCE FROM N.A.
RP MEDLINE=90169514; PubMed=2106471;
RA Fan C.M., Maniatis T.;
RT "A DNA-binding protein containing two widely separated zinc finger
RT motifs that recognize the same DNA sequence.";
RL Genes Dev. 4:29-42(1990).
[2]
RP STRUCTURE BY NMR OF 2113-2142.
RX MEDLINE=91064333; PubMed=2248949;
RA Omichinski J.G., Clore G.M., Appella E., Sakaguchi K.,
RA Gronenborn A.M.;
RT "High-resolution three-dimensional structure of a single zinc finger
RT from a human enhancer binding protein in solution.";
RL Biochemistry 29:9324-9334(1990).
[3]
RP STRUCTURE BY NMR OF 2087-2142.
RX MEDLINE=92232684; PubMed=1567844;
RA Omichinski J.G., Clore G.M., Robien M., Sakaguchi K., Appella E.,
RA Gronenborn A.M.;
RT "High-resolution solution structure of the double Cys2His2 zinc
RT finger from the human enhancer binding protein MBP-1.";
RL Biochemistry 31:3907-3917(1992).
-!- FUNCTION: THIS PROTEIN SPECIFICALLY BINDS TO THE DNA SEQUENCE
CC 5'-GGGACTTCC-3' WHICH IS FOUND IN THE ENHANCER ELEMENTS OF
CC NUMEROUS VIRAL PROMOTERS SUCH AS THOSE OF SV40, CMV, OR HIV1.
CC IN ADDITION, RELATED SEQUENCES ARE FOUND IN THE ENHANCER ELEMENTS
CC OF A NUMBER OF CELLULAR PROMOTERS, INCLUDING THOSE OF THE CLASS I
CC MHC, INTERLEUKIN-2 RECEPTOR, AND INTERFERON-BETA GENES. IT MAY ACT
CC IN T-CELL ACTIVATION.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- INDUCTION: By mitogens and phorbol ester.
CC -!- DOMAIN: CONTAINS TWO SETS OF 2 ZINC-FINGERS, WHICH ARE WIDELY
CC SEPARATED AND RECOGNIZE THE SAME DNA SEQUENCE. THERE IS A FIFTH
CC ZINC-FINGER IN-BETWEEN.
CC -!- SIMILARITY: STRONG, TO HIVEP2.
CC
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CC
CC EMBL; X51435; CAA35798.1; -.
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DR PIR; A34203; A34203.
DR PDB; 3ZNF; 15-JAN-92.
DR PDB; 4ZNF; 15-JAN-92.
DR PDB; 1BBO; 31-OCT-93.
DR TRANSFAC; T00497; -.
DR Genew; HGNC:4920; HIVEP1.
DR MIM; 194540; -.
DR GO; GO:0005634; C:nucleus; TAS.
DR GO; GO:0003677; F:DNA binding; TAS.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF00096; zf_C2H2; 5.
DR SMART; SMO0355; Znf_C2H2; 4.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_2; 4.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_1; 4.
KW Transcription regulation; Zinc-finger; Metal-binding; DNA-binding;
KW Nuclear protein; Repeat; 3D-structure.
FT ZN_FING 406 428
FT ZN_FING 434 456
FT ZN_FING 958 981
FT ZN_FING 2087 2109
FT ZN_FING 2115 2139
FT DOMAIN 803 806
FT STRAND 2088 2088
FT TURN 2090 2092
FT STRAND 2095 2095
FT HELIX 2099 2108
FT TURN 2109 2109
FT STRAND 2115 2116
FT STRAND 2123 2124
FT HELIX 2127 2135
SQ SEQUENCE 2717 AA; 297217 MW; D45D3CA951FEA561 CRC64;
Query Match 48.6%; Score 34.5; DB 1; Length 2717;
Best Local Similarity 63.6%; Pred. No. 8.4e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 1; Gaps 1;
QY 1 SHEGCR-SGEA 10
||:| | | |
Db 921 SHQCHARGEA 931

RESULT 48
YOR4_EAV
ID YOR4_EAV STANDARD; PRT; 152 AA.
AC P28994;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE Hypothetical 17.2 kDa protein (ORF4).
OS Equine arteritis virus (EAV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Arteriviridae; Arterivirus.
OX NCBI_TaxID=11047;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BUCYTUS;
RX MEDLINE=91237805; PubMed=1851863;
RA den Boon J.A., Snijder E.J., Chirnside E.D., de Vries A.A.F.,
RA Horzinek M.C., Spaan W.J.M.;
RT "Equine arteritis virus is not a togavirus but belongs to the
RT coronaviruslike superfamily.";
RL J. Virol. 65:2910-2920(1991).
CC -!- FUNCTION: Possible envelope protein.
CC
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CC
CC EMBL; X53459; CAA37543.1; -.
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DR PIR; E39925; E39925.
DR InterPro; IPR004257; GP4.
DR Pfam; PF03010; GP4; 1.
DR ProDom; PD006770; GP4; 1.
KW Hypothetical protein; Envelope protein.
FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .) (POTENTIAL)..
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (POTENTIAL)..
FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL)..
SQ SEQUENCE 152 AA; 17161 MW; 1065AE55C5811CA8 CRC64;

Query Match      47.9%; Score 34; DB 1; Length 152;
Best Local Similarity 83.3%; Pred. No. 51;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 HEGCRS 7
    |||||
Db 47 HEGCRN 52

RESULT 49
YFDN_ECOLI
ID YFDN_ECOLI STANDARD; PRT; 164 AA.
AC P76510;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE Hypothetical protein yfdN.
GN YFDN OR B2357.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregory J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE OF 70-164 FROM N.A.
RX MEDLINE=87016348; PubMed=3532033;
RA Kurose N., Watanabe K., Kimura A.;
RT "Nucleotide sequence of the gene responsible for D-xylose uptake in
RL Escherichia coli.";
RL Nucleic Acids Res. 14:7115-7123(1986).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AE000324; AAC75416.1; -.
DR EMBL; X04387; -. NOT_ANNOTATED_CDS.
DR PIR; B65009; B65009.
DR EcoGene; EG12949; yfdN.
KW Hypothetical protein; Complete proteome.
FT CONFLICT 73 73 P -> L (IN REF. 2).
SQ SEQUENCE 164 AA; 18766 MW; EC3C6404F98B484D CRC64;

Query Match      47.9%; Score 34; DB 1; Length 164;
Best Local Similarity 55.6%; Pred. No. 55;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SHEGCRSGE 9
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Db 15 AHPGCTSGD 23

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## RESULT 50

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Y334_RALSO
ID Y334_RALSO STANDARD; PRT; 171 AA.
AC Q8Y2K1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein RSC0334.
GN RSC0334 OR RS03301.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=GM11000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choisme N., Claudel-Renard C., Cunac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Siguiet P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
CC -!- SIMILARITY: Belongs to the UPF0189 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AL646058; CAD13862.1; -.
DR HAMAP; MF_01205; -. 1.
DR InterPro; IPR002589; Alpp.
DR Pfam; PF01661; Alpp; 1.
DR SMART; SM00506; Alpp; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 171 AA; 18018 MW; 7DC99AF217882657 CRC64;

Query Match      47.9%; Score 34; DB 1; Length 171;
Best Local Similarity 62.5%; Pred. No. 58;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCRSGEAE 11
    |||||
Db 58 GCRTGQAK 65

Search completed: April 19, 2004, 17:18:47
Job time : 8.33871 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 19, 2004, 17:08:00 ; Search time 58.0806 Seconds  
(without alignments)  
63.242 Million cell updates/sec

Title: US-10-726-692-22

Perfect score: 71

Sequence: 1 SHEGRCRGEAEGS 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : A: Geneseq 29Jan04:.\*  
1: geneseqp1980s:.\*  
2: geneseqp1990s:.\*  
3: geneseqp2000s:.\*  
4: geneseqp2001s:.\*  
5: geneseqp2002s:.\*  
6: geneseqp2003as:.\*  
7: geneseqp2003bs:.\*  
8: geneseqp2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	64.8	740	3 AAY99411	Aay99411 Human PRO
2	46	64.8	740	4 AAB66160	Aab66160 Protein o
3	46	64.8	802	3 AAB40501	Aab40501 Human ORF
4	46	64.8	802	4 AAU29179	Aau29179 Human PRO
5	46	64.8	802	6 ABU58555	Abu58555 Human PRO
6	46	64.8	802	6 ABU88103	Abu88103 Novel hum
7	46	64.8	802	6 ABU84418	Abu84418 Human sec
8	46	64.8	802	6 ABR66292	Abu66292 Human sec
9	46	64.8	802	6 ABR65682	Abu65682 Human sec
10	46	64.8	802	6 ABU99622	Abu99622 Human sec
11	46	64.8	802	6 ABU82861	Abu82861 Human PRO
12	46	64.8	802	6 ABU89982	Abu89982 Novel hum
13	46	64.8	802	6 ABR68231	Abu68231 Human sec
14	46	64.8	802	6 ABU09342	Abu09342 Human cho
15	46	64.8	802	6 ABU96284	Abu96284 Novel hum
16	46	64.8	802	6 ABU92715	Abu92715 Human sec
17	46	64.8	802	6 ABU08792	Abu08792 Human sec
18	46	64.8	802	6 ABO02844	Abu02844 Human sec
19	46	64.8	802	6 ABR74998	Abu74998 Human sec
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21	46	64.8	802	6 ABU85733	Abu85733 Human PRO
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23	46	64.8	802	6 ABU98108	Abu98108 Novel hum
24	46	64.8	802	6 ABU91814	Abu91814 Novel hum
25	46	64.8	802	6 ABU89507	Abu89507 Human PRO

26	46	64.8	802	6 ABU86348	Abu86348 Human sec
27	46	64.8	802	6 ABU67561	Abu67561 Human sec
28	46	64.8	802	6 ABU80589	Abu80589 Human PRO
29	46	64.8	802	6 ABR99507	Abu99507 Human sec
30	46	64.8	802	6 ABR98897	Abu98897 Human sec
31	46	64.8	802	6 ABO16420	Abu16420 Human sec
32	46	64.8	802	6 ABR92320	Abu92320 Human sec
33	46	64.8	802	6 ABO18961	Abu18961 Human sec
34	46	64.8	802	6 ABR78382	Abu78382 Human sec
35	46	64.8	802	6 ABU85118	Abu85118 Novel hum
36	46	64.8	802	6 ABO00257	Abu000257 Novel hum
37	46	64.8	802	6 ABO11589	Abu11589 Human sec
38	46	64.8	802	6 ABO02234	Abu022234 Human sec
39	46	64.8	802	6 ABU88808	Abu88808 Novel hum
40	46	64.8	802	6 ABU83503	Abu83503 Human sec
41	46	64.8	802	6 ABO06304	Abu06304 Novel hum
42	46	64.8	802	6 ABR59340	Abu59340 Human sec
43	46	64.8	802	6 ABO09402	Abu09402 Human sec
44	46	64.8	802	6 ABO19266	Abu19266 Novel hum
45	46	64.8	802	6 ABO11284	Abu11284 Human sec
46	46	64.8	802	6 ABR66902	Abu66902 Human sec
47	46	64.8	802	6 ABO16115	Abu16115 Human sec
48	46	64.8	802	6 ABO13821	Abu13821 Human sec
49	46	64.8	802	6 ABU65724	Abu65724 Human sec
50	46	64.8	802	6 ABO07572	Abu07572 Human PRO

ALIGNMENTS

RESULT 1  
AAY99411  
ID AAY99411 standard; protein; 740 AA.

AC AAY99411;  
XX  
DT 08-AUG-2000 (first entry)  
XX

DE Human PRO1487 (UNQ756) amino acid sequence SEQ ID NO:260.

KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;  
KW transmembrane; secretion; immunoadhesion; pharmaceutical; screening.

OS Homo sapiens.

PN WO200012708-A2.

XX 09-MAR-2000.

XX 01-SEP-1999; 99WO-US020111.  
XX 01-SEP-1998; 98US-0098716P.  
XX 01-SEP-1998; 98US-0098749P.  
XX 01-SEP-1998; 98US-0098750P.  
XX 02-SEP-1998; 98US-0098803P.  
XX 02-SEP-1998; 98US-0098821P.  
XX 02-SEP-1998; 98US-0098843P.  
XX 09-SEP-1998; 98US-0099536P.  
XX 09-SEP-1998; 98US-0099596P.  
XX 09-SEP-1998; 98US-0099598P.  
XX 09-SEP-1998; 98US-0099602P.  
XX 09-SEP-1998; 98US-0099642P.  
XX 10-SEP-1998; 98US-0099741P.  
XX 10-SEP-1998; 98US-0099754P.  
XX 10-SEP-1998; 98US-0099763P.  
XX 10-SEP-1998; 98US-0099792P.  
XX 10-SEP-1998; 98US-0099808P.  
XX 10-SEP-1998; 98US-0099812P.  
XX 10-SEP-1998; 98US-0099815P.  
XX 10-SEP-1998; 98US-0099816P.  
XX 15-SEP-1998; 98US-0100385P.  
XX 15-SEP-1998; 98US-0100388P.  
XX 15-SEP-1998; 98US-0100390P.

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PR 16-SEP-1998; 98US-0100584P.
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PR 29-OCT-1998; 98US-0106248P.

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PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108859P.
PR 18-NOV-1998; 98US-0108904P.
XX
XX (GETH ) GENENTECH INC.
PA
XX Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WT;
PI WPI: 2000-237871/20.
XX N-PSDB; AAA37093.
PT New mammalian DNA sequences encoding transmembrane, receptor or secreted
PT PRO polypeptides, useful for screening of potential peptide or small
PT molecule inhibitors of the relevant receptor/ligand interactions.
XX Claim 12; Fig 144; 773pp; English.
XX AAA37022 to AAA37144 encode the new isolated human transmembrane,
XX receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The
XX transmembrane and receptor PRO proteins can be used for screening of
XX potential peptide or small molecule inhibitors of the relevant
XX receptor/ligand interactions. The polypeptides and nucleotide sequences
XX encoding then have various industrial applications, including uses as
XX pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR
XX primers and hybridisation probes used in the isolation of the PRO
XX polypeptides from the present invention
XX SQ Sequence 740 AA;

Query Match 64.8%; Score 46; DB 3; Length 740;
Best Local Similarity 69.2%; Pred. No. 62;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SHEGCRSGEAGCS 13
Db 44 SPEGCRSGQAAAS 56

RESULT 2
AAB66160
ID AAB66160 standard; protein; 740 AA.
XX
AC AAB66160;
XX
DT 02-APR-2001 (first entry)
XX
DE Protein of the invention #72.
XX
KW Secreted; transmembrane; gene therapy.
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XX PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;  
 KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;  
 KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;  
 XX adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.  
 OS Homo sapiens.  
 XX WO200168848-A2.  
 XX 20-SEP-2001.  
 XX 28-FEB-2001; 2001WO-US006520.  
 XX 01-MAR-2000; 2000WO-US005601.  
 PR 02-MAR-2000; 2000WO-US005841.  
 PR 03-MAR-2000; 2000US-0187202P.  
 PR 06-MAR-2000; 2000US-0186968P.  
 PR 14-MAR-2000; 2000US-0189320P.  
 PR 14-MAR-2000; 2000US-0189320P.  
 PR 15-MAR-2000; 2000WO-US006884.  
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 PR 30-MAR-2000; 2000WO-US008439.  
 PR 04-APR-2000; 2000US-0194449P.  
 PR 04-APR-2000; 2000US-0194647P.  
 PR 11-APR-2000; 2000US-0195975P.  
 PR 11-APR-2000; 2000US-0196000P.  
 PR 11-APR-2000; 2000US-0196187P.  
 PR 11-APR-2000; 2000US-0196690P.  
 PR 11-APR-2000; 2000US-0196820P.  
 PR 18-APR-2000; 2000US-0198121P.  
 PR 18-APR-2000; 2000US-0198585P.  
 PR 25-APR-2000; 2000US-0199397P.  
 PR 25-APR-2000; 2000US-0199550P.  
 PR 25-APR-2000; 2000US-0199654P.  
 PR 03-MAY-2000; 2000US-0201516P.  
 PR 17-MAY-2000; 2000WO-US013705.  
 PR 22-MAY-2000; 2000WO-US014042.  
 PR 30-MAY-2000; 2000WO-US014941.  
 PR 02-JUN-2000; 2000WO-US015264.  
 PR 05-JUN-2000; 2000US-0209832P.  
 PR 28-JUL-2000; 2000WO-US020710.  
 PR 22-AUG-2000; 2000US-00644848.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 08-NOV-2000; 2000WO-US030952.  
 PR 01-DEC-2000; 2000WO-US032678.  
 PR 20-DEC-2000; 2000WO-US034956.  
 XX (GETH ) GENENTECH INC.  
 XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;  
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;  
 XX WPI; 2001-602746/68.  
 DR N-PSDB; AAS46080.  
 XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the  
 PT presence of tumors, such as prostate and breast tumors, in mammals and to  
 PT screen for modulators of the compounds.  
 XX Claim 11; Fig 312; 774pp; English.  
 PS Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.  
 XX The PRO polypeptides and their associated nucleic acids can be used to  
 CC detect the presence of a tumour in a mammal by comparing the level of  
 CC expression of a PRO polypeptide in a test sample of cells from the animal  
 CC and a control sample of normal cells, whereby a higher level of

CC expression in the test sample indicates the presence of a tumour in the  
 CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats  
 CC and rabbits but are preferably human. The polypeptides can be used to  
 CC stimulate tumour necrosis factor (TNF) alpha release from human blood,  
 CC when contacted with it. A specific polypeptide can be used to stimulate  
 CC the proliferation or differentiation of chondrocyte cells. The PRO  
 CC proteins can be used to determine the presence of tumours and also  
 CC susceptibility to tumour development, particularly adrenal, lung, colon,  
 CC breast, prostate, rectal, cervical, or liver tumours, in mammalian  
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids  
 CC can be used for genetic analysis of individuals with genetic disorders  
 XX  
 SQ Sequence 802 AA;

Query Match 64.8%; Score 46; DB 4; Length 802;  
 Best Local Similarity 69.2%; Pred. No. 67;  
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SHEGCRSGEAGS 13  
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 Db 44 SPEGCRSQAAAS 56

## RESULT 5

ABUS8555  
 ID ABUS8555 standard; protein; 802 AA.

XX AC ABUS8555;

XX 15-APR-2003 (first entry)

XX Human PRO polypeptide #156.

XX Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;  
 KW dog; cat; cow; horse; sheep; pig; goat; rabbit; ADPPT;  
 KW antibody-dependent enzyme mediated prodrug therapy.

XX Homo sapiens.

XX US2003027272-A1.

XX 06-FEB-2003.

XX 21-JUN-2002; 2002US-00176492.

XX 18-SEP-1997; 97US-0059263P.

PR 18-SEP-1997; 97US-0059266P.

PR 17-OCT-1997; 97US-0062250P.

PR 21-OCT-1997; 97US-0063486P.

PR 24-OCT-1997; 97US-0063120P.

PR 24-OCT-1997; 97US-0063121P.

PR 28-OCT-1997; 97US-0063540P.

PR 28-OCT-1997; 97US-0063541P.

PR 28-OCT-1997; 97US-0063544P.

PR 28-OCT-1997; 97US-0063564P.

PR 29-OCT-1997; 97US-0063734P.

PR 31-OCT-1997; 97US-0063870P.

PR 31-OCT-1997; 97US-0064103P.

PR 13-NOV-1997; 97US-0065311P.

PR 21-NOV-1997; 97US-0066120P.

PR 24-NOV-1997; 97US-0066466P.

PR 24-NOV-1997; 97US-0066772P.

PR 11-DEC-1997; 97US-0069335P.

PR 12-DEC-1997; 97US-0069425P.

PR 17-DEC-1997; 97US-0069870P.

PR 18-DEC-1997; 97US-0068017P.

PR 10-MAR-1998; 98US-0077450P.

PR 11-MAR-1998; 98US-0077632P.

PR 11-MAR-1998; 98US-0077649P.

PR 20-MAR-1998; 98US-0078886P.

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PR 27-MAR-1998; 98US-0079664P.

PR 27-MAR-1998; 98US-0079786P.

PR 31-MAR-1998; 98US-0080107P.  
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PR 01-APR-1998; 98US-0080333P.  
PR 08-APR-1998; 98US-0081049P.  
PR 08-APR-1998; 98US-0081070P.  
PR 09-APR-1998; 98US-0081195P.  
PR 15-APR-1998; 98US-0081838P.  
PR 21-APR-1998; 98US-0082568P.  
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PR 22-APR-1998; 98US-0082797P.  
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PR 05-MAY-1998; 98US-0084366P.  
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Query Match 64.8%; Score 46; DB 6; Length 802;

Best Local Similarity 69.2%; Pred. No. 67;

Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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DB 44 SPEGCRSGQAAS 56

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KW chondrocyte; proliferation; differentiation; cartilage disorder;  
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;  
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;  
KW liver; drug screening; transgenic animal; genetic analysis;  
KW antiarthritic; vulnery; gene therapy.  
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Query Match 64.8%; Score 46; DB 6; Length 802;
Best Local Similarity 69.2%; Pred. No. 67;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SHEGCRSGEAGEGS 13
Db 44 SPEGCRSGQAAS 56

RESULT 14
ABU09342
ID ABU09342 standard; protein; 802 AA.
XX
AC ABU09342;
XX
DT 01-JUL-2003 (first entry)
XX
DE Human chondroitin synthase.
XX
KW Human; chondroitin synthase; vector; sugar chain production;
KW chondroitin disaccharide repetitive unit; enzyme.
OS Homo sapiens.
XX
PN WO2003012099-A1.
XX
PD 13-FEB-2003.
XX
PF 01-AUG-2002; 2002WO-JP007859.
XX
PR 01-AUG-2001; 2001JP-00234112.
XX
PA (NEWI-) NEW IND RES ORG.
XX
PI Sugahara K, Kitagawa H;
XX
WPI; 2003-248181/24.
N-PSDB; ABX95723.
XX
PT New vector for use in producing human chondroitin synthase applicable in
PT production of sugar chains and having a disaccharide repetitive unit of
PT chondroitin.
XX
PS Claim 1; Fig 1; 61pp; Japanese.
XX
CC The present invention relates to a vector containing DNA that encodes
CC human chondroitin synthase. The vector is useful for producing
CC chondroitin synthase which may be used in the production of a sugar chain
CC having a disaccharide repetitive unit of chondroitin. The polynucleotide
```

CC sequence encoding chondroitin synthase is useful as a hybridisation probe  
CC for chondroitin synthase. The present sequence represents human  
XX chondroitin synthase

SQ Sequence 802 AA;

Query Match 64.8%; Score 46; DB 6; Length 802;  
Best Local Similarity 69.2%; Pred. No. 67;  
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SHEGCRSGEAECS 13  
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Db 44 SPEGCRSGOAAAS 56

#### RESULT 15

ABU96284

ID ABU96284 standard; protein; 802 AA.

XX

AC ABU96284;

XX

DT 25-JUL-2003 (first entry)

XX

DE Novel human secreted and transmembrane protein PRO1487.

XX

KW Human; secreted and transmembrane protein; PRO; transgenic animal;

KW knockout; chromosome identification; tissue typing; tumour;

KW chondrocyte proliferation; chondrocyte differentiation;

KW tumor necrosis factor-alpha release stimulator.

XX

OS Homo sapiens.

XX

PN US2003036144-A1.

XX

PD 20-FEB-2003.

XX

PF 01-JUL-2002; 2002US-00187601.

XX

PR 18-SEP-1997; 97US-0059263P.

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Best Local Similarity 69.2%; Pred. No. 67;  
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SHEGCRSGEAGS 13  
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Db 44 SPEGCRSGQAAS 56

RESULT 16  
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ID ABU92715 standard; protein; 802 AA.  
XX  
AC ABU92715;  
XX  
DT 18-JUL-2003 (first entry)  
XX  
DE Human secreted/transmembrane protein (PRO) #156.  
XX  
DE Human; secreted protein; transmembrane protein; PRO; tumour;  
KW proliferation; differentiation; chondrocyte cell; TNF-alpha;  
KW tumour necrosis factor-alpha; gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN US2003036149-A1.  
XX  
PD 20-FEB-2003.  
XX  
PF 02-JUL-2002; 2002US-00187746.  
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PR 07-OCT-1998; 98US-0016897B.

Query Match 64.8%; Score 46; DB 6; Length 802;

Best Local Similarity 69.2%; Pred. No. 67;

Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SHEGCRSGEAGS 13

DB 44 SPEGCRSGQAAS 56

RESULT 17  
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ID ABO08792 standard; protein; 802 AA.  
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AC ABO08792;  
XX  
DT 17-AUG-2003 (first entry)  
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DE Human secreted/transmembrane protein (PRO) #156.  
XX  
KW Human; secreted and transmembrane protein; PRO; TNF-alpha;  
KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;  
KW tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour;  
KW prostate tumour; rectal tumour; cervical tumour; liver tumour.  
XX  
OS Homo sapiens.  
XX  
PN US2003044923-A1.  
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PD 06-MAR-2003.  
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Query Match 64.8%; Score 46; DB 6; Length 802;
Best Local Similarity 69.2%; Pred. No. 67;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SHEGCRSGEAGS 13
Db 44 SPEGCRSGQAAAS 56

RESULT 18
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ID ABO02844 standard; protein; 802 AA.
XX
AC ABO02844;
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DT 09-AUG-2003 (first entry)
XX Human secreted/transmembrane protein (PRO) #156.
XX Human; secreted and transmembrane protein; PRO; TNF-alpha;
KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour;
XX prostate tumour; rectal tumour; cervical tumour; liver tumour.
OS Homo sapiens.
XX
PN US2003040062-A1.
XX 27-FEB-2003.
XX
PF 25-JUN-2002; 2002US-00180545.
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Query Match 64.8%; Score 46; DB 6; Length 802;
Best Local Similarity 69.2%; Pred. No. 67;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SHEGCRSGEAGGS 13
Db 44 SPEGCRSGQAAS 56

RESULT 19
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ID ABR74998 standard; protein; 802 AA.
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AC ABR74998;
XX
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DE Human secreted polypeptide PRO1487, SEQ ID NO:312.
XX
KW Human; PRO; secreted protein; transmembrane protein;
extracellular domain; tumour necrosis factor-alpha;
chondrocyte; proliferation; differentiation; cartilage disorder;
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KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;  
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;  
KW liver; drug screening; transgenic animal; genetic analysis;  
KW antithratic; vulnery; gene therapy.

XX OS Homo sapiens.  
XX US2003040056-A1.  
XX PD 27-FEB-2003.  
XX PF 21-JUN-2002; 2002US-00176916.  
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Best Local Similarity 69.2%; Pred. No. 67;  
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Db 44 SPEGCRSGQAAS 56

## RESULT 21

ABU85733  
ID ABU85733 standard; protein; 802 AA.

XX AC ABU85733;

XX DT 02-JUL-2003 (first entry)

XX DE Human PRO polypeptide #156.

XX KW Human; PRO; secreted polypeptide; transmembrane polypeptide;  
tumour necrosis factor alpha; TNF-alpha; chondrocyte cell; tumour;  
cytostatic.

XX OS Homo sapiens.

XX PN US2003036140-A1.

XX PD 20-FEB-2003.

XX PF 01-JUL-2002; 2002US-00187588.

XX PR 26-JUN-1998; 98US-00105413.

XX PR 16-SEP-1998; 98WO-US019330.

XX PR 07-OCT-1998; 98US-00168978.

XX PR 07-OCT-1998; 98WO-US021141.

XX PR 06-NOV-1998; 98US-00187368.







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 PR 30-SEP-1998; 98US-0102570P.  
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Query Match 64.8%; Score 46; DB 6; Length 802;

Best Local Similarity 69.2%; Pred. No. 67;

Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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DB 44 SPEGCRSGQAAAS 56

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ABU98108  
 ID ABU98108 standard; protein; 802 AA.

XX AC ABU98108;

DT 30-JUL-2003 (first entry)

DE Novel human secreted and transmembrane protein PRO1487.

KW Human; secreted and transmembrane protein; PRO; cytostatic; gene therapy;

KW chondrocyte stimulator; tumour; adrenal tumour; lung tumour;

KW colon tumour; breast tumour; prostate tumour; rectal tumour;

KW cervical tumour; liver tumour; chromosome identification.

XX OS Homo sapiens.

XX PN US2003017544-A1.

XX PD 23-JAN-2003.

XX 21-JUN-2002; 2002US-00176915.

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Db 44 SPEGCRSQAAAS 56

RESULT 24
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AC ABU91814;
XX
DT 11-AUG-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO1487.
XX
KW Human; gene therapy; chromosome identification; tissue typing.
XX
OS Homo sapiens.
XX
PN US2003027277-A1.
XX
PD 06-FEB-2003.
XX
PF 21-JUN-2002; 2002US-00176985.
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RESULT 25
ABU89507
ID ABU89507 standard; protein; 802 AA.
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AC ABU89507;
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DT 09-JUL-2003 (first entry)
XX
DE Human PRO polypeptide #156.
XX
KW Human; PRO polypeptide; secreted protein; transmembrane protein;
KW Chromosome mapping; gene mapping; tumour; adrenal; lung; colon; breast;
KW prostate; rectal; cervical; liver; cancer; TNF-alpha;
KW tumour necrosis factor-alpha; proliferation; differentiation;
KW chondrocyte cell; bone disorder; cartilage disorder; sports injury;
KW arthritis; cytostatic; antiarthritic; osteopathic.
XX
OS Homo sapiens.
XX
PN US2003036141-A1.
XX
PD 20-FEB-2003.
XX
PF 01-JUL-2002; 2002US-00187597.
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PR 02-OCT-1998; 98US-0102687P.
PR 02-OCT-1998; 98US-0102965P.

Query Match 64.8%; Score 46; DB 6; Length 802;
Best Local Similarity 69.2%; Pred. No. 67;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SHEGCRSGAAGS 13
DB 44 SPEGCRSGQAAS 56

RESULT 26
ABU86348
ID ABU86348 standard; protein; 802 AA.
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XX ABU86348;
XX 01-JUL-2003 (first entry)
XX Human secreted/transmembrane protein (PRO) #156.
XX Human; immunogen; secreted protein; transmembrane protein; PRO; tumour;
XX proliferation; differentiation; chondrocyte cells;
XX tumour necrosis factor-alpha; TNF-alpha; blood; gene therapy.
XX Homo sapiens.
XX US2003036146-A1.
XX 20-FEB-2003.
XX 02-JUL-2002; 2002US-00187603.
XX 26-JUN-1998; 98US-00105413.
XX 16-SEP-1998; 98WO-US019330.
XX 07-OCT-1998; 98US-00168978.
XX 07-OCT-1998; 98WO-US021141.
XX 06-NOV-1998; 98US-00187368.
XX 01-DEC-1998; 98WO-US025108.
XX 07-DEC-1998; 98US-00202054.
XX 03-MAR-1999; 99US-00254311.
XX 08-MAR-1999; 99WO-US005028.
XX 14-MAY-1999; 99US-00311832.
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XX 18-OCT-1999; 99US-00403297.
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XX 01-DEC-1999; 99WO-US028301.
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XX 30-DEC-1999; 99WO-US031274.
XX 05-JAN-2000; 2000WO-US000219.
XX 18-FEB-2000; 2000WO-US004341.
XX 18-FEB-2000; 2000WO-US004342.
XX 22-FEB-2000; 2000WO-US004414.
XX 24-FEB-2000; 2000WO-US005004.
XX 01-MAR-2000; 2000WO-US005601.
XX 02-MAR-2000; 2000WO-US005841.
XX 15-MAR-2000; 2000WO-US006884.
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XX 17-MAY-2000; 2000WO-US013705.
XX 22-MAY-2000; 2000WO-US014042.
XX 30-MAY-2000; 2000WO-US014941.
XX 02-JUN-2000; 2000WO-US015264.
XX 28-JUL-2000; 2000WO-US020710.
XX 22-AUG-2000; 2000US-00644848.
XX 24-AUG-2000; 2000WO-US023328.
XX 18-SEP-2000; 2000US-00664610.
XX 18-SEP-2000; 2000US-00665350.
XX 08-NOV-2000; 2000US-00709238.
XX 08-NOV-2000; 2000WO-US030952.
XX 01-DEC-2000; 2000WO-US032678.
XX 20-DEC-2000; 2000US-00747259.
XX 20-DEC-2000; 2000WO-US034956.
XX 28-FEB-2001; 2001WO-US006520.
XX 22-MAR-2001; 2001US-00816744.
XX 10-MAY-2001; 2001US-00854208.
XX 10-MAY-2001; 2001US-00854280.
XX 25-MAY-2001; 2001US-00866028.
XX 01-JUN-2001; 2001WO-US017800.
XX 05-JUN-2001; 2001US-00874503.
XX 20-JUN-2001; 2001WO-US019692.
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PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 18-JUL-2001; 2001US-00908827.  
PR 30-JUL-2001; 2001US-00918585.  
PR 06-AUG-2001; 2001US-00924419.  
PR 13-AUG-2001; 2001US-00929404.  
PR 16-AUG-2001; 2001US-00931836.  
PR 28-AUG-2001; 2001US-00941992.  
PR 29-AUG-2001; 2001WO-US027099.  
PR 04-SEP-2001; 2001WO-US046374.  
PR 15-JAN-2002; 2002US-00052586.  
XX (GETH ) GENENTECH INC.  
XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;  
XX Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;  
XX WPI: 2003-332039/31.  
XX N-PSDB; ACA05855.  
XX New secreted and transmembrane PRO polypeptides and nucleic acids, useful  
PT in gene therapy, in chromosome and gene mapping, as chromosome markers,  
PT in tissue typing, and in chromosome identification.  
XX Claim 11; Fig 312; 706pp; English.  
XX The invention discloses human nucleic acids encoding secreted and  
CC transmembrane (PRO) polypeptides. Also disclosed is an antibody that  
CC specifically binds to the PRO polypeptide, a method for stimulating the  
CC release of tumour necrosis factor alpha (TNF-alpha) from human blood by  
CC contacting the blood with a PRO polypeptide, a method for stimulating the  
CC proliferation or differentiation of chondrocyte cells by contacting the  
CC cells with a PRO polypeptide, a method for detecting the presence of a  
CC tumour in a mammal and an oligonucleotide probe derived from any of the  
CC PRO nucleotide sequences. The nucleotide sequences are useful as probes,  
CC in chromosome and gene mapping, in generating antisense RNA and DNA, in  
CC preparing PRO polypeptides by recombinant techniques and in gene therapy  
CC (e.g. for replacement of defective gene). The PRO polypeptides are useful  
CC as molecular weight markers for protein electrophoresis purposes, for  
CC chromosome identification, as chromosome markers, as therapeutic agents,  
CC for stimulating the release of TNF-alpha from human blood, for  
CC stimulating the proliferation or differentiation of chondrocytes and  
CC detecting the presence of a tumour. The PRO polypeptides and nucleic  
CC acids may also be used diagnostically for tissue typing. The sequences  
CC presented in ABU67406-ABU67710 are the PRO polypeptides of the invention  
XX Sequence 802 AA;  
SQ Query Match 64.8%; Score 46; DB 6; Length 802;  
Best Local Similarity 69.2%; Pred. NO. 67;  
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 1 SHEGCRSGEAGCS 13  
Db 44 SPEGCRSGGAAS 56  
RESULT 28  
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ID ABU0589 standard; protein; 802 AA.  
XX AC ABU0589;  
XX DT 23-JUN-2003 (first entry)  
XX DE Human PRO protein #156.  
XX KW Human; tumour; adrenal; lung; colon; breast; prostate; rectal; cervical;  
XX KW liver; PRO; gene therapy.  
XX OS Homo sapiens.  
XX PN US2003036137-A1.

XX 20-FEB-2003.  
XX 27-JUN-2002; 2002US-00184640.  
XX 26-JUN-1998; 98US-00105413.  
XX 16-SEP-1998; 98WO-US019330.  
XX 07-OCT-1998; 98US-00168978.  
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XX 06-NOV-1998; 98US-00187368.  
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XX 14-MAY-1999; 99US-00311832.  
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XX 01-SEP-1999; 99WO-US020111.  
XX 15-SEP-1999; 99WO-US021090.  
XX 18-OCT-1999; 99US-00403297.  
XX 12-NOV-1999; 99US-00423844.  
XX 01-DEC-1999; 99WO-US028301.  
XX 02-DEC-1999; 99WO-US028551.  
XX 30-DEC-1999; 99WO-US031274.  
XX 05-JAN-2000; 2000WO-US000219.  
XX 18-FEB-2000; 2000WO-US004341.  
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XX 24-FEB-2000; 2000WO-US005004.  
XX 01-MAR-2000; 2000WO-US005601.  
XX 02-MAR-2000; 2000WO-US005841.  
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XX 30-MAR-2000; 2000WO-US008439.  
XX 17-MAY-2000; 2000WO-US013705.  
XX 22-MAY-2000; 2000WO-US014042.  
XX 30-MAY-2000; 2000WO-US014941.  
XX 02-JUN-2000; 2000WO-US015264.  
XX 28-JUL-2000; 2000WO-US020710.  
XX 22-AUG-2000; 2000US-00644848.  
XX 24-AUG-2000; 2000WO-US023328.  
XX 18-SEP-2000; 2000US-00664610.  
XX 18-SEP-2000; 2000US-00665350.  
XX 08-NOV-2000; 2000US-00709238.  
XX 08-NOV-2000; 2000WO-US030952.  
XX 01-DEC-2000; 2000WO-US032678.  
XX 20-DEC-2000; 2000US-00747259.  
XX 20-DEC-2000; 2000WO-US034956.  
XX 28-FEB-2001; 2001WO-US006520.  
XX 22-MAR-2001; 2001US-00816744.  
XX 10-MAY-2001; 2001US-00854208.  
XX 10-MAY-2001; 2001WO-US021735.  
XX 25-MAY-2001; 2001US-00866028.  
XX 01-JUN-2001; 2001WO-US017800.  
XX 05-JUN-2001; 2001US-00874503.  
XX 20-JUN-2001; 2001WO-US019692.  
XX 29-JUN-2001; 2001WO-US021066.  
XX 09-JUL-2001; 2001WO-US021735.  
XX 18-JUL-2001; 2001US-00908827.  
XX 30-JUL-2001; 2001US-00918585.  
XX 06-AUG-2001; 2001US-00924419.  
XX 13-AUG-2001; 2001US-00929404.  
XX 16-AUG-2001; 2001US-00931836.  
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XX 29-AUG-2001; 2001WO-US027099.  
XX 04-SEP-2001; 2001US-00946374.  
XX 15-JAN-2002; 2002US-00052586.  
XX (GETH ) GENENTECH INC.  
XX

PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;  
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;  
 XX WPI; 2003-342038/32.  
 DR N-PSDB; ACA66689.  
 XX  
 XX Three hundred and five nucleic acids encoding secreted and transmembrane  
 PT PRO polypeptides, useful for the diagnosis, prevention and/or treatment  
 PT of tumors, such as adrenal, lung, colon, breast, prostate, rectal,  
 PT cervical or liver tumors.  
 XX  
 XX Claim 11; Fig 312; 708pp; English.  
 PS  
 XX The invention relates to three hundred and five nucleic acids encoding  
 CC PRO polypeptides (secreted and transmembrane). Methods and compositions  
 CC of the present invention are useful for the diagnosis, prevention and/or  
 CC treatment of tumors, such as adrenal, lung, colon, breast, prostate,  
 CC rectal, cervical or liver tumours. The PRO polypeptides are also useful  
 CC as molecular weight markers, or for chromosome identification. The PRO  
 CC genes are useful as hybridisation probes, or for screening libraries of  
 CC human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene  
 CC therapy, particularly for replacing a defective gene. The present  
 CC sequence represents a human PRO polypeptide of the invention  
 XX  
 XX Sequence 802 AA;  
 SQ  
 Query Match 64.8%; Score 46; DB 6; Length 802;  
 Best Local Similarity 69.2%; Pred. No. 67;  
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 SHEGCRSGEAGGS 13  
 Db | ||||| |  
 44 SPEGCRSGQAAS 56  
 RESULT 29  
 ABR99507  
 ID ABR99507 standard; protein; 802 AA.  
 XX  
 AC ABR99507;  
 XX  
 DT 18-SEP-2003 (first entry)  
 XX  
 DE Human secreted polypeptide PRO1487, SEQ ID NO:312.  
 XX  
 KW Human; PRO; secreted protein; transmembrane protein;  
 KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;  
 KW chondrocyte; proliferation; differentiation; cartilage disorder;  
 KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;  
 KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;  
 KW liver; drug screening; transgenic animal; genetic analysis;  
 KW antiarthritic; vulnery; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 XX US2003040063-A1.  
 PN  
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 PD 27-FEB-2003.  
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 XX 26-JUN-2002; 2002US-00183006.  
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 PR 21-OCT-1997; 97US-0063486P.  
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ABR98897  
ID ABR98897 standard; protein; 802 AA.

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AC ABR98897;

DT 17-SEP-2003 (first entry)

DE Human secreted polypeptide PRO1487, SEQ ID NO:312.

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KW Human; PRO; secreted protein; transmembrane protein;  
extracellular domain; tumour necrosis factor-alpha; TNF-alpha;  
chondrocyte; proliferation; differentiation; cartilage disorder;  
bone disorder; arthritis; sports injury; cancer; diagnosis;  
adrenal tumour; lung; colon; breast; prostate; rectum; cervix;  
liver; drug screening; transgenic animal; genetic analysis;  
antiarthritic; vulnery; gene therapy.

OS Homo sapiens.

XX US2003040064-A1.

PD 27-FEB-2003.

PF 26-JUN-2002; 2002US-00183008.

XX 18-SEP-1997; 97US-0059263P.

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Db 44 SPEGCRSGQAAAS 56

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XX AC ABO16420;  
XX DT 25-AUG-2003 (first entry)  
XX DE Human secreted/transmembrane protein (PRO) #156.  
XX KW Human; secreted and transmembrane protein; PRO; TNF-alpha;  
KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;  
KW tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour;  
KW prostate tumour; rectal tumour; cervical tumour; liver tumour.  
XX OS Homo sapiens.  
XX PN US2003027267-A1.  
XX PD 06-FEB-2003.  
XX PF 19-JUN-2002; 2002US-00175739.  
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Best Local Similarity 69.2%; Pred. No. 67;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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DB 44 SPEGCRSGQAAAS 56

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AC ABR92320;
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XX
KW Human; PRO; secreted protein; transmembrane protein;
extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
chondrocyte; proliferation; differentiation; cartilage disorder;
bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
liver; drug screening; transgenic animal; genetic analysis;
antiarthritic; vulneryary; gene therapy.
XX
OS Homo sapiens.
XX
PN US2003036160-A1.
XX
PD 20-FEB-2003.
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PF 02-JUL-2002; 2002US-00188781.
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Query Match 64.8%; Score 46; DB 6; Length 802;  
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QY 1 SHEGCRSGEAGS 13  
 Db 44 SPEGCKSGQAAS 56

# RESULT 34

ABR78382  
 ID ABR78382 standard; protein; 802 AA.

XX ABR78382;

XX DT 19-SEP-2003 (first entry)

XX Human secreted polypeptide PRO1487, SEQ ID NO:312.

XX Human; PRO; secreted protein; transmembrane protein;  
 extracellular domain; tumour necrosis factor-alpha; TNF-alpha;  
 chondrocyte; proliferation; differentiation; cartilage disorder;  
 bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;  
 adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;  
 liver; drug screening; transgenic animal; genetic analysis;  
 antiarthritic; vulnery; gene therapy.

XX Homo sapiens.

XX US2003054474-A1.

XX 20-MAR-2003.

XX 22-JUL-2002; 2002US-00201530.

XX 22-JUN-1998; 98US-0090254P.

XX 02-JUN-1999; 99WO-US012252.

XX 25-AUG-1999; 99US-00380137.

XX 28-FEB-2001; 2001WO-US006520.

XX 15-JAN-2002; 2002US-00052586.

XX (GETH ) GENENTECH INC.

XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;  
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

XX WPI; 2003-503631/47.

XX N-PSDB; ACF00255.

XX New secreted and transmembrane PRO polypeptides and nucleic acids, useful  
 in gene therapy, or for preparing a medicament for treating a condition  
 that is responsive to the PRO polypeptide or anti-PRO antibody.

XX Claim 11; Fig 312; 700pp; English.

XX The invention relates to human PRO secreted/transmembrane polypeptides  
 (ABR78227-ABR78531) and nucleic acids encoding them (ACF00100-00404). The  
 invention also relates to sequences at least 80% identical to the PRO  
 nucleic acid and polypeptide sequences of the invention, recombinant  
 vectors and host cells comprising a PRO nucleic acid, a method for the  
 recombinant production of a PRO polypeptide, antibodies against a PRO  
 polypeptide, and fusion proteins comprising a PRO polypeptide. Nucleic  
 acids encoding PRO polypeptides of the invention were initially  
 identified via homology screening using consensus sequences based on the  
 extracellular domain sequences from known secreted proteins. Human cDNA  
 libraries containing sequences of interest were identified using  
 oligonucleotides based on the consensus sequences, and cDNA clones were  
 isolated and characterised. The PRO polypeptides are useful for  
 stimulating release of tumour necrosis factor-alpha (TNF-alpha) from  
 human blood and may thus be used in the treatment of conditions in which  
 enhanced TNF-alpha release would be beneficial. They are also useful for  
 stimulating the proliferation or differentiation of chondrocytes and as  
 such may be used in the treatment of various bone and/or cartilage  
 disorders such as arthritis and sports injuries. The PRO polypeptides may  
 be used in a method for detecting the presence of a tumour (e.g., an  
 adrenal tumour, lung tumour, colon tumour, breast tumour, prostate  
 tumour, rectal tumour, cervical tumour or liver tumour) in a mammal. This  
 method involves comparing the level of expression of the PRO polypeptide  
 in test and control samples, where a higher level of expression of PRO  
 polypeptide in the test sample as compared to the control sample is  
 indicative of the presence of a tumour. The PRO polypeptides are  
 additionally useful for in drug screening to identify agonists and





PR 21-APR-1998; 98US-0082568P.  
PR 21-APR-1998; 98US-0082569P.  
PR 22-APR-1998; 98US-0082704P.  
PR 22-APR-1998; 98US-0082797P.  
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XX	Human; secreted and transmembrane protein; PRO; TNF-alpha;	
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KW	prostate tumour; rectal tumour; cervical tumour; liver tumour.	
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Best Local Similarity 69.2%; Pred. No. 67; Mismatches 1; Indels 3; Gaps 0;

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DB 44 SPEGCRSGQAAAS 56

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XX AC ABO02234;  
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XX DE Human secreted/transmembrane protein (PRO) #156.  
XX KW Human; secreted and transmembrane protein; PRO; TNF-alpha;  
KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;  
KW tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour;  
KW prostate tumour; rectal tumour; cervical tumour; liver tumour.  
XX OS Homo sapiens.  
XX PN US2003040054-A1.  
XX PD 27-FEB-2003.  
XX PF 20-JUN-2002; 2002US-00176479.  
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Db 44 SPEGCRSGQAAS 56

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ID ABO06304 standard; protein; 802 AA.

XX ABO06304;

XX 13-AUG-2003 (first entry)

XX Novel human secreted and transmembrane protein PRO1487.

XX Human; secreted and transmembrane protein; PRO; gene therapy;  
KW chondrocyte stimulator; chromosome mapping; gene mapping;  
KW transgenic animal; knockout animal; tissue typing;  
KW chondrocyte proliferation; chondrocyte differentiation;  
KW tumour necrosis factor-alpha stimulation; TNF-alpha stimulation.

XX Homo sapiens.

XX US2003022294-A1.

XX PD 30-JAN-2003.  
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Query Match 64.8%; Score 46; DB 6; Length 802;
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Db 44 SPEGCRSGQAAS 56

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AC ABR59340;
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KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulneryary; gene therapy.
XX
OS Homo sapiens.
XX
XX US2003027275-A1.
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PD 06-FEB-2003.
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XX 20-JUN-2002; 2002US-00176918.
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Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 SHEGCRSGEAGCS 13
DB 44 SPEGCRSGQAAS 56
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ID ABO09402 standard; protein; 802 AA.
XX
AC ABO09402;
XX
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DT 17-AUG-2003 (first entry)
XX
DE Human secreted/transmembrane protein (PRO) #156.
XX
KW Human; secreted and transmembrane protein; PRO; TNF-alpha;
KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour.
XX
OS Homo sapiens.
XX
US2003027324-A1.
PN
XX
PD 06-FEB-2003.
XX
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PF 21-JUN-2002; 2002US-00176991.
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QY 1 SHEGCRSGEAGS 13  
 Db 44 SPEGCRSGQAAS 56

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XX ABO19266;

XX 27-AUG-2003 (first entry)

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XX Human; secreted and transmembrane protein; PRO; chromosome mapping;  
 KW gene mapping; transgenic animal; knockout animal; tissue typing;  
 KW chromosome identification; tumour; chondrocyte proliferation;  
 KW chondrocyte differentiation; tumour necrosis factor-alpha release;  
 KW gene therapy.

XX Homo sapiens.

XX US2003036118-A1.

XX 20-FEB-2003.

XX 21-JUN-2002; 2002US-00176760.

XX 26-JUN-1998; 98US-00105413.

XX 16-SEP-1998; 98WO-US019330.

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XX 06-NOV-1998; 98US-00187368.

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XX 07-DEC-1998; 98US-00202054.

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XX 08-MAR-1999; 98WO-US005028.

XX 14-MAY-1999; 98US-00311832.

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XX 25-AUG-1999; 98US-00380137.

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 PR 01-JUN-2001; 2001WO-US017800.  
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 PR 20-JUN-2001; 2001WO-US019692.  
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 PR 09-JUL-2001; 2001WO-US021735.  
 PR 18-JUL-2001; 2001US-00908827.  
 PR 30-JUL-2001; 2001US-00918585.  
 PR 06-AUG-2001; 2001US-00924419.  
 PR 13-AUG-2001; 2001US-00929404.  
 PR 16-AUG-2001; 2001US-00931836.  
 PR 28-AUG-2001; 2001US-00941992.  
 PR 29-AUG-2001; 2001WO-US027099.  
 PR 04-SEP-2001; 2001US-00946374.  
 PR 15-JAN-2002; 2002US-00052586.

(GETH ) GENENTECH INC.

Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;  
 Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-402071/38.  
 N-PSDB; ACD25513.

New secreted and transmembrane PRO polypeptides and nucleic acids, useful  
 in gene therapy, chromosome identification, tissue typing, for detecting  
 the presence of tumor in a mammal, or as hybridization probes in gene  
 mapping.

Claim 11; SEQ ID NO 312; 707pp; English.

The invention describes a novel isolated PRO polypeptide. The PRO  
 polypeptide or anti-PRO antibody is useful for preparing a medicament for  
 treating a condition that is responsive to the PRO polypeptide or anti-  
 PRO antibody. The PRO nucleotide sequences are useful as hybridization  
 probes in chromosome and gene mapping, or in generating antisense RNA and  
 DNA. PRO nucleic acids are also useful in preparing PRO polypeptides, in  
 assays to identify other proteins or molecules involved in binding  
 reaction, to generate transgenic animals or knockout animals, which in

CC turn are useful in the development and screening of therapeutically  
 CC useful reagents, for chromosome identification, and tissue typing. The  
 CC PRO polypeptides and nucleic acid molecules are also useful for detecting  
 CC the presence of tumour in a mammal, stimulating proliferation or  
 CC differentiation of chondrocyte cells, stimulating the release of tumour  
 CC necrosis factor-alpha from human blood, in gene therapy, or as molecular  
 CC weight markers for protein electrophoresis purposes. The anti-PRO  
 CC antibodies may be used in diagnostic assays for PRO, or for the affinity  
 CC purification of PRO from recombinant cell culture or natural sources.  
 CC This is the amino acid sequence of a novel human secreted and  
 CC transmembrane PRO polypeptide

XX Sequence 802 AA;

Query Match 64.8%; Score 46; DB 6; Length 802;  
 Best Local Similarity 69.2%; Pred. NO. 67;  
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SHEGCRSGRAEGS 13

Db 44 SPEGCRSGQAAS 56

RESULT 45

ABO11284

ID ABO11284 standard; protein; 802 AA.

XX AC

XX AC ABO11284;

XX 25-AUG-2003 (first entry)

XX DE Human secreted/transmembrane protein (PRO) #156.

XX KW Human; secreted and transmembrane protein; PRO; TNF-alpha;

XX KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;

XX KW tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour;

XX KW prostate tumour; rectal tumour; cervical tumour; liver tumour.

XX OS Homo sapiens.

XX PN US2003036123-A1.

XX PD 20-FEB-2003.

XX PF 25-JUN-2002; 2002US-00180551.

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XX PR 28-OCT-1997; 97US-0063541P.

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DB 44 SPEGCRSGQAAAS 56

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ABR66902  
ID ABR66902 standard; protein; 802 AA.

XX ABR66902;

XX 05-AUG-2003 (first entry)

DE Human secreted polypeptide PRO1487, SEQ ID NO:312.

Human; PRO; secreted protein; transmembrane protein;  
extracellular domain; tumour necrosis factor-alpha; TNF-alpha;  
chondrocyte; proliferation; differentiation; cartilage disorder;  
bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;  
adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;  
liver; drug screening; transgenic animal; genetic analysis;  
antiarthritic; vulnery; gene therapy.

OS Homo sapiens.

XX US2003036148-A1.

XX 20-FEB-2003.

XX 02-JUL-2002; 2002US-00187743.

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KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;  
KW tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour;  
KW prostate tumour; rectal tumour; cervical tumour; liver tumour.  
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XX  
XX US2003040060-A1.  
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XX 27-FEB-2003.  
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Best Local Similarity 69.2%; Pred. No. 67;

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DB 44 SPEGCRSGQAAS 56

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KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;  
KW tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour;  
KW prostate tumour; rectal tumour; cervical tumour; liver tumour.  
XX  
OS Homo sapiens.  
XX  
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XX  
PD 06-MAR-2003.  
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KW Human; PRO; secreted protein; transmembrane protein; cytostatic;  
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KW breast tumour; prostate tumour; rectal tumour; cervical tumour;  
KW liver tumour; TNF-alpha release; arthritis; tumour necrosis factor alpha;  
KW chondrocyte cell; bone disorder; cartilage disorder; sports injury.  
XX  
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XX  
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PR 01-OCT-1998; 98US-0102887P.
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PR 06-OCT-1998; 98US-0103258P.

Query Match 64.8%; Score 46; DB 6; Length 802;
Best Local Similarity 69.3%; Pred. NO. 67;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SHEGCRSGEAGS 13
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Db 44 SPEGCRSGGQAAS 56

RESULT 50
ABO07572
ID ABO07572 standard; protein; 802 AA.
AC ABO07572;
XX
XX
DT 18-AUG-2003 (first entry)
DE Human PRO polypeptide #156.
XX Human; PRO; secreted polypeptide; transmembrane polypeptide; cytostatic;
KW tumour necrosis factor-alpha; TNF-alpha; blood; tumour; chondrocyte cell;
KW
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KW cancer.
XX Homo sapiens.
OS
PN US2003032117-A1.
XX 13-FEB-2003.
PD
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PF 24-JUN-2002; 2002US-00179510.
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PR 18-SEP-1997; 97US-0059263P.
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PR 24-OCT-1997; 97US-0063121P.
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PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063544P.
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PR 29-OCT-1997; 97US-0063734P.
PR 31-OCT-1997; 97US-0063870P.
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PR 10-JUN-1998; 98US-0088824P.  
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PR 04-AUG-1998; 98US-0095282P.  
PR 10-AUG-1998; 98US-0095998P.  
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PR 26-AUG-1998; 98US-0098014P.

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PR 01-SEP-1998; 98US-0098723P.  
PR 02-SEP-1998; 98US-0098803P.  
PR 02-SEP-1998; 98US-0098821P.  
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PR 16-SEP-1998; 98US-0100662P.  
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PR 29-SEP-1998; 98US-0102331P.  
PR 30-SEP-1998; 98US-0102487P.  
PR 30-SEP-1998; 98US-0102570P.  
PR 30-SEP-1998; 98US-0102571P.  
PR 01-OCT-1998; 98US-0102684P.  
PR 01-OCT-1998; 98US-0102687P.  
PR 02-OCT-1998; 98US-0102965P.  
PR 06-OCT-1998; 98US-0103258P.  
PR 06-OCT-1998; 98US-0103449P.  
PR 07-OCT-1998; 98US-00168978.

Query Match 64.8%; Score 46; DB 6; Length 802;  
Best Local Similarity 69.2%; Pred. No. 67;  
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 SHEGCRSGEAEGS 13  
Db 44 SPEGCRSQMAAS 56

Search completed: April 19, 2004, 17:18:03  
Job time : 59.0806 secs



Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	46	64.8	802	10	US-09-346-374-260	Sequence 260, App	
2	46	64.8	802	12	US-10-206-915-312	Sequence 312, App	
3	46	64.8	802	12	US-10-199-670-312	Sequence 312, App	
4	46	64.8	802	12	US-10-201-858-312	Sequence 312, App	
5	46	64.8	802	12	US-10-205-890-312	Sequence 312, App	
6	46	64.8	802	12	US-10-208-020-312	Sequence 312, App	
7	46	64.8	802	12	US-10-201-853-312	Sequence 312, App	
8	46	64.8	802	12	US-10-174-581-312	Sequence 312, App	
9	46	64.8	802	12	US-10-176-483-312	Sequence 312, App	
10	46	64.8	802	12	US-10-176-749-312	Sequence 312, App	
11	46	64.8	802	12	US-10-176-914-312	Sequence 312, App	
12	46	64.8	802	12	US-10-176-915-312	Sequence 312, App	
13	46	64.8	802	12	US-10-006-485A-260	Sequence 260, App	
14	46	64.8	802	12	US-10-013-907A-260	Sequence 260, App	
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; PRIOR APPLICATION NUMBER: 60/103679  
; PRIOR FILING DATE: 1998-10-08  
; PRIOR APPLICATION NUMBER: 60/103711  
; PRIOR FILING DATE: 1998-10-08  
; PRIOR APPLICATION NUMBER: 60/104257  
; PRIOR FILING DATE: 1998-10-14  
; PRIOR APPLICATION NUMBER: 60/104987  
; PRIOR FILING DATE: 1998-10-20  
; PRIOR APPLICATION NUMBER: 60/105000  
; PRIOR FILING DATE: 1998-10-20  
; PRIOR APPLICATION NUMBER: 60/105002  
; PRIOR FILING DATE: 1998-10-20  
; PRIOR APPLICATION NUMBER: 60/105104  
; PRIOR FILING DATE: 1998-10-21  
; PRIOR APPLICATION NUMBER: 60/105169  
; PRIOR FILING DATE: 1998-10-22  
; PRIOR APPLICATION NUMBER: 60/105266  
; PRIOR FILING DATE: 1998-10-22  
; PRIOR APPLICATION NUMBER: 60/105693  
; PRIOR FILING DATE: 1998-10-26  
; PRIOR APPLICATION NUMBER: 60/105694  
; PRIOR FILING DATE: 1998-10-26  
; PRIOR APPLICATION NUMBER: 60/105807

Query Match 64.8%; Score 46; DB 10; Length 802;  
Best Local Similarity 69.2%; Pred. No. 53;  
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 SHEGCRSGEAGS 13  
| | | | | | | | | |  
Db 44 SPEGCRSGQAAS 56

## RESULT 2

US-10-206-915-312  
; Sequence 312, Application US/10206915  
; Publication No. US20040029221A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P34301C513

; CURRENT APPLICATION NUMBER: US/10/206,915  
; CURRENT FILING DATE: 2002-07-26

; PRIOR APPLICATION NUMBER: 10/052586  
; PRIOR FILING DATE: 2002-01-15  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059266  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063120  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063121  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063486  
; PRIOR FILING DATE: 1997-10-21  
; PRIOR APPLICATION NUMBER: 60/063540  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063541  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063544

; PRIOR FILING DATE: 1997-10-28  
; Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 312  
; LENGTH: 802  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-206-915-312

Query Match 64.8%; Score 46; DB 12; Length 802;  
Best Local Similarity 69.2%; Pred. No. 53;  
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 SHEGCRSGEAGS 13  
| | | | | | | | | |  
Db 44 SPEGCRSGQAAS 56

## RESULT 3

US-10-199-670-312  
; Sequence 312, Application US/10199670  
; Publication No. US20040033560A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P34301C401

; CURRENT APPLICATION NUMBER: US/10/199,670  
; CURRENT FILING DATE: 2002-07-19

; PRIOR APPLICATION NUMBER: 10/052586  
; PRIOR FILING DATE: 2002-01-15

; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059266  
; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/063120  
; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063121  
; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063486  
; PRIOR FILING DATE: 1997-10-21

; PRIOR APPLICATION NUMBER: 60/063540  
; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063541  
; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063544  
; PRIOR FILING DATE: 1997-10-28

; Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 312  
; LENGTH: 802  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-199-670-312

Query Match 64.8%; Score 46; DB 12; Length 802;  
Best Local Similarity 69.2%; Pred. No. 53;  
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 SHEGCRSGEAGS 13  
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Db 44 SPEGCRSGQAAAS 56

# RESULT 4

US-10-201-858-312  
; Sequence 312, Application US/10201858  
; Publication No. US20040038337A1

## GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430RIC464

; CURRENT APPLICATION NUMBER: US/10/201,858  
; CURRENT FILING DATE: 2002-07-23

; PRIOR APPLICATION NUMBER: 10/052586

; PRIOR FILING DATE: 2002-01-15

; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059266

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/063120

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063121

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063486

; PRIOR FILING DATE: 1997-10-21

; PRIOR APPLICATION NUMBER: 60/063540

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063541

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063544

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 312

; LENGTH: 802

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-201-858-312

Query Match 64.8%; Score 46; DB 12; Length 802;

Best Local Similarity 69.2%; Pred. No. 53;

Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 SHEGCRSGEAGS 13

| | | | | | | | | | | | | | |

Db 44 SPEGCRSGQAAAS 56

# RESULT 5

US-10-205-890-312

; Sequence 312, Application US/10205890

; Publication No. US20040048334A1

## GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430RIC519

; CURRENT APPLICATION NUMBER: US/10/205,890

; CURRENT FILING DATE: 2002-07-26

; PRIOR APPLICATION NUMBER: 10/052586

; PRIOR FILING DATE: 2002-01-15

; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059266

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/063120

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063121

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063486

; PRIOR FILING DATE: 1997-10-21

; PRIOR APPLICATION NUMBER: 60/063540

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063541

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063544

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 312

; LENGTH: 802

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-205-890-312

Query Match 64.8%; Score 46; DB 12; Length 802;

Best Local Similarity 69.2%; Pred. No. 53;

Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 SHEGCRSGEAGS 13

| | | | | | | | | | | | | | |

Db 44 SPEGCRSGQAAAS 56

# RESULT 6

US-10-208-024-312

; Sequence 312, Application US/10208024

; Publication No. US20040048335A1

## GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3430RIC538

; CURRENT APPLICATION NUMBER: US/10/208,024

; CURRENT FILING DATE: 2002-07-29

; PRIOR APPLICATION NUMBER: 10/052586

; PRIOR FILING DATE: 2002-01-15

; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059266

; PRIOR FILING DATE: 1997-09-18

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; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 312
; LENGTH: 802
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-208-024-312
```

```
Query Match 64.8%; Score 46; DB 12; Length 802;
Best Local Similarity 69.2%; Pred. No. 53;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 SHEGCRSGEAGEGS 13
| | | | | | | | | | | | | |
Db 44 SPEGCRSGQAAS 56
```

## RESULT 7

```
US-10-201-853-312
; Sequence 312, Application US/10201853
; Publication No. US20040053358A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C465
; CURRENT APPLICATION NUMBER: US/10/201,853
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
```

```
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 312
; LENGTH: 802
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-201-853-312
```

```
Query Match 64.8%; Score 46; DB 12; Length 802;
Best Local Similarity 69.2%; Pred. No. 53;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 SHEGCRSGEAGEGS 13
| | | | | | | | | | | | | |
Db 44 SPEGCRSGQAAS 56
```

## RESULT 8

```
US-10-174-581-312
; Sequence 312, Application US/10174581
; Publication No. US20030017540A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C41
; CURRENT APPLICATION NUMBER: US/10/174,581
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063564
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063734
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063870
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066120
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/066466
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066772
; PRIOR FILING DATE: 1997-11-24
```

[illegible]

```

; ORGANISM: Homo Sapien
US-10-176-749-312

; Query Match      64.8%      Score 46;   DB 12;   Length 802;
Best Local Similarity 59.2%      Pred. No. 53;
Matches 9;   Conservative 1;   Mismatches 3;   Indels 0;   Gaps 0;

Oy      1  SHEGCRSGEAGGS 13
      |||||
Db      44  SPEGCRSGOAAAS 56

```

Db 44 SPEGCRSGQAAS 56

RESULT 11  
US-10-176-914-312  
; Sequence 312, Application US/10176914  
; Publication No. US20030017543A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3430RIC83  
; CURRENT APPLICATION NUMBER: US/10/176,914  
; CURRENT FILING DATE: 2002-06-20  
; Prior Application removed - See file Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 312  
; LENGTH: 802  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-176-914-312

```

; TYPE: PKI
; ORGANISM: Homo Sapien
US-10-176-914-312

Query/Match      64.8%; Score 46; DB 12; Length 802;
Best Local Similarity 69.2%; Pred. No. 53;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      1 SHEGCRSGEAGS 13
      | | | | | | | |
Db      44 SPFGCFSGGAAAS 56

```

Db 44 SPEGCRSGQAAAS 56

RESULT 12

US-10-176--915-312

Sequence 312, Application US/10176915

Publication No. US20030017544A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Chen, Jian

APPLICANT: Desnoyers, Luc

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Pan, James

APPLICANT: Smith, Victoria

APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P3430R1C110

CURRENT APPLICATION NUMBER: US/10/176,915

CURRENT FILING DATE: 2002-06-21

Prior Application removed - See File Wrapper or Palm

NUMBER OF SEQ ID NOS: 612

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; SEQ ID NO 312
; LENGTH: 802
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-915-312

Query Match          64.8%; Score 46; DB 12; Length 802;
Best Local Similarity 69.2%; Pred. No. 53;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SHEGCRSGEAEQS 13
   |||||:|
Db 44 SPEGCRSGQAAS 56

RESULT 13
US-10-006-485A-260
; Sequence 260, Application US/10006485A
; Publication No. US20030064062A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Fan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C9
; CURRENT APPLICATION NUMBER: US/10/006,485A
; CURRENT FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099602
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099642
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099741
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099754
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099763
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099792
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099808
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099815
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100388
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100584
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100661
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100662
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100664
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100683
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100684
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100710
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100711
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100849
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101014
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101068
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/101471
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101472
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101474
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101475
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101476
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101479
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101743
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101915
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/102207
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102240
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; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 477  
; SEQ ID NO 260  
; LENGTH: 802  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-015-499A-260

Query Match 64.8%; Score 46; DB 12; Length 802;  
Best Local Similarity 69.2%; Pred. No. 53;  
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SHEGCRSGEAGS 13  
| | | | | | | | | |  
Db 44 SPEGCRSGQAAS 56

RESULT 16  
US-10-176-484-312  
; Sequence 312, Application US/10176484  
; Publication No. US20030059876A9  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430R1C64  
; CURRENT APPLICATION NUMBER: US/10/176,484  
; CURRENT FILING DATE: 2002-06-20  
; Prior application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 312  
; LENGTH: 802  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-176-484-312

Query Match 64.8%; Score 46; DB 12; Length 802;  
Best Local Similarity 69.2%; Pred. No. 53;  
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SHEGCRSGEAGS 13  
| | | | | | | | | |  
Db 44 SPEGCRSGQAAS 56

RESULT 17  
US-10-180-550-312  
; Sequence 312, Application US/10180550  
; Publication No. US2003006440A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430R1C64  
; CURRENT APPLICATION NUMBER: US/10/176,484  
; CURRENT FILING DATE: 2002-06-20  
; Prior application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 312  
; LENGTH: 802  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-176-484-312

; FILE REFERENCE: P3430R1C149  
; CURRENT APPLICATION NUMBER: US/10/180,550  
; CURRENT FILING DATE: 2002-06-25  
; Prior application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 312  
; LENGTH: 802  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-180-550-312

Query Match 64.8%; Score 46; DB 12; Length 802;  
Best Local Similarity 69.2%; Pred. No. 53;  
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SHEGCRSGEAGS 13  
| | | | | | | | | |  
Db 44 SPEGCRSGQAAS 56

RESULT 18  
US-10-183-014-312  
; Sequence 312, Application US/10183014  
; Publication No. US2003006441A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430R1C170  
; CURRENT APPLICATION NUMBER: US/10/183,014  
; CURRENT FILING DATE: 2002-06-26  
; Prior application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 312  
; LENGTH: 802  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-183-014-312

Query Match 64.8%; Score 46; DB 12; Length 802;  
Best Local Similarity 69.2%; Pred. No. 53;  
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SHEGCRSGEAGS 13  
| | | | | | | | | |  
Db 44 SPEGCRSGQAAS 56

RESULT 19  
US-10-187-738-312  
; Sequence 312, Application US/10187738  
; Publication No. US2003006442A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.

```
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430RIC241
; CURRENT APPLICATION NUMBER: US/10/187,738
; CURRENT FILING DATE: 2002-07-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 312
; LENGTH: 802
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-187-738-312

Query Match 64.8%; Score 46; DB 12; Length 802;
Best Local Similarity 69.2%; Pred. No. 53;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SHEGCRSGEAGS 13
DB 44 SPEGCRSGQAAS 56

RESULT 20
US-10-187-740-312
; Sequence 312, Application US/10187740
; Publication No. US2003006443A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430RIC251
; CURRENT APPLICATION NUMBER: US/10/187,740
; CURRENT FILING DATE: 2002-07-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 312
; LENGTH: 802
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-187-740-312

Query Match 64.8%; Score 46; DB 12; Length 802;
Best Local Similarity 69.2%; Pred. No. 53;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SHEGCRSGEAGS 13
DB 44 SPEGCRSGQAAS 56

RESULT 21
US-10-187-883-312
; Sequence 312, Application US/10187883
; Publication No. US2003006444A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
```

```
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430RIC248
; CURRENT APPLICATION NUMBER: US/10/187,883
; CURRENT FILING DATE: 2002-07-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 312
; LENGTH: 802
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-187-883-312

Query Match 64.8%; Score 46; DB 12; Length 802;
Best Local Similarity 69.2%; Pred. No. 53;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SHEGCRSGEAGS 13
DB 44 SPEGCRSGQAAS 56

RESULT 22
US-10-194-363-312
; Sequence 312, Application US/10194363
; Publication No. US20030064445A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430RIC310
; CURRENT APPLICATION NUMBER: US/10/194,363
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 312
; LENGTH: 802
; TYPE: PRT
; ORGANISM: Homo Sapien
```



PRIOR APPLICATION NUMBER: 60/086392  
PRIOR FILING DATE: 1998-05-22  
PRIOR APPLICATION NUMBER: 60/086486  
PRIOR FILING DATE: 1998-05-22  
PRIOR APPLICATION NUMBER: 60/087098  
PRIOR FILING DATE: 1998-05-28  
PRIOR APPLICATION NUMBER: 60/087208  
PRIOR FILING DATE: 1998-05-28  
PRIOR APPLICATION NUMBER: 60/087609  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087759  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087827  
PRIOR FILING DATE: 1998-06-03  
PRIOR APPLICATION NUMBER: 60/088025  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088028  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088029  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088033  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088167  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088202  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088212  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088217  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088326  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088655  
PRIOR FILING DATE: 1998-06-09  
PRIOR APPLICATION NUMBER: 60/088722  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088738  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088740  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088811  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088824  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088825  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088826  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088861  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/088863  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/088876  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/089090  
PRIOR FILING DATE: 1998-06-12  
PRIOR APPLICATION NUMBER: 60/089105  
PRIOR FILING DATE: 1998-06-12  
PRIOR APPLICATION NUMBER: 60/089512  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089514  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089538  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089598  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089653

Query Match 64.8%; Score 46; DB 12; Length 802;  
Best Local Similarity 69.2%; Pred. No. 53;  
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SHEGCRSGAEGS 13

Db 44 SPEGCRSGQAAS 56  
RESULT 24  
US-10-194-463-312  
Sequence 312, Application US/10194463  
Publication No. US20030064447A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Chen, Jian  
APPLICANT: Desnoyers, Luc  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Pan, James  
APPLICANT: Smith, Victoria  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3430R1C300  
CURRENT APPLICATION NUMBER: US/10/194,463  
CURRENT FILING DATE: 2002-07-11  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 612  
SEQ ID NO 312  
LENGTH: 802  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-194-463-312

Query Match 64.8%; Score 46; DB 12; Length 802;  
Best Local Similarity 69.2%; Pred. No. 53;  
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SHEGCRSGAEGS 13  
Db 44 SPEGCRSGQAAS 56

RESULT 25  
US-10-194-484-312  
Sequence 312, Application US/10194484  
Publication No. US20030064448A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Chen, Jian  
APPLICANT: Desnoyers, Luc  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Pan, James  
APPLICANT: Smith, Victoria  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3430R1C313  
CURRENT APPLICATION NUMBER: US/10/194,484  
CURRENT FILING DATE: 2002-07-12  
PRIOR APPLICATION NUMBER: 10/052586  
PRIOR FILING DATE: 2002-01-15  
PRIOR APPLICATION NUMBER: 60/059263  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/059266  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063120  
PRIOR FILING DATE: 1997-10-24

;; PRIOR APPLICATION NUMBER: 60/063121  
;; PRIOR FILING DATE: 1997-10-24  
;; PRIOR APPLICATION NUMBER: 60/063486  
;; PRIOR FILING DATE: 1997-10-21  
;; PRIOR APPLICATION NUMBER: 60/063540  
;; PRIOR FILING DATE: 1997-10-28  
;; PRIOR APPLICATION NUMBER: 60/063541  
;; PRIOR FILING DATE: 1997-10-28  
;; PRIOR APPLICATION NUMBER: 60/063544  
;; PRIOR FILING DATE: 1997-10-28  
;; PRIOR Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 612  
;; SEQ ID NO 312  
;; LENGTH: 802  
;; TYPE: PRT  
;; ORGANISM: Homo Sapien  
US-10-194-484-312

Query Match 64.8%; Score 46; DB 12; Length 802;  
Best Local Similarity 69.2%; Pred. No. 53;  
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SHEGCRSGEARGS 13  
| | | | | | | | | | | | | | | | | |  
Db 44 SPEGCRSGQAAS 56

## RESULT 26

US-10-195-884-312  
;; Sequence 312, Application US/10195884  
;; Publication No. US20030064449A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Baker, Kevin P.  
;; APPLICANT: Chen, Jian  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Pan, James  
;; APPLICANT: Smith, Victoria  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
;; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
;; CURRENT APPLICATION NUMBER: US/10/195,884  
;; CURRENT FILING DATE: 2002-07-15  
;; PRIOR APPLICATION NUMBER: 10/052586  
;; PRIOR FILING DATE: 2002-01-15  
;; PRIOR APPLICATION NUMBER: 60/059263  
;; PRIOR FILING DATE: 1997-09-18  
;; PRIOR APPLICATION NUMBER: 60/059266  
;; PRIOR FILING DATE: 1997-09-18  
;; PRIOR APPLICATION NUMBER: 60/062250  
;; PRIOR FILING DATE: 1997-10-17  
;; PRIOR APPLICATION NUMBER: 60/063120  
;; PRIOR FILING DATE: 1997-10-24  
;; PRIOR APPLICATION NUMBER: 60/063121  
;; PRIOR FILING DATE: 1997-10-24  
;; PRIOR APPLICATION NUMBER: 60/063486  
;; PRIOR FILING DATE: 1997-10-21  
;; PRIOR APPLICATION NUMBER: 60/063540  
;; PRIOR FILING DATE: 1997-10-28  
;; PRIOR APPLICATION NUMBER: 60/063541  
;; PRIOR FILING DATE: 1997-10-28  
;; PRIOR APPLICATION NUMBER: 60/063544  
;; PRIOR FILING DATE: 1997-10-28  
;; PRIOR Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 612  
;; SEQ ID NO 312  
;; LENGTH: 802  
;; TYPE: PRT

;; ORGANISM: Homo Sapien  
US-10-195-884-312

Query Match 64.8%; Score 46; DB 12; Length 802;  
Best Local Similarity 69.2%; Pred. No. 53;  
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SHEGCRSGEARGS 13  
| | | | | | | | | | | | | | | | | |  
Db 44 SPEGCRSGQAAS 56

## RESULT 27

US-10-195-896-312  
;; Sequence 312, Application US/10195896  
;; Publication No. US20030063112A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Baker, Kevin P.  
;; APPLICANT: Chen, Jian  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Pan, James  
;; APPLICANT: Smith, Victoria  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
;; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
;; FILE REFERENCE: P3430R1C327  
;; CURRENT APPLICATION NUMBER: US/10/195,896  
;; CURRENT FILING DATE: 2002-07-15  
;; PRIOR Application removed - See File Wrapper or PALM  
;; NUMBER OF SEQ ID NOS: 612  
;; SEQ ID NO 312  
;; LENGTH: 802  
;; TYPE: PRT  
;; ORGANISM: Homo Sapien  
US-10-195-896-312

Query Match 64.8%; Score 46; DB 12; Length 802;  
Best Local Similarity 69.2%; Pred. No. 53;  
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SHEGCRSGEARGS 13  
| | | | | | | | | | | | | | | | | |  
Db 44 SPEGCRSGQAAS 56

## RESULT 28

US-10-196-744-312  
;; Sequence 312, Application US/10196744  
;; Publication No. US20030064450A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Baker, Kevin P.  
;; APPLICANT: Chen, Jian  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Pan, James  
;; APPLICANT: Smith, Victoria  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
;; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
;; FILE REFERENCE: P3430R1C353  
;; CURRENT APPLICATION NUMBER: US/10/196,744  
;; CURRENT FILING DATE: 2002-07-16  
;; PRIOR APPLICATION NUMBER: 10/052586  
;; PRIOR FILING DATE: 2002-01-15

```

; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 312
; LENGTH: 802
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-196-744-312

```

```

Query Match      64.8%; Score 46; DB 12; Length 802;
Best Local Similarity 69.2%; Pred. No. 53;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 1 SHEGCRSGEAGS 13
| | | | | | | | | |
DB 44 SPEGCRSQAAAS 56

```

## RESULT 29

```

US-10-196-755-312
; Sequence 312, Application US/10196755
; Publication No. US20030064451A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C350
; CURRENT APPLICATION NUMBER: US/10/196,755
; CURRENT FILING DATE: 2002-07-16
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 312
; LENGTH: 802
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-196-755-312

```

```

Query Match      64.8%; Score 46; DB 12; Length 802;
Best Local Similarity 69.2%; Pred. No. 53;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 1 SHEGCRSGEAGS 13
| | | | | | | | | |
DB 44 SPEGCRSQAAAS 56

```

```

RESULT 30
US-10-196-757-312
; Sequence 312, Application US/10196757
; Publication No. US20030065159A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C345
; CURRENT APPLICATION NUMBER: US/10/196,757
; CURRENT FILING DATE: 2002-07-16
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 312
; LENGTH: 802
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-196-757-312

```

```

Query Match      64.8%; Score 46; DB 12; Length 802;
Best Local Similarity 69.2%; Pred. No. 53;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 1 SHEGCRSGEAGS 13
| | | | | | | | | |
DB 44 SPEGCRSQAAAS 56

```

## RESULT 31

```

US-10-197-704-312
; Sequence 312, Application US/10197704
; Publication No. US20030064452A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C364
; CURRENT APPLICATION NUMBER: US/10/197,704
; CURRENT FILING DATE: 2002-07-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 312
; LENGTH: 802
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-197-704-312

```

```

Query Match      64.8%; Score 46; DB 12; Length 802;
Best Local Similarity 69.2%; Pred. No. 53;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 1 SHEGCRSGEAGS 13
| | | | | | | | | |

```

Db 44 SPEGCRSGQAAS 56

## RESULT 32

US-10-197-710-312

; Sequence 312, Application US/10197710

; Publication No. US20030064453A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3430R1C375

; CURRENT FILING DATE: 2002-07-17

; PRIOR APPLICATION NUMBER: US/10/197,710

; PRIOR FILING DATE: 2002-07-17

; PRIOR APPLICATION NUMBER: 60/052586

; PRIOR FILING DATE: 2002-01-15

; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059266

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/063120

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063121

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063486

; PRIOR FILING DATE: 1997-10-21

; PRIOR APPLICATION NUMBER: 60/063540

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063541

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063544

; PRIOR FILING DATE: 1997-10-28

; Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 312

; LENGTH: 802

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-197-710-312

Query Match 64.8%; Score 46; DB 12; Length 802;

Best Local Similarity 69.2%; Pred. No. 53;

Matches 9; Conservative 1; Mismatches 0; Gaps 0;

QY 1 SHEGCRSGQAAS 13

| | | | | | | | | | | | | | |

Db 44 SPEGCRSGQAAS 56

## RESULT 33

US-10-198-758-312

; Sequence 312, Application US/10198758

; Publication No. US2003006445A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3430R1C383

; CURRENT APPLICATION NUMBER: US/10/198,758

; CURRENT FILING DATE: 2002-07-18

; PRIOR APPLICATION NUMBER: 10/052586

; PRIOR FILING DATE: 2002-01-15

; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059266

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/063120

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063121

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063486

; PRIOR FILING DATE: 1997-10-21

; PRIOR APPLICATION NUMBER: 60/063540

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063541

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063544

; PRIOR FILING DATE: 1997-10-28

; Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 312

; LENGTH: 802

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-198-758-312

Query Match 64.8%; Score 46; DB 12; Length 802;

Best Local Similarity 69.2%; Pred. No. 53;

Matches 9; Conservative 1; Mismatches 0; Gaps 0;

QY 1 SHEGCRSGQAAS 13

| | | | | | | | | | | | | | |

Db 44 SPEGCRSGQAAS 56

## RESULT 34

US-10-198-766-312

; Sequence 312, Application US/10198766

; Publication No. US20030064455A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3430R1C379

; CURRENT APPLICATION NUMBER: US/10/198,766

; CURRENT FILING DATE: 2002-07-18

; PRIOR APPLICATION NUMBER: 10/052586

; PRIOR FILING DATE: 2002-01-15

; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059266

; PRIOR FILING DATE: 1997-09-18



; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063120  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063121  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063486  
; PRIOR FILING DATE: 1997-10-21  
; PRIOR APPLICATION NUMBER: 60/063540  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063541  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063544  
; PRIOR FILING DATE: 1997-10-28  
; Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 312  
; LENGTH: 802  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-198-766-312

Query Match 64.8%; Score 46; DB 12; Length 802;  
Best Local Similarity 69.2%; Pred. No. 53;  
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SHEGCRSGEAGS 13  
| | | | | | | | | | | | | | | | |  
Db 44 SPEGCRSGQAAS 56

## RESULT 35

US-10-199-304-312  
; Sequence 312, Application US/10199304  
; Publication No. US20030064456A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430R1C402  
; CURRENT APPLICATION NUMBER: US/10/199,304  
; CURRENT FILING DATE: 2002-07-19  
; PRIOR APPLICATION NUMBER: 10/052586  
; PRIOR FILING DATE: 2002-01-15  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059266  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063120  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063486  
; PRIOR FILING DATE: 1997-10-21  
; PRIOR APPLICATION NUMBER: 60/063540  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063541  
; PRIOR FILING DATE: 1997-10-28  
; Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 312  
; LENGTH: 802  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-198-766-312

## RESULT 36

US-10-199-309-312  
; Sequence 312, Application US/10199309  
; Publication No. US20030064457A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430R1C394  
; CURRENT APPLICATION NUMBER: US/10/199,309  
; CURRENT FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 10/052586  
; PRIOR FILING DATE: 2002-01-15  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059266  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063120  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063121  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063486  
; PRIOR FILING DATE: 1997-10-21  
; PRIOR APPLICATION NUMBER: 60/063540  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063541  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063544  
; PRIOR FILING DATE: 1997-10-28  
; Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 312  
; LENGTH: 802  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-199-309-312

Query Match 64.8%; Score 46; DB 12; Length 802;  
Best Local Similarity 69.2%; Pred. No. 53;  
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SHEGCRSGEAGS 13  
| | | | | | | | | | | | | | | | |  
Db 44 SPEGCRSGQAAS 56

```
RESULT 37
US-10-199-313-312
; Sequence 312, Application US/10199313
; Publication No. US20030064458A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C396
; CURRENT APPLICATION NUMBER: US/10/199,313
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 312
; LENGTH: 802
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-199-313-312
```

```
Query Match 64.8%; Score 46; DB 12; Length 802;
Best Local Similarity 69.2%; Pred. No. 53;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 SHEGCRSGEAGS 13
Db 44 SPEGCRSGQAAS 56
```

```
RESULT 38
US-10-199-456-312
; Sequence 312, Application US/10199456
; Publication No. US20030064459A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
```

```
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C400
; CURRENT APPLICATION NUMBER: US/10/199,456
; CURRENT FILING DATE: 2002-07-18
; Prior Application removed - See File Wrapper or PALM
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 312
; LENGTH: 802
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-199-456-312
```

```
Query Match 64.8%; Score 46; DB 12; Length 802;
Best Local Similarity 69.2%; Pred. No. 53;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 SHEGCRSGEAGS 13
Db 44 SPEGCRSGQAAS 56
```

```
RESULT 39
US-10-201-329-312
; Sequence 312, Application US/10201329
; Publication No. US20030064460A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C438
; CURRENT APPLICATION NUMBER: US/10/201,329
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 312
; LENGTH: 802
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-201-329-312
```

Query Match 64.8%; Score 46; DB 12; Length 802;  
Best Local Similarity 69.2%; Pred. No. 53;  
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SHEGCRSGEAGS 13  
| | | | | | | | | |  
DB 44 SPEGCRSGQAAS 56

## RESULT 40

US-10-202-412-312  
; Sequence 312, Application US/10202412  
; Publication No. US20030064461A1  
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430R1C456

; CURRENT APPLICATION NUMBER: US/10/202,412  
; CURRENT FILING DATE: 2002-07-23

; PRIOR FILING DATE: 2002-01-15  
; PRIOR APPLICATION NUMBER: 60/052586  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059266  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063120  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063121  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063486  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063540  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063541  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063544  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063544  
; Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 312  
; LENGTH: 802  
; TYPE: PRT  
; ORGANISM: Homo Sapien

## US-10-202-412-312

Query Match 64.8%; Score 46; DB 12; Length 802;  
Best Local Similarity 69.2%; Pred. No. 53;  
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SHEGCRSGEAGS 13  
| | | | | | | | | |  
DB 44 SPEGCRSGQAAS 56

## RESULT 41

US-10-206-919-312  
; Sequence 312, Application US/10206919  
; Publication No. US20030064462A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430R1C518

; CURRENT APPLICATION NUMBER: US/10/206,919  
; CURRENT FILING DATE: 2002-07-26

; PRIOR FILING DATE: 2002-01-15  
; PRIOR APPLICATION NUMBER: 60/052586  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059266  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063120  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063121  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063486  
; PRIOR FILING DATE: 1997-10-21  
; PRIOR APPLICATION NUMBER: 60/063540  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063541  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063544  
; PRIOR FILING DATE: 1997-10-28  
; Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 312  
; LENGTH: 802  
; TYPE: PRT  
; ORGANISM: Homo Sapien

## US-10-206-919-312

Query Match 64.8%; Score 46; DB 12; Length 802;  
Best Local Similarity 69.2%; Pred. No. 53;  
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SHEGCRSGEAGS 13  
| | | | | | | | | |  
DB 44 SPEGCRSGQAAS 56

## RESULT 42

US-10-206-922-312  
; Sequence 312, Application US/10206922  
; Publication No. US20030064463A1  
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430R1C525

; CURRENT APPLICATION NUMBER: US/10/206,922  
; CURRENT FILING DATE: 2002-07-26

; PRIOR APPLICATION NUMBER: 10/052586  
; PRIOR FILING DATE: 2002-01-15  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059266  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063120  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063121  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063486  
; PRIOR FILING DATE: 1997-10-21  
; PRIOR APPLICATION NUMBER: 60/063540  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063541  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063544  
; PRIOR FILING DATE: 1997-10-28  
; Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 312  
; LENGTH: 802  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-206-924-312

Query Match 64.8%; Score 46; DB 12; Length 802;  
Best Local Similarity 69.2%; Pred. No. 53;  
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SHEGCRSGEAGS 13  
| | | | | | | | | | | | | | | | | |  
DB 44 SPEGCRSGQAAS 56

RESULT 43  
US-10-206-924-312  
; Sequence 312, Application US/10206924  
; Publication No. US20030064464A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430R1C512  
; CURRENT APPLICATION NUMBER: US/10/206,924  
; CURRENT FILING DATE: 2002-07-26  
; PRIOR APPLICATION NUMBER: 10/052586  
; PRIOR FILING DATE: 2002-01-15  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059266  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063120  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063121  
; PRIOR FILING DATE: 1997-10-24  
; Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 312  
; LENGTH: 802  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-206-924-312

; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063541  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063544  
; PRIOR FILING DATE: 1997-10-28  
; Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 312  
; LENGTH: 802  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-206-924-312

Query Match 64.8%; Score 46; DB 12; Length 802;  
Best Local Similarity 69.2%; Pred. No. 53;  
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SHEGCRSGEAGS 13  
| | | | | | | | | | | | | | | | | |  
DB 44 SPEGCRSGQAAS 56

RESULT 44  
US-10-206-928-312  
; Sequence 312, Application US/10206928  
; Publication No. US20030064465A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430R1C490  
; CURRENT APPLICATION NUMBER: US/10/206,928  
; CURRENT FILING DATE: 2002-07-25  
; PRIOR APPLICATION NUMBER: 10/052586  
; PRIOR FILING DATE: 2002-01-15  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059266  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063120  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063121  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063486  
; PRIOR FILING DATE: 1997-10-21  
; PRIOR APPLICATION NUMBER: 60/063540  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063541  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063544  
; PRIOR FILING DATE: 1997-10-28  
; Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 312  
; LENGTH: 802  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-206-928-312

Query Match 64.8%; Score 46; DB 12; Length 802;  
Best Local Similarity 69.2%; Pred. No. 53;

Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SHEGCRSGAEGS 13  
| | | | | | | | | |  
Db 44 SPEGCRSGQAAS 56

## RESULT 45

US-10-207-914-312  
; Sequence 312, Application US/10207914

; Publication No. US20030064466A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C548

; CURRENT APPLICATION NUMBER: US/10/207,914

; CURRENT FILING DATE: 2002-07-29

; PRIOR APPLICATION NUMBER: 10/052586

; PRIOR FILING DATE: 2002-01-15

; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059266

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/063120

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063121

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063486

; PRIOR FILING DATE: 1997-10-21

; PRIOR APPLICATION NUMBER: 60/063540

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063541

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063544

; PRIOR FILING DATE: 1997-10-28

; Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 312

; LENGTH: 802

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-207-914-312

Query Match 64.8%; Score 46; DB 12; Length 802;

Best Local Similarity 69.2%; Pred. No. 53;

Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SHEGCRSGAEGS 13  
| | | | | | | | | |  
Db 44 SPEGCRSGQAAS 56

## RESULT 46

US-10-207-921-312

; Sequence 312, Application US/10207921

; Publication No. US20030064467A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C546

; CURRENT APPLICATION NUMBER: US/10/207,921

; CURRENT FILING DATE: 2002-07-29

; PRIOR APPLICATION NUMBER: 10/052586

; PRIOR FILING DATE: 2002-01-15

; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059266

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/063120

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063121

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063486

; PRIOR FILING DATE: 1997-10-21

; PRIOR APPLICATION NUMBER: 60/063540

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063541

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063544

; PRIOR FILING DATE: 1997-10-28

; Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 312

; LENGTH: 802

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-207-921-312

Query Match 64.8%; Score 46; DB 12; Length 802;

Best Local Similarity 69.2%; Pred. No. 53;

Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SHEGCRSGAEGS 13  
| | | | | | | | | |  
Db 44 SPEGCRSGQAAS 56

## RESULT 47

US-10-207-922-312

; Sequence 312, Application US/10207922

; Publication No. US20030064468A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C542

; CURRENT APPLICATION NUMBER: US/10/207,922

; CURRENT FILING DATE: 2002-07-29

; PRIOR APPLICATION NUMBER: 10/052586

; PRIOR FILING DATE: 2002-01-15

; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059266  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063120  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063121  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063486  
; PRIOR FILING DATE: 1997-10-21  
; PRIOR APPLICATION NUMBER: 60/063540  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063541  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063544  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 312  
; LENGTH: 802  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-207-922-312

Query Match 64.8%; Score 46; DB 12; Length 802;  
Best Local Similarity 69.2%; Pred. No. 53;  
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SHEGCRSGEAGS 13  
| | | | | | | | | |  
DB 44 SPEGCRSGQAAS 56

## RESULT 48

US-10-208-027-312  
; Sequence 312, Application US/10208027  
; Publication No. US20030064469A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430R1C544  
; CURRENT APPLICATION NUMBER: US/10/208,027  
; CURRENT FILING DATE: 2002-07-29  
; PRIOR APPLICATION NUMBER: 10/052586  
; PRIOR FILING DATE: 2002-01-15  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059266  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063120  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063121  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063486  
; PRIOR FILING DATE: 1997-10-21  
; PRIOR APPLICATION NUMBER: 60/063540  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063541

; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063544  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 312  
; LENGTH: 802  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-208-027-312

Query Match 64.8%; Score 46; DB 12; Length 802;  
Best Local Similarity 69.2%; Pred. No. 53;  
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SHEGCRSGEAGS 13  
| | | | | | | | | |  
DB 44 SPEGCRSGQAAS 56

## RESULT 49

US-10-013-910A-260  
; Sequence 260, Application US/10013910A  
; Publication No. US20030187192A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan I.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2830F1C33  
; CURRENT APPLICATION NUMBER: US/10/013,910A  
; CURRENT FILING DATE: 2001-12-10  
; PRIOR APPLICATION NUMBER: 60/098716  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098723  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098749  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098750  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098803  
; PRIOR FILING DATE: 1998-09-02  
; PRIOR APPLICATION NUMBER: 60/098821  
; PRIOR FILING DATE: 1998-09-02  
; PRIOR APPLICATION NUMBER: 60/098843  
; PRIOR FILING DATE: 1998-09-02  
; PRIOR APPLICATION NUMBER: 60/099536  
; PRIOR FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: 60/099596  
; PRIOR FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: 60/099598  
; PRIOR FILING DATE: 1998-09-09  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 477  
; SEQ ID NO 260  
; LENGTH: 802  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-013-910A-260

Query Match 64.8%; Score 46; DB 12; Length 802;

Best Local Similarity 69.2%; Pred. No. 53;  
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SHEGCRSGEAGS 13  
| | | | | | | | | |  
Db 44 SPEGCRSGQAAAS 56

## RESULT 50

US-10-174-570-312  
; Sequence 312, Application US/10174570  
; Publication No. US20030211572A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430RIC26  
; CURRENT APPLICATION NUMBER: US/10/174,570  
; CURRENT FILING DATE: 2002-06-18  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 312  
; LENGTH: 802  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-174-570-312

Query Match 64.8%; Score 46; DB 12; Length 802;  
Best Local Similarity 69.2%; Pred. No. 53;  
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SHEGCRSGEAGS 13  
| | | | | | | | | |  
Db 44 SPEGCRSGQAAAS 56

Search completed: April 19, 2004, 17:46:52  
Job time : 44.4032 secs

**This Page Blank (usp10)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 19, 2004, 17:12:35 ; Search time 13 Seconds  
(without alignments)  
96.192 Million cell updates/sec

Title: US-10-726-692-22

Perfect score: 71

Sequence: 1 SHEGCRSGEAEAGS 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 50 summaries

Database : PIR 78:\*

1: piri:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	59.2	261	S51678	chitinase (EC 3.2.1.14)
2	41	57.7	1053	S34172	sucrose-phosphate
3	40	56.3	111	H97316	hypothetical prote
4	39	54.9	226	S37105	phosphoribosylglyc
5	39	54.9	264	A84868	probable endochiti
6	39	54.9	292	D86438	phosphoribosylglyc
7	39	54.9	716	H85089	hypothetical prote
8	39	54.9	1213	T51032	hypothetical prote
9	39	54.9	1607	T02837	long chain fatty a
10	38	53.5	72	S39416	metallothionein 10
11	38	53.5	72	S39418	metallothionein 10
12	38	53.5	72	S39419	metallothionein 10
13	38	53.5	72	S39417	metallothionein 10
14	38	53.5	448	S41725	integrinase - Saccha
15	38	53.5	501	S45914	probable glucan 1,
16	38	53.5	577	T00416	hypothetical prote
17	38	53.5	1015	C84918	probable ATP-depen
18	37.5	52.8	646	H96665	protein F2C12.10
19	37	52.1	220	D82139	conserved hypothet
20	37	52.1	227	H82344	rfbt protein VC025
21	37	52.1	286	S16969	O-antigen - Vibrio
22	37	52.1	286	A42699	serotype specific
23	37	52.1	286	H90066	hypothetical prote
24	37	52.1	350	F86804	basic membrane pro
25	37	52.1	415	H83067	probable c-type cy
26	37	52.1	627	S37954	RNA polymerase I t
27	37	52.1	844	T00529	hypothetical prote
28	37	52.1	1621	T30200	protein-tyrosine k
29	36	50.7	186	S65723	extracellular hemo

30	36	50.7	207	2	D65095	hypothetical prote
31	36	50.7	207	2	A98123	hypothetical prote
32	36	50.7	207	2	H85967	hypothetical prote
33	36	50.7	237	2	B82986	hypothetical prote
34	36	50.7	263	2	AC1685	dihydrodipicolinat
35	36	50.7	276	2	AB2037	hypothetical prote
36	36	50.7	308	2	AE3415	integrinase (importe
37	36	50.7	409	2	E91246	probable L-sorbose
38	36	50.7	413	2	B86094	probable L-sorbose
39	36	50.7	471	2	C82825	UDP-N-acetylmurama
40	36	50.7	541	2	T23689	hypothetical prote
41	36	50.7	594	2	T04545	protein cs/ch-42
42	36	50.7	598	2	T05329	hypothetical prote
43	36	50.7	626	2	A41284	translation initia
44	36	50.7	708	2	T48022	hypothetical prote
45	36	50.7	1197	2	T13956	timeless protein h
46	36	50.7	1429	2	T19422	hypothetical prote
47	35.5	50.0	136	2	S59313	hypothetical prote
48	35.5	50.0	284	2	S18957	fix23-5 protein -
49	35	49.3	89	1	TKMYT	tuberculin-activ
50	35	49.3	101	2	D83375	hypothetical prote

ALIGNMENTS

RESULT 1

S51678

chitinase (EC 3.2.1.14) class I - European elder (fragment)

N/Alternate names: pathogenesis-related protein PR-3 type

C/Species: Sambucus nigra (European elder)

C/Date: 07-May-1995 #sequence\_revision 01-Sep-1995 #text\_change 22-Jun-1999

C/Accession: S51678

R/Coupe, S.A.; Taylor, J.E.; Roberts, J.A.

submitted to the EMBL Data Library, December 1994

A/Description: Characterisation of mRNAs that encode pathogenesis-related proteins that

A/Reference number: S51645

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-261 <COU>

A/Cross-references: EMBL:Z46948; NID:G603881; PID:CAA87072.1; PID:G603882

C/Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; p1

C/Keywords: glycosidase; hydrolase; polysaccharide degradation

F16-51/Domain: hevein chitin-binding domain homology <HCB>

F161-261/Domain: plant chitinase homology <PCH>

Query Match 59.2%; Score 42; DB 2; Length 261;  
Best Local Similarity 72.7%; Pred. No. 12;  
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 EGCRSGEAEAGS 13

DB 41 EGCRSGPCVGS 51

RESULT 2

S34172

sucrose-phosphate synthase (EC 2.4.1.14) - potato

C/Species: Solanum tuberosum (potato)

C/Date: 22-Nov-1993 #sequence\_revision 03-Aug-1995 #text\_change 18-Jun-1999

C/Accession: S34172

R/Sonnenwald, U.; Basner, A.

submitted to the EMBL Data Library, June 1993

A/Reference number: S34172

A/Accession: S34172

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1053 <SON>

A/Cross-references: EMBL:X73477; NID:G313264; PID:CAA51872.1; PID:G313265

C/Function:

A/Description: catalyzes the formation of sucrose-6-phosphate from UDPglucose and D-fru

A/Pathway: sucrose biosynthesis

C:Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homology  
C:Keywords: glycosyltransferase; hexosyltransferase; sucrose biosynthesis  
P:168-651/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>

Query Match 57.7%; Score 41; DB 2; Length 1053;  
Best Local Similarity 66.7%; Pred. No. 58;  
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 HEGCRSGEAEGS 13  
||| |||  
DB 439 HEGDMDETEGS 450

RESULT 3  
H97316  
hypothetical protein CAC3393 [imported] - Clostridium acetobutylicum  
C:Species: Clostridium acetobutylicum  
C:Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 14-Sep-2001  
C:Accession: H97316  
R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,  
.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001  
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo  
A:Reference number: A96900; MUID:21359325; PMID:21359325  
A:Accession: H97316  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-111 <KUR>  
A:Cross-references: GB:AE001437; PIDN:AAK81323.1; PID:g15026479; GSPDB:GN00168  
A:Experimental source: Clostridium acetobutylicum ATCC824  
C:Genetics:  
A:Gene: CAC3393

Query Match 56.3%; Score 40; DB 2; Length 111;  
Best Local Similarity 60.0%; Pred. No. 13;  
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SHEGCRSGEA 10  
||:|::||  
DB 55 SHKGCKAAEA 64

RESULT 4  
S37105  
phosphoribosylglycinamide formyltransferase (EC 2.1.2.2) - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 06-Jan-1994 #sequence\_revision 28-Oct-1994 #text\_change 11-Jun-1999  
C:Accession: S37105  
R:Schnorr, K.M.  
submitted to the EMBL Data Library, August 1993  
A:Reference number: S37104  
A:Accession: S37105  
A:Molecule type: mRNA  
A:Residues: 1-226 <SCH>  
A:Cross-references: EMBL:X74767; NID:g398611; PIDN:CAA52779.1; PID:g398612  
C:Genetics:  
A:Gene: PUR3  
C:Superfamily: phosphoribosylglycinamide formyltransferase; phosphoribosylglycinamide fo  
F:34-226/Domain: phosphoribosylglycinamide formyltransferase homology <PRGF>

Query Match 54.9%; Score 39; DB 1; Length 226;  
Best Local Similarity 54.5%; Pred. No. 35;  
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 HEGCRSGEAE 12  
||| |  
DB 49 HEGCSDGSVNG 59

RESULT 5  
A84868  
probable endochitinase [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 16-Feb-2001  
C:Accession: A84868  
R:Jin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083487; PMID:10617197  
A:Accession: A84868  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-264 <STO>  
A:Cross-references: GB:AE002093; NID:g2281111; PIDN:AAB64047.1; GSPDB:GN00139  
C:Genetics:  
A:Gene: At2g43590  
A:Map position: 2  
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl

Query Match 54.9%; Score 39; DB 2; Length 264;  
Best Local Similarity 70.0%; Pred. No. 39;  
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GCRSGEAEGS 13  
||| ||  
DB 51 GCRSGPCRGS 60

RESULT 6  
D86438  
phosphoribosylglycinamide formyltransferase - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 02-Nov-2001  
C:Accession: D86438  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Accession: D86438  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-292 <STO>  
A:Cross-references: GB:AE005172; NID:g4512619; PIDN:AAD21688.1; GSPDB:GN00141  
C:Genetics:  
A:Map position: 1  
C:Superfamily: phosphoribosylglycinamide formyltransferase; phosphoribosylglycinamide fo

Query Match 54.9%; Score 39; DB 2; Length 292;  
Best Local Similarity 54.5%; Pred. No. 43;  
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 HEGCRSGEAE 12  
||| |  
DB 95 HEGCSDGSVNG 105

RESULT 7  
H85089  
hypothetical protein AT4g08920 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 16-Feb-2001  
C:Accession: H85089  
R:Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprir  
Nature 402, 769-777, 1999  
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.  
A:Reference number: A85001; MUID:20083488; PMID:10617198

A:Accession: H85089  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-716 <STO>  
 A:Cross-references: GB:NC\_001268; NID:g7267534; PIDN:CAB78016.1; GSPDB:GN00140  
 C:Genetics:  
 A:Gene: AT4g08920  
 A:Map position: 4

Query Match 54.9%; Score 39; DB 2; Length 716;  
 Best Local Similarity 75.0%; Pred. No. 91;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 HEGCRSGE 9  
 DB 696 HRCGSGE 703  
 ||| |||

RESULT 8  
 T51032  
 Hypothetical protein B15120.20 [imported] - Neurospora crassa  
 C:Species: Neurospora crassa  
 C:Date: 21-Jul-2000 #sequence\_revision 21-Jul-2000 #text\_change 21-Jul-2000  
 C:Accession: T51032  
 R:Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, July 2000  
 A:Reference number: Z25286  
 A:Accession: T51032  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-1213 <SCH>  
 A:Cross-references: EMBL:AL389900; GSPDB:GN00116; NCSP:B15120.20  
 A:Experimental source: BAC clone B15120; strain OR74A  
 C:Genetics:  
 A:Gene: NCSP:B15120.20  
 A:Map position: 6  
 A:Map position: 72/3; 958/3; 1055/3

Query Match 54.9%; Score 39; DB 2; Length 1213;  
 Best Local Similarity 54.5%; Pred. No. 1.4e+02;  
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 ECRSGEARGS 13  
 DB 164 DACRSGEKDGA 174  
 : ||||| :|

RESULT 9  
 T02837  
 long chain fatty acyl CoA synthetase LCFACAS5 [imported] - Leishmania major (strain Frie  
 C:Species: Leishmania major  
 C:Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 19-May-2000  
 C:Accession: A81461; T02837  
 R:Myler, P.J.; Audleman, L.; deVos, T.; Hixson, G.; Kiser, P.; Lemley, C.; Magness, C.; Proc. Natl. Acad. Sci. U.S.A. 96, 2902-2906, 1999  
 A:Title: Leishmania major Friedlin chromosome 1 has an unusual distribution of protein-c  
 A:Reference number: A81455; MUID:99178987; PMID:10077609  
 A:Accession: A81461  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-1507 <PVL>  
 A:Cross-references: GB:AE001274; NID:g3264850; PIDN:AAC24660.1; PID:g1617560; GSPDB:GN00  
 A:Experimental source: strain MHOM/IL/81/Friedlin  
 C:Genetics:  
 A:Gene: LCFACAS5  
 A:Map position: 1

Query Match 54.9%; Score 39; DB 2; Length 1607;  
 Best Local Similarity 70.0%; Pred. No. 1.8e+02;  
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 SHEGCRSGEA 10  
 || | |||||

Db 714 SHSACASGEA 723

RESULT 10  
 S39416  
 metallothionein 10-I - blue mussel  
 C:Species: Mytilus edulis (blue mussel)  
 C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 17-Mar-1999  
 R:MacKay, E.A.; Overnell, J.; Dunbar, B.; Davidson, I.; Hunziker, P.E.; Kaegi, J.H.R.; Eur. J. Biochem. 218, 183-194, 1993  
 A:Title: Complete amino acid sequences of five dimeric and four monomeric forms of metal  
 A:Reference number: S39416; MUID:94062828; PMID:8243463  
 A:Accession: S39416  
 A:Molecule type: protein  
 A:Residues: 1-72 <MAC>  
 C:Superfamily: metallothionein  
 C:Keywords: metal binding

Query Match 53.5%; Score 38; DB 2; Length 72;  
 Best Local Similarity 70.0%; Pred. No. 20;  
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SHEGCRSGEA 10  
 DB 19 SGEGRCCGDA 28  
 ||||| :|

RESULT 11  
 S39418  
 metallothionein 10-III - blue mussel  
 C:Species: Mytilus edulis (blue mussel)  
 C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 17-Mar-1999  
 C:Accession: S39418  
 R:MacKay, E.A.; Overnell, J.; Dunbar, B.; Davidson, I.; Hunziker, P.E.; Kaegi, J.H.R.; Eur. J. Biochem. 218, 183-194, 1993  
 A:Title: Complete amino acid sequences of five dimeric and four monomeric forms of metal  
 A:Reference number: S39416; MUID:94062828; PMID:8243463  
 A:Accession: S39418  
 A:Molecule type: protein  
 A:Residues: 1-72 <MAC>  
 C:Superfamily: metallothionein  
 C:Keywords: metal binding

Query Match 53.5%; Score 38; DB 2; Length 72;  
 Best Local Similarity 70.0%; Pred. No. 20;  
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SHEGCRSGEA 10  
 DB 19 SGEGRCCGDA 28  
 ||||| :|

RESULT 12  
 S39419  
 metallothionein 10-IV - blue mussel  
 C:Species: Mytilus edulis (blue mussel)  
 C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 17-Mar-1999  
 C:Accession: S39419  
 R:MacKay, E.A.; Overnell, J.; Dunbar, B.; Davidson, I.; Hunziker, P.E.; Kaegi, J.H.R.; Eur. J. Biochem. 218, 183-194, 1993  
 A:Title: Complete amino acid sequences of five dimeric and four monomeric forms of metal  
 A:Reference number: S39416; MUID:94062828; PMID:8243463  
 A:Accession: S39419  
 A:Molecule type: protein  
 A:Residues: 1-72 <MAC>  
 C:Superfamily: metallothionein  
 C:Keywords: metal binding

Query Match 53.5%; Score 38; DB 2; Length 72;  
 Best Local Similarity 70.0%; Pred. No. 20;  
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SHEGCRSGEA 10  
 Db 19 SGEGRGCGDA 28

RESULT 13  
 S39417  
 metallothionein 10-II - blue mussel  
 C:Species: Mytilus edulis (blue mussel)  
 C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 17-Mar-1999  
 C:Accession: S39417  
 R:MacKay, E.A.; Overnell, J.; Dunbar, B.; Davidson, I.; Hunziker, P.E.; Kaegi, J.H.R.; R  
 Eur. J. Biochem. 218, 183-194, 1993  
 A>Title: Complete amino acid sequences of five dimeric and four monomeric forms of metal  
 A:Reference number: S39416; MUID:194062828; PMID:8243463  
 A:Accession: S39417  
 A:Molecule type: protein  
 A:Residues: 1-72 <MAC>  
 C:Superfamily: metallothionein  
 C:Keywords: metal binding

Query Match 53.5%; Score 38; DB 2; Length 72;  
 Best Local Similarity 70.0%; Pred. NO. 20;  
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SHEGCRSGEA 10  
 Db 19 SGEGRGCGDA 28

RESULT 14  
 S41725  
 integrase - Saccharopolyspora erythraea  
 C:Species: Saccharopolyspora erythraea  
 C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 22-Oct-1999  
 C:Accession: S41725  
 R:Brown, D.P.; Idler, K.B.; Backer, D.M.; Donadio, S.; Katz, L.  
 Mol. Gen. Genet. 242, 185-193, 1994  
 A>Title: Characterization of the genes and attachment sites for site-specific integratio  
 A:Reference number: S41722; MUID:94211208; PMID:8159169  
 A:Accession: S41725  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-448 <BRO>  
 A:Cross-references: EMBL:L11597; NID:9404798; PIDN:AAA26480.1; PID:9404802

Query Match 53.5%; Score 38; DB 2; Length 448;  
 Best Local Similarity 77.8%; Pred. NO. 90;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCRSGEAG 12  
 Db 215 GCRQGEALG 223

RESULT 15  
 S45914  
 probable glucan 1,3-beta-glucosidase (EC 3.2.1.58) YBR056w - yeast (Saccharomyces cerevisi  
 N:Alternate names: hypothetical protein YBR0510  
 C:Species: Saccharomyces cerevisiae  
 C>Date: 26-Aug-1994 #sequence\_revision 09-Sep-1994 #text\_change 19-Apr-2002  
 C:Accession: S45914; S49511; S55855  
 R:Aljinovic, G.; Pohl, F.M.; Pohl, T.M.  
 submitted to the Protein Sequence Database, August 1994  
 A:Reference number: S45906  
 A:Accession: S45914  
 A:Molecule type: DNA  
 A:Residues: 1-501 <ALJ>  
 A:Cross-references: EMBL:X35925; NID:9536292; PID:9536293; MIPS:YBR056w  
 A:Experimental source: strain S288C  
 R:Aljinovic, G.  
 submitted to the EMBL Data Library, October 1994  
 A:Description: Sequence and analysis of 24 kb on chromosome II of Saccharomyces cerevisi

A:Reference number: S49503  
 A:Accession: S49511  
 A:Molecule type: DNA  
 A:Residues: 1-501 <AL2>  
 A:Cross-references: EMBL:Z46260; NID:9559942; PID:9559952  
 A:Experimental source: strain S288C  
 R:Aljinovic, G.; Pohl, T.M.  
 Yeast 11, 475-479, 1995  
 A>Title: Sequence and analysis of 24 kb on chromosome II of Saccharomyces cerevisiae.  
 A:Reference number: S55846; MUID:95321020; PMID:7597852  
 A:Accession: S55855  
 A:Molecule type: DNA  
 A>Status: nucleic acid sequence not shown; translation not shown  
 A:Residues: 1-501 <ALW>  
 A:Cross-references: EMBL:Z46260; NID:9559942; PIDN:CAA86399.1; PID:9559952  
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1994  
 C:Genetics:  
 A:Cross-references: SGD:S0000260  
 A:Map position: 2R  
 C:Keywords: glycosidase; hydrolase

Query Match 53.5%; Score 38; DB 2; Length 501;  
 Best Local Similarity 70.0%; Pred. NO. 99;  
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SHEGCRSGEA 10  
 Db 188 SHSGRSGEA 197

RESULT 16  
 T00416  
 hypothetical protein T30B22.1 - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C>Date: 01-Feb-1999 #sequence\_revision 01-Feb-1999 #text\_change 24-Nov-1999  
 C:Accession: T00416  
 R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Maso  
 submitted to the EMBL Data Library, October 1998  
 A:Description: Arabidopsis thaliana chromosome II BAC T30B22 genomic sequence.  
 A:Reference number: Z14149  
 A:Accession: T00416  
 A>Status: translated from GB/EMBL/DBDJ  
 A:Molecule type: DNA  
 A:Residues: 1-577 <ROU>  
 A:Cross-references: EMBL:AC002535; NID:92529657; PID:92529658  
 A:Experimental source: cultivar Columbia  
 C:Genetics:  
 A:Map position: 2  
 A:Introns: 87/3; 126/3; 175/1; 264/3; 329/3; 507/3  
 C:Superfamily: Arabidopsis thaliana hypothetical protein T30B22.1

Query Match 53.5%; Score 38; DB 2; Length 577;  
 Best Local Similarity 60.0%; Pred. NO. 1.1e+02;  
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SHEGCRSGEA 10  
 Db 327 SSQGRNGES 336

RESULT 17  
 C84918  
 probable ATP-dependent RNA helicase A [imported] - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C>Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
 C:Accession: C84918  
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.  
 eus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, L.  
 Nature 402, 761-768, 1999  
 A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
 A:Reference number: A84420; MUID:20083487; PMID:10617197  
 A:Accession: C84918

A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-1015 <STO>  
 A:Cross-references: GB:AE002093; NID:g3738282; PIDN:AA63624.1; GSPDB:GN00139  
 C:Genetics:  
 A:Gene: AF2947680  
 A:Map position: 2

Query Match 53.5%; Score 38; DB 2; Length 1015;  
 Best Local Similarity 60.0%; Pred. No. 1.8e+02;  
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SHEGCRSGBA 10  
 DB 765 SSGCGRNGES 774

RESULT 18  
 H96665  
 protein F22C12.10 [imported] - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C>Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
 C:Accession: H96665  
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
 ansen, N.F.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
 Nature 408, 816-820, 2000  
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
 C.A.; Li, J.H.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luross, J.S.; Maiti, R.; Marziali,  
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
 A:Reference number: A86141; MUID:21016719; PMID:11130712  
 A:Accession: H96665  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-646 <STO>  
 A:Cross-references: GB:AE005173; NID:g6692098; PIDN:AAF24563.1; GSPDB:GN00141  
 C:Genetics:  
 A:Gene: F22C12.10  
 A:Map position: 1

Query Match 52.8%; Score 37.5; DB 2; Length 646;  
 Best Local Similarity 61.5%; Pred. No. 1.5e+02;  
 Matches 8; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 SHEGCRSGBAEGS 13  
 DB 410 THSGCTKG-AEGS 421

RESULT 19  
 D82139  
 conserved hypothetical protein VC1940 [imported] - Vibrio cholerae (strain N16961 serogr  
 C:Species: Vibrio cholerae  
 C>Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Feb-2001  
 C:Accession: D82139  
 R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;  
 chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, H  
 l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
 Nature 406, 477-483, 2000  
 A>Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
 A:Reference number: A82035; MUID:20406833; PMID:10952301  
 A:Accession: D82139  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-220 <HEI>  
 A:Cross-references: GB:AE004269; GB:AE003852; NID:g9556466; PIDN:AAF95088.1; GSPDB:GN001  
 A:Experimental source: serogroup O1; strain N16961; biotype El Tor  
 C:Genetics:  
 A:Gene: VC1940  
 A:Map position: 1

Query Match 52.1%; Score 37; DB 2; Length 220;  
 Best Local Similarity 58.3%; Pred. No. 73;  
 Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 SHEGCRSGBAEG 12  
 DB 139 SONGCYSGNIEG 150

RESULT 20  
 H82344  
 rfbT protein VC0258 [imported] - Vibrio cholerae (strain N16961 serogroup O1)  
 C:Species: Vibrio cholerae  
 C>Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Feb-2001  
 C:Accession: H82344  
 R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;  
 chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I.;  
 l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
 Nature 406, 477-483, 2000  
 A>Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
 A:Reference number: A82035; MUID:20406833; PMID:10952301  
 A:Accession: H82344  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-227 <HEI>  
 A:Cross-references: GB:AE004114; GB:AE003852; NID:g9654662; PIDN:AAF93433.1; GSPDB:GN001  
 A:Experimental source: serogroup O1; strain N16961; biotype El Tor  
 C:Genetics:  
 A:Gene: VC0258  
 A:Map position: 1

Query Match 52.1%; Score 37; DB 2; Length 227;  
 Best Local Similarity 63.6%; Pred. No. 75;  
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 HEGCRSGBAEG 12  
 DB 75 HFGCAIGENEG 85

RESULT 21  
 S16969  
 O-antigen - Vibrio cholerae  
 C:Species: Vibrio cholerae  
 C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 08-Oct-1999  
 C:Accession: S16969  
 R:Rito, T.; Ohshita, Y.; Hiramatsu, K.; Yokota, T.  
 FEBS Lett. 286, 159-162, 1991  
 A>Title: Identification and nucleotide sequence determination of the gene responsible for  
 A:Reference number: S16969; MUID:91323507; PMID:1713857  
 A:Accession: S16969  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-286 <ITO>  
 A:Cross-references: EMBL:X58834; NID:g48423; PIDN:CAA41643.1; PID:g48424

Query Match 52.1%; Score 37; DB 2; Length 286;  
 Best Local Similarity 63.6%; Pred. No. 91;  
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 HEGCRSGBAEG 12  
 DB 134 HFGCAIGENEG 144

RESULT 22  
 A42699  
 serotype specificity determinant rfbT - Vibrio cholerae  
 C:Species: Vibrio cholerae  
 C>Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 08-Oct-1999  
 A:Experimental source: serogroup O1; strain N16961; biotype El Tor  
 C:Accession: A42699; S28484  
 R:Stroehner, U.H.; Karageorgos, L.E.; Morona, R.; Manning, P.A.

Proc. Natl. Acad. Sci. U.S.A. 89, 2566-2570, 1992  
 A:Title: Serotype conversion in *Vibrio cholerae* O1.  
 A:Reference number: A42699; MUID:92212870; PMID:1372980  
 A:Contents: 01, Ogawa O17  
 A:Accession: A42699  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-286 <STR>  
 A:Cross-references: EMBL:X59554; NID:g48381; PIDN:CRA42150.1; PID:g48399  
 A>Note: sequence extracted from NCBI backbone (NCBIN:191922, NCBIP:191924)  
 C:Genetics:  
 A:Gene: rfbT

Query Match 52.1%; Score 37; DB 2; Length 286;  
 Best Local Similarity 63.6%; Pred. No. 91;  
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 HEGCRSGEARG 12  
 ||||| :|||  
 Db 134 HFGCAIGENEG 144

RESULT 23  
 H90066  
 hypothetical protein SA2393 [imported] - *Staphylococcus aureus* (strain N315)  
 C:Species: *Staphylococcus aureus*  
 C>Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 22-Oct-2001  
 C:Accession: H90066  
 R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogud  
 ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, R.; Inoue, R.; Kaito, C.; Sekimizu, K.;  
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.  
 Lancet 357, 1225-1240, 2001  
 A:Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.  
 A:Reference number: A89758; MUID:21311952; PMID:11418146  
 A:Accession: H90066  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-286 <KUR>  
 A:Cross-references: GB:BA000018; PID:g13702557; PIDN:BAB43698.1; GSPDB:GN00149  
 A:Experimental source: strain N315  
 C:Genetics:  
 A:Gene: SA2393

Query Match 52.1%; Score 37; DB 2; Length 286;  
 Best Local Similarity 60.0%; Pred. No. 91;  
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGRSGEARG 12  
 :||| :|||  
 Db 204 DGRVQAEG 213

RESULT 24  
 F86804  
 basic membrane protein A [imported] - *Lactococcus lactis* subsp. *lactis* (strain IL1403)  
 C:Species: *Lactococcus lactis* subsp. *lactis*  
 C>Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 03-Aug-2001  
 C:Accession: F86804  
 R:Boilotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarre, K.; Weissensbach, J.; Ehrli  
 Genome Res. 11, 731-753, 2001  
 A:Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* se  
 A:Reference number: A86625; MUID:21235186; PMID:11337471  
 A:Accession: F86804  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-350 <STO>  
 A:Cross-references: GB:AE005176; PID:g12724428; PIDN:AAK05536.1; GSPDB:GN00146  
 A:Experimental source: strain IL1403  
 C:Genetics:  
 A:Gene: bmpA

Query Match 52.1%; Score 37; DB 2; Length 350;  
 Best Local Similarity 70.0%; Pred. No. 1.1e+02;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 4 GCRSGEARGS 13  
 ||||| :|||  
 Db 21 GCRSHDAAGS 30

RESULT 25  
 H83067  
 probable c-type cytochrome PA4619 [imported] - *Pseudomonas aeruginosa* (strain PAO1)  
 C:Species: *Pseudomonas aeruginosa*  
 C>Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 21-Jul-2003  
 C:Accession: H83067  
 R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br  
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,  
 .; Lory, S.; Olson, M.V.  
 Nature 406, 959-964, 2000  
 A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PAO1, an opportunistic patho  
 A:Reference number: A82950; MUID:20437337; PMID:10984043  
 A:Accession: H83067  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-415 <STO>  
 A:Cross-references: GB:AE004876; GB:AE004091; NID:g9950869; PIDN:AAG08007.1; GSPDB:GN001  
 A:Experimental source: strain PAO1  
 C:Genetics:  
 A:Gene: PA4619  
 C:Superfamily: membrane-bound alcohol dehydrogenase, cytochrome c; cytochrome c6 homolog  
 C:Keywords: chromoprotein; heme; iron; metalloprotein  
 F:42.45/Binding site: heme (Cys) (covalent) #status predicted  
 F:46/Binding site: heme iron (His) (axial ligand) #status predicted  
 F:188.191/Binding site: heme (Cys) (covalent) #status predicted  
 F:192/Binding site: heme iron (His) (axial ligand) #status predicted  
 F:310.313/Binding site: heme (Cys) (covalent) #status predicted  
 F:314/Binding site: heme iron (His) (axial ligand) #status predicted

Query Match 52.1%; Score 37; DB 2; Length 415;  
 Best Local Similarity 66.7%; Pred. No. 1.2e+02;  
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GCRSGEARG 12  
 ||||| :|||  
 Db 312 GCHGGEAG 320

RESULT 26  
 S37954  
 RNA polymerase I transcription factor RRN3 - yeast (*Saccharomyces cerevisiae*)  
 N:Alternate names: protein YKL125w  
 C:Species: *Saccharomyces cerevisiae*  
 C>Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 13-Mar-1998  
 R:Ramezani Rad, M.; Xu, G.; Kirchrath, L.; Fritz, C.; Keuchel, H.; Hollenberg, C.P.  
 submitted to the Protein Sequence Database, March 1994  
 A:Reference number: S37953  
 A:Accession: S37954  
 A:Molecule type: DNA  
 A:Residues: 1-627 <RAM>  
 A:Cross-references: EMBL:Z28125; NID:g486210; PID:g486211; MIPS:YKL125w  
 A:Experimental source: strain S288C  
 R:Yanamoto, R.T.; Nogi, Y.; Dodd, J.A.; Nomura, M.  
 EMBO J. 15, 3964-3973, 1996  
 A:Title: RRN3 gene of *Saccharomyces cerevisiae* encodes an essential RNA polymerase I tra  
 A:Reference number: S71600; MUID:96324404; PMID:8670901  
 A:Accession: S71600  
 A:Molecule type: DNA  
 A:Residues: 1-627 <YAM>  
 C:Genetics:  
 A:Gene: SGD:RRN3  
 A:Cross-references: SGD:S0001608; MIPS:YKL125w  
 A:Map position: 11L  
 C:Keywords: nucleus

Query Match 52.1%; Score 37; DB 2; Length 627;  
Best Local Similarity 61.5%; Pred. No. 1.8e+02;  
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 SHEGCRSGEAGS 13  
|:| | | | | | | | | |  
DB 286 SNEELRSGADGS 298

## RESULT 27

T00529  
hypothetical protein At2g19090 [imported] - Arabidopsis thaliana  
N:Alternate names: hypothetical protein T20K24.10  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 01-Feb-1999 #sequence\_revision 01-Feb-1999 #text\_change 16-Feb-2001  
C:Accession: T00529; D84572  
R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, July 1997  
A:Description: Arabidopsis thaliana chromosome II BAC T20K24 genomic sequence.  
A:Reference number: Z14167  
A:Accession: T00529  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-844 <ROU>  
A:Cross-References: EMBL:AC002392; NID:g3176701; PID:g3176711  
A:Experimental source: cultivar Columbia  
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; eus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083487; PMID:10617197  
A:Accession: D84572  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-844 <STO>  
A:Cross-References: GB:AE002093; NID:g3176711; PIDN:AAI2027.1; GSPDB:GN00139

C:Genetics:  
A:Gene: At2g19090; T20K24.10  
A:Map position: 2  
A:Introns: 439/1; 519/3; 594/2  
C:Superfamily: Arabidopsis thaliana hypothetical protein F6G3.160

Query Match 52.1%; Score 37; DB 2; Length 844;  
Best Local Similarity 63.6%; Pred. No. 2.3e+02;  
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 ECGRSGEAGS 13  
|:| | | | | | | | | |  
DB 341 EVCGRGEATGN 351

## RESULT 28

T30200  
protein-tyrosine kinase (EC 2.7.1.112) alk - mouse  
N:Alternate names: anaplastic lymphoma kinase  
C:Species: Mus musculus (house mouse)  
C:Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 21-Jul-2000  
C:Accession: T30200  
R:Wahara, T.; Fujimoto, J.; Wen, D.; Cupples, R.; Bucay, N.; Arakawa, T.; Mori, S.; Rat Oncogene 14, 439-449, 1997  
A:Title: Molecular characterization of ALK, a receptor tyrosine kinase expressed specifically  
A:Reference number: Z20774; MUID:97178863; PMID:9053841  
A:Accession: T30200  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1621 <IWA>  
A:Cross-References: EMBL:D83002; NID:g1864006; PIDN:BAAL1673.1; PID:g1864007  
A:Experimental source: brain and testis  
C:Genetics:  
A:Gene: alk  
A:Function:  
A:Description: may play an important role in development of the brain

C:Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase

Query Match 52.1%; Score 37; DB 2; Length 1621;  
Best Local Similarity 54.5%; Pred. No. 3.9e+02;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 HEGCRSGEAG 12  
|:| | | | | | | | | |  
DB 462 HQDCAQGEDEG 472

## RESULT 29

S65723  
extracellular hemoglobin linker chain L3 - earthworm (Lumbricus terrestris) (fragments)  
C:Species: Lumbricus terrestris (common earthworm)  
C:Date: 06-Dec-1996 #sequence\_revision 13-Mar-1997 #text\_change 02-Sep-2000  
C:Accession: S65723; B46586  
R:Pushitani, K.; Higashiyama, K.; Asao, M.; Hosokawa, K. Biochim. Biophys. Acta 1292, 273-280, 1996  
A:Title: Characterization of the constituent polypeptides of the extracellular hemoglobin  
A:Reference number: S65721; MUID:96176855; PMID:8597573  
A:Accession: S65723  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-77; 78-102; 103-129; 130-186 <FUS>  
R:Owby, D.W.; Zhu, H.; Schneider, K.; Beavis, R.C.; Chait, B.T.; Riggs, A.F. J. Biol. Chem. 268, 13539-13547, 1993  
A:Title: The extracellular hemoglobin of the earthworm, Lumbricus terrestris. Determina-  
A:Reference number: A46586; MUID:93293879; PMID:8514787  
A:Accession: B46586  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-15 <OWN>  
A:Note: sequence extracted from NCBI backbone (NCBIP:134510)  
C:Superfamily: hemoglobin linker chain: LDL receptor ligand-binding repeat homology  
F:60-96/Domain: LDL receptor ligand-binding repeat homology (fragments) <LDL>

Query Match 50.7%; Score 36; DB 2; Length 186;  
Best Local Similarity 60.0%; Pred. No. 94;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 HEGCRSGEAG 11  
|:| | | | | | | | | |  
DB 84 HNDRCNGEDE 93

## RESULT 30

D65095  
hypothetical protein b3071 - Escherichia coli (strain K-12)  
C:Species: Escherichia coli  
C:Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 01-Mar-2002  
C:Accession: D65095  
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997  
A:Title: The complete genome sequence of Escherichia coli K-12.  
A:Reference number: A64720; MUID:97426617; PMID:9278503  
A:Accession: D65095  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-207 <BLAT>  
A:Cross-References: GB:AE000389; GB:U00096; NID:g1789451; PIDN:AAC76106.1; PID:g1789452  
A:Experimental source: strain K-12, substrain MG1655

Query Match 50.7%; Score 36; DB 2; Length 207;  
Best Local Similarity 75.0%; Pred. No. 1e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 HEGCRSGE 9  
|:| | | | | | | | | |  
DB 17 HEGCCKGE 24



```

RESULT 31
A98123
Hypothetical protein EC83953 [imported] - Escherichia coli (strain O157:H7, substrain R1
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C:Accession: A98123
R:Hayashi, T.; Makino, K.; Onishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
gaawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: A98123
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-207 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA837376.1; PID:g13363426; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain R1MD 0509952
C:Genetics:
A:Gene: EC83953

Query Match 50.7%; Score 36; DB 2; Length 207;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 HEGCRSGE 9
|||||
Db 17 HEGCCKGE 24

RESULT 32
HB5967
Hypothetical protein yqjI [imported] - Escherichia coli (strain O157:H7, substrain EDL93
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: HB5967
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: HB5967
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-207 <STO>
A:Cross-references: GB:AE005174; NID:g12517652; PIDN:AGS8204.1; GSPDB:GN00145; UWGP:244
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: yqjI

Query Match 50.7%; Score 36; DB 2; Length 207;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 HEGCRSGE 9
|||||
Db 17 HEGCCKGE 24

RESULT 33
HB2986
Hypothetical protein PA5273 [imported] - Pseudomonas aeruginosa (strain PAO1)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: HB2986
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bu
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: HB2986
A:Status: preliminary
A:Molecule type: DNA

```

```

A:Residues: 1-237 <STO>
A:Cross-references: GB:AE004940; GB:AE004091; NID:g9951584; PIDN:AAG08658.1; GSPDB:GN001
A:Experimental source: strain PAO1
C:Genetics:
A:Gene: PA5273

Query Match 50.7%; Score 36; DB 2; Length 237;
Best Local Similarity 61.5%; Pred. No. 1.2e+02;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 SHEGCRSGEAGS 13
|||||
Db 187 SHIGCSGCASDS 199

RESULT 34
AC1685
dihydrodipicolinate reductase homolog dapB [imported] - Listeria innocua (strain Clip112
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C:Accession: AC1685
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkut, G.; Madueno, E.; Maitournam, A.; Ma
OK, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AC1685
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-263 <GLA>
A:Cross-references: GB:AL592022; PIDN:CAC97251.1; PID:g16414522; GSPDB:GN00178
A:Experimental source: strain Clip11262
C:Genetics:
A:Gene: dapB
C:Superfamily: dihydrodipicolinate reductase

Query Match 50.7%; Score 36; DB 2; Length 263;
Best Local Similarity 70.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 EGCRCSEAGG 12
|||||
Db 190 EGARGGEYEG 199

RESULT 35
AB2037
Hypothetical protein all1848 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C:Accession: AB2037
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriqichu
Nakazaki, N.; Shimpou, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AB2037
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-276 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA873547.1; PID:g17130938; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all1848

Query Match 50.7%; Score 36; DB 2; Length 276;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```



QY 2 HEGCRSGE 9  
| | | | |  
DB 108 HAGCSSGE 115

## RESULT 36

AE3415  
integrase [imported] - Brucella melitensis (strain 16M)  
C:Species: Brucella melitensis  
C>Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 01-Feb-2002  
C:Accession: AE3415  
R:DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,  
.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess  
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis  
A:Reference number: AD3252; PMID:11756688  
A:Accession: AE3415  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-308 <KOR>  
A:Cross-references: GB:AE008917; PIDN:AAL52488.1; PID:gl17983297; GSPDB:GN00190  
A:Experimental source: strain 16M  
C:Genetics:  
A:Gene: BME11307  
A:Map position: 1

Query Match 50.7%; Score 36; DB 2; Length 308;  
Best Local Similarity 77.8%; Pred. No. 1.4e+02;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCRSGEAG 12  
| | | | |  
DB 172 GCRSGEAG 180

## RESULT 37

E91246  
probable L-sorbose 1-phosphate dehydrogenase [imported] - Escherichia coli (strain O157:  
C:Species: Escherichia coli  
C>Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 18-Jul-2001  
C:Accession: E91246  
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
Gawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.  
DNA Res. 8, 11-22, 2001  
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene  
A:Reference number: A99629; PMID:21156231; PMID:11258796  
A:Accession: E91246  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-409 <HAY>  
A:Cross-references: GB:BA000007; PIDN:BA038364.1; PID:gl13364417; GSPDB:GN00154  
A:Experimental source: strain O157:H7, substrain RMD 0509952  
C:Genetics:  
A:Gene: ECs4941

Query Match 50.7%; Score 36; DB 2; Length 409;  
Best Local Similarity 70.0%; Pred. No. 1.8e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 HEGCRSGEAE 11  
| | | | |  
DB 387 HQGIWSGEAE 396

## RESULT 38

B86094  
probable L-sorbose-1-P-reductase Z5613 [imported] - Escherichia coli (strain O157:H7, su  
C:Species: Escherichia coli  
C>Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001  
C:Accession: B86094  
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,  
Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A:Reference number: A85480; MUID:21074935; PMID:11206551  
A:Accession: B86094  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-413 <STO>  
A:Cross-references: GB:AE005174; NID:gl12518955; PIDN:AAG59214.1; GSPDB:GN00145; UWGP:Z5  
A:Experimental source: strain O157:H7, substrain EDL933  
C:Genetics:  
A:Gene: Z5613

Query Match 50.7%; Score 36; DB 2; Length 413;  
Best Local Similarity 70.0%; Pred. No. 1.8e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 HEGCRSGEAE 11  
| | | | |  
DB 391 HQGIWSGEAE 400

## RESULT 39

C82825  
UDP-N-acetylmuramate-L-alanine ligase XF0276 [imported] - Xylella fastidiosa (strain 9a  
C:Species: Xylella fastidiosa  
C>Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 17-Nov-2000  
C:Accession: C82825  
R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen  
Nature 406, 151-157, 2000  
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
A:Reference number: A82515; MUID:20365717; PMID:10910347  
A:Note: for a complete list of authors see reference number A59328 below  
A:Accession: C82825  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-471 <SIM>  
A:Cross-references: GB:AE003881; GB:AE003849; NID:99105093; PIDN:AAF83089.1; GSPDB:GN001  
A:Experimental source: strain 9a5c  
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; I  
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carreir  
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.  
submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Froh  
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuranae, E.E.; Laig  
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins,  
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.  
., P.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.  
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawaes  
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir  
M.; Teuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.;

C:Superfamily: UDP-N-acetylmuramate-alanine ligase

Query Match 50.7%; Score 36; DB 2; Length 471;  
Best Local Similarity 50.0%; Pred. No. 2e+02;  
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 HEGCRSGEAE 13  
| | | | |  
DB 285 HEGCEVGQVRWS 296

## RESULT 40

T23689  
hypothetical protein M03C11.4 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: T23689  
R:McMurray, A.  
submitted to the EMBL Data Library, April 1995  
A:Reference number: Z19783



Query Match 50.7%; Score 36; DB 2; Length 708;  
 Best Local Similarity 58.3%; Pred. No. 2.9e+02;  
 Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 SHEGCRSGAEG 12  
 |||||  
 Db 560 SEEGCRGDAIG 571

RESULT 45  
 T13956  
 timeless protein homolog mTm1 - mouse  
 C:Species: Mus musculus (house mouse)  
 C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 21-Jul-2000  
 C:Accession: T13956  
 R:Koike, N.; Hida, A.; Numano, R.; Hirose, M.; Sakaki, Y.; Tei, H.  
 PDBS Lett. 441: 427-431, 1998  
 A:Title: Identification of the mammalian homologues of the Drosophila timeless gene, Tim  
 A:Reference number: Z17832; MUID:99107002; PMID:9891984  
 A:Accession: T13956  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-1197 <KOI>  
 A:Cross-references: EMBL:AB015598; NID:g4115715; PIDN:BAA36500.1; PID:g4115716  
 A:Experimental source: strain BALB/c  
 C:Genetics:  
 A:Gene: mTm1

Query Match 50.7%; Score 36; DB 2; Length 1197;  
 Best Local Similarity 53.8%; Pred. No. 4.4e+02;  
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 SHEGCRSGAEGS 13  
 |||||  
 Db 983 SEEGLPSCGGQS 995

RESULT 46  
 T19422  
 hypothetical protein C24F3.5 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 29-Oct-1999  
 C:Accession: T19422; T23313; T24960  
 R:McMurray, A.  
 submitted to the EMBL Data Library, April 1998  
 A:Reference number: Z19122  
 A:Accession: T19422  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-1429 <WIL>  
 A:Cross-references: EMBL:AL022716; PIDN:CAA18775.1; GSPDB:GN000022; CESP:C24F3.5  
 A:Experimental source: clone C24F3  
 R:Wild, A.  
 submitted to the EMBL Data Library, February 1996  
 A:Reference number: Z19725  
 A:Accession: T23313  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-1429 <WIL>  
 A:Cross-references: EMBL:Z69664; PIDN:CAA93518.1; GSPDB:GN000022; CESP:C24F3.5  
 A:Experimental source: clone K04D7  
 R:Ainscough, R.  
 submitted to the EMBL Data Library, January 1998  
 A:Reference number: Z19961  
 A:Accession: T24960  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-1429 <WIL>  
 A:Cross-references: EMBL:AL021570; PIDN:CAA16510.1; GSPDB:GN000022; CESP:C24F3.5  
 A:Experimental source: clone T17B5  
 C:Genetics:  
 A:Gene: CESP:C24F3.5

A:Map position: 4  
 A:Introns: 23/3; 57/2; 120/3; 150/3; 189/3; 230/1; 235/1; 466/2; 544/2; 583/2; 642/2; 6;  
 Query Match 50.7%; Score 36; DB 2; Length 1429;  
 Best Local Similarity 75.0%; Pred. No. 5.2e+02;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 HEGCRSGE 9  
 |||||  
 Db 407 HHGCGSGE 414

RESULT 47  
 S59313  
 hypothetical protein YLR125W - yeast (Saccharomyces cerevisiae)  
 N:Alternate names: hypothetical protein L3101  
 C:Species: Saccharomyces cerevisiae  
 C>Date: 29-Nov-1995 #sequence\_revision 23-Feb-1996 #text\_change 19-Apr-2002  
 C:Accession: S59313; S64962; S64967; S69412  
 R:Delius, H.  
 submitted to the EMBL Data Library, June 1995  
 A:Description: 36.8 kb of S.cerevisiae chromosome XII including ACE2, CKI1, PDC5, SLS1,  
 A:Reference number: S59313  
 A:Accession: S59313  
 A:Molecule type: DNA  
 A:Residues: 1-136 <DEL>  
 A:Cross-references: EMBL:X91258; NID:g995686; PIDN:CAA62636.1; PID:g995687  
 A:Experimental source: strain S288C  
 R:Verhasselt, P.; Voet, M.; Volckaert, G.  
 submitted to the Protein Sequence Database, May 1996  
 A:Reference number: S64943  
 A:Accession: S64962  
 A:Molecule type: DNA  
 A:Residues: 1-136 <VER>  
 A:Cross-references: EMBL:Z73297; NID:gl360530; PIDN:CAA97694.1; PID:e245565; PID:gl360530  
 A:Experimental source: strain S288C  
 R:Delius, H.; Hebling, U.  
 submitted to the Protein Sequence Database, May 1996  
 A:Reference number: S64967  
 A:Accession: S64967  
 A:Molecule type: DNA  
 A:Residues: 1-136 <DEW>  
 A:Cross-references: EMBL:Z73297; NID:gl360530; PIDN:CAA97694.1; PID:e245565; PID:gl360530  
 A:Experimental source: strain S288C  
 R:Verhasselt, P.; Volckaert, G.  
 submitted to the EMBL Data Library, September 1995  
 A:Reference number: S69393  
 A:Accession: S69412  
 A:Molecule type: DNA  
 A:Residues: 1-136 <VEW>  
 A:Cross-references: EMBL:X89514; NID:gl297019; PIDN:CAA61703.1; PID:e198754; PID:gl297019  
 C:Genetics:  
 A:Cross-references: SGD:S0004115  
 A:Map position: 12R

Query Match 50.0%; Score 35.5; DB 2; Length 136;  
 Best Local Similarity 64.3%; Pred. No. 88;  
 Matches 9; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 SHEGC-RSGEAGS 13  
 |||||  
 Db 61 SEEGCGSSGEXENS 74

RESULT 48  
 S18957  
 fix23-5 protein - Rhizobium meliloti  
 C:Species: Rhizobium meliloti  
 C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 08-Oct-1999  
 C:Accession: S18957  
 R:Petrovics, G.; Putnoky, P.; Kondorosi, A.  
 submitted to the EMBL Data Library, January 1992  
 A:Description: A fatty acid synthase like gene cluster of Rhizobium meliloti is involved

Db 19 EGCPDQAE 27

Search completed: April 19, 2004, 17:23:19  
Job time : 14 secs

A;Reference number: S18953  
A;Accession: S18957  
A;Status: Preliminary  
A;Molecule type: DNA  
A;Residues: 1-284 <PET>  
A;Cross-references: EMBL:X64131; NID:g1235585; PIDN:CAA45487.1; PID:g46275  
C;Superfamily: short-chain alcohol dehydrogenase homology  
F;36-216/Domain: short-chain alcohol dehydrogenase homology <SADH>

Query Match 50.0%; Score 35.5; DB 2; Length 284;  
Best Local Similarity 58.3%; Pred. No. 1.6e+02;  
Matches 7; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 2 HEGCRS-GEAEG 12  
DB 97 HHCGRGRGDASG 108

RESULT 49  
TKMYT  
tuberculin-active protein - Mycobacterium tuberculosis (strain Aoyama/B)  
C;Species: Mycobacterium tuberculosis  
C;Date: 22-Jun-1981 #sequence\_revision 22-Jun-1981 #text\_change 21-Nov-1998  
C;Accession: A03444  
R;Kuwabara, S.  
J; Biol. Chem. 250, 2563-2568, 1975  
A;Title: Amino acid sequence of tuberculin-active protein from Mycobacterium tuberculosis  
A;Reference number: A03444; MUID:75133468; PMID:804477  
A;Accession: A03444  
A;Molecule type: protein  
A;Residues: 1-89 <KUM>  
A;Experimental source: human type Aoyama/B strain  
C;Comment: Tuberculin is the soluble protein produced by the bacterium to which infected  
C;Comment: This protein is the most potent component with tuberculin activity so far pur  
C;Superfamily: tuberculin-active protein  
F;27-59/Disulfide bonds: #status experimental

Query Match 49.3%; Score 35; DB 1; Length 89;  
Best Local Similarity 61.5%; Pred. No. 75;  
Matches 8; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 2 HEGCRSG--EAEG 12  
DB 56 HEICRDGSGSEEG 68

RESULT 50  
D83375  
hypothetical protein PA2161 [imported] - Pseudomonas aeruginosa (strain PA01)  
C;Species: Pseudomonas aeruginosa  
C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C;Accession: D83375  
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,  
.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho  
A;Reference number: A82950; MUID:20437337; PMID:10984043  
A;Accession: D83375  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-101 <STO>  
A;Cross-references: GB:AE004643; GB:AE004091; NID:g9948178; PIDN:AG05549.1; GSPDB:GN001  
A;Experimental source: strain PA01  
C;Genetics:  
A;Gene: PA2161

Query Match 49.3%; Score 35; DB 2; Length 101;  
Best Local Similarity 66.7%; Pred. No. 83;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGCRSGEAE 11  
||| |